

The Genetic Basis for Evolution

No two individuals are alike. Not even identical twins. Somewhere in their DNA their base pairs are different. This difference in base pairs between individuals can lead to different expression of genotypes. It's this genetic variation in species that drives the process of evolution. Another way of looking at evolution is the change which occurs in gene frequencies. What brings about those changes in DNA, and thus gene frequencies, are the driving factors of evolution. Potential for evolutionary change depends upon variations within a population's gene pool.

Variation within species can be either continuous or discrete (sometimes called discontinuous). Continuous variations are simply very small differences between individuals, many not even noticeable. Discrete variations provide clear-cut differences between individuals. These variations are genetically inherited.

An example of continuous variation in humans is height. You have a full range of heights in humans from the very short to the exceptionally tall and every gradation in between. Other examples of continuous variation are weight, length of hand span, length of feet, and even the amount of milk produced by nursing mothers. Much of this variation is due to genetics and the differences in DNA; however, environment also plays a part. For example, the amount of milk produced may also be tied to diet and nutrition. A person's height may be stunted with poor nutrition or lack of vitamins.

An example of discrete or discontinuous variation is the blood types of humans. Humans are either one blood type or another - there is no gradation of blood type - you can't be a little bit AB.

A Look At Continuous Variation

Dr. John Manning at the University of Liverpool reported the ratio of the length of the index finger and the ring finger on human hands provides insight as to athletic ability (University of Liverpool 2002). According to Manning, the shorter the index finger compared to the ring finger *on the left hand*, the greater the likelihood the male is to become a football (soccer) star. Additionally, running speed can be predicted by comparison with the *right hand*.

The basis for these conclusions is the influence of testosterone in males. Manning reports (University of Liverpool 1999) fetal testosterone has a role not only in the development of the male genital system but also in finger length, thumb length and the central nervous system. Individuals with high levels of fetal testosterone have long ring fingers compared to their index finger. In the same study, Manning shows a positive correlation between the length of a man's fingers relative to his height. The longer the fingers are in relation to the height, the greater the chance of depression in that male. The same study also indicates that men with relatively long ring fingers have high fertility and women with relatively short ring fingers have high fertility.

On the other hand, women's index and ring finger length are almost equal since they are exposed to less testosterone as a fetus. Those women with greater exposure to testosterone have longer ring fingers (BBC n.d.).

You perhaps remember from first semester biology that index finger and ring finger length is a sex-influenced trait. In males, the dominant trait is for the index finger to be shorter than the ring finger. In females, it's reversed. The dominant trait in females is for the index finger to be equal to or longer than the ring finger.

Exercise A: Index-Ring Finger Ratio

In this exercise, you will carefully measure the length of the index and ring finger on both hands and calculate the ratio between the two lengths for each hand and separate your data according to gender. The key is to be consistent with your measurements. Each student will be assigned a number to insure accurate accumulation of data.

figure 1. Measure the length of index and ring finger according to photograph.



Procedure

1. With the ruler provided, measure, in millimeters the length of your index finger (palm side) on your right hand from the base of the index finger to the tip of the index finger (see figure 1.)
2. Repeat the measurement for your ring finger.
3. Record your data in the spreadsheet provided. Use red fonts for females and blue fonts for males. The spreadsheet will calculate your index finger/ring finger ratio.
4. Construct a bar graph showing ranges of ratios and the number of students within those ranges.

Exercise B: Total Lung Capacity

One of Manning’s findings was a strong correlation of the length of the ring finger relative to the index finger on the *left* hand for runners. One characteristic long distance runners *may* have is good lung capacity. The average human’s lungs hold about 6 liters of air but volumes can vary with height and age. Total lung capacity depends on person’s age, height, sex, weight and degree of physical activity. Females tend to have 20-25% lower capacity than males. Tall people tend to have more lung capacity than shorter people and heavy smokers have less lung capacity. Additionally, altitude affects lung capacity. Let’s see if there is a correlation between total lung capacity and index finger/ring finger length ratio on the *left hand*.

First, we need a few definitions. The chart provided defines various terms and provides average values for healthy adults.

TERM	ABBREVAITION	DEFINITION	AVERAGE VALUES FOR HEALTHY ADULT
Tidal volume	TV	Amount of air moved into lungs during inhalation or out of lungs during exhalation	500ml
Inspiratory Reserve Volume	IRV	Maximum amount of air which can be inhaled after a normal inhalation	3100 ml
Expiratory Reserve Volume	ERV	Maximum amount of air which can be exhaled after a normal exhalation	1200 ml
Residual Volume	RV	Amount of air which remains in the lungs after a maximum exhalation	1200 ml
Inspiratory Capacity	IC	$IC = TV + IRV$	3600 ml
Functional Residual Capacity	FRC	$FRC = RV + ERV$	2400 ml
Vital Capacity	VC	$VC = IRV + TV + ERV$	4800 ml
Total Lung Capacity	TLC	$TLC = IRV + TV + ERV + RV$	6000 ml

We will use either a device called a wet spirometer or a dry spirometer to measure lung volumes and from that calculate capacities. Use the same student number from the previous exercise.

Procedure

1. Attach a disposable mouthpiece to the hose of the wet or dry spirometer. **When finished with this experiment, dispose of the mouthpiece in the biohazard bag!**
2. If using a wet spirometer, position the pointer on the zero line of the scale nearest the right end of the scale arm by adjusting the pointer guide which must be to the right of the pointer. If using a dry spirometer, rotate the spirometer dial until the pointer is aligned with zero.

Vital Capacity (VC)

3. Position yourself as straight as possible in your chair. You will need to make sure no air escapes through your nostrils, so either pinch your nostrils together with one hand or use the nose clips provided.
4. Inhale as deeply as possible. Exhale through the mouthpiece into the wet spirometer. **Caution! Make sure no air escapes from the nostrils or from around your mouth on the disposable mouthpiece. Never inhale with the mouthpiece.**
5. Read the value on the spirometer gauge to the nearest 100 cc. Record your data in the data table provided.
6. Repeat this 3 times and use the largest volume of gas exhaled as your measurement. Record your data.

Tidal Volume (TV)

You should rest approximately five minutes before attempting this exercise after doing Vital Capacity. Allow other students in your group to do Vital Capacity while you are waiting to do Tidal Volume.

7. Adjust the pointer to zero as before on the far right of the scale.
8. Again, pinch the nose or use nose clamps.
9. Breathe normally with the mouthpiece in your mouth but let air escape through the sides of your mouth. Establish a regular pattern of breathing while doing this.
10. Exhale 5 successive times (without inhaling between) into the mouthpiece while preventing any escape around the lips. You will need to use some force for the first exhalation to get the pointer to move the first time.
11. Record the total volume of the five successive breaths and divide by five to get the Tidal Volume. Record your data.

Expiratory Reserve Volume (ERV)

This process is similar to the one for Tidal Volume (TV) in that you establish the normal breathing pattern as indicated above. However, in this one you do 1 forceful exhalation.

12. Adjust the pointer to zero as before on the far right of the scale.
13. Again, pinch the nose or use nose clamps.
14. Breathe normally with the mouthpiece in your mouth but let air escape through the sides of your mouth. Establish a regular pattern of breathing while doing this.
15. Exhale as forcefully as possible as much air as possible (making sure to prevent any leaking around the mouthpiece).
16. Record the volume to the nearest 100 cc.
17. Repeat twice more and calculate the average of the three totals. Record this data.

Inspiratory Reserve Volume (IRV)

This can be calculated using the formula $IRV = VC - (TV + ERV)$.

Inspiratory Capacity (IC)

This can be calculated using the formula $IC = VC - ERV$.

Residual Volume (RV)

This is not measurable with our instruments. Assume 1200 cc for males and 900 cc for females.

Total Lung Capacity (TLC)

This is calculated from the formula $TLC = VC + RV$.

Data table 1. Vital Capacity.

	Trial 1	Trial 2	Trial 3	VC Highest Value
Vital Capacity (VC)				

Data table 2. Tidal Volume.

	Total for 5 Breaths	Average
Tidal Volume (TC)		

Data table 3. Expiratory Reserve Volume.

	Trial 1	Trial 2	Trial 3	Average
Expiratory Reserve Volume (ERV)				

Data table 4. Calculation of Total Lung Capacity (TLC).

Inspiratory Reserve Volume $IRV = VC - (TV + ERV)$	
Inspiratory Capacity $IC = VC - ERV$	
Residual Volume	Assume 1200 cc males Assume 900 cc females
Total Lung Capacity $TLC = VC + RV$	

Questions

1. What is the class average index finger/ring finger ratio for males? _____
2. What is the class average index finger/ring finger ratio for females? _____
3. For which gender is the range of ratios the greatest? _____
4. What is the penetrance for the dominant trait in males? _____
5. What is the penetrance for the dominant trait in females? _____
6. What is the class average total lung capacity for females? _____
7. What is the class average total lung capacity for males? _____
8. Do you see any correlation between index finger/ring finger ratio and total lung capacity?

9. Regardless of what your data indicated in question 8, assume there was a positive correlation between index/ring finger ratio and total lung capacity. Explain how natural selection could play a role in this. _____

Hardy-Weinberg Equilibrium and the Hardy Weinberg Equation

At the beginning of this lab, we described evolution as the change in gene (and thus allele) frequencies. Remember when you covered genetics last semester, humans have 23 chromosomes and 23 homologs. A specific points on a chromosome (locus) you may find a unit of heredity - the gene. On the homolog, at the same locus, is the allele of that gene.

Assume we have a population where a particular genetic trait is represented by two alleles, A and a. Further assume our population is 100% heterozygous for the condition, in other words, Aa. We then know the allelic frequency for the gene A is 0.5 (because half the alleles in the total population is "A"). It's important to distinguish what is meant by genotypic frequency and allelic frequency. If I tell you a population was sampled and it was determined 25% exhibited the genotype AA, 60% exhibited Aa genotype and 15% exhibited aa genotype, I am expressing genotypic frequencies. However, allelic frequencies are based on the percentage of the "A" allele in the population as opposed to the "a" allele.

Let's consider another population. Suppose the breakdown in our population is as follows: 20% is AA, 50% is Aa and 30% is aa. Let's calculate the allelic frequency of "A".

Since 20% (0.20) is AA and 100% (1.0) of the alleles are A, then the frequency of the A allele in this group is $(0.20)(1.0) = .20$.

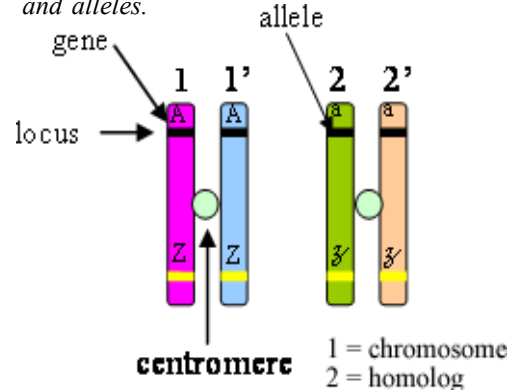
Fifty percent (0.50) is Aa but only 1/2 the genotype is "A" or (0.5) so the frequency of the A allele in this group is $(0.50)(0.5) = 0.25$.

Next, 30% are aa, so that means there are no "A" alleles in this group. The frequency of allele A in this group is $(0.30)(0.0) = 0$.

The allelic frequency of "A" in this population is therefore $.20 + .25 + 0$ or 0.45.

From this, you can conclude that the frequency of the recessive allele "a" is $1.0 - 0.45$ which is

figure 2. chromosomes, homologs, genes and alleles.



0.55.

Mathematically we say if there are only two alleles at a locus with one dominant (A) and one recessive (a), then p = the frequency of the dominant allele and q = the frequency of the recessive allele and $p + q = 1$.

Hardy and Weinberg

Godfrey Harold Hardy (1887-1947), a British mathematician who played cricket with the English geneticist Reginal Punnett of Punnett square fame, became intrigued by a population genetics problem presented by Punnett. In 1908, Hardy independently came up with a mathematical application to deal with the problem (Wikipedia 2006). In the same year, Wilhelm Weinberg (1862-1937), a German physician, independent of Hardy, formulated the same principle today known as the Hardy-Weinberg Equilibrium, Hardy-Weinberg Principle, or Hardy-Weinberg Law (Wikipedia 2006b).

The Hardy-Weinberg Principle assumes no evolution is taking place in a population. This is important because in real life scenarios, evolution is always occurring. Otherwise, we would need chaos theory to describe what happens in populations. For the Hardy-Weinberg Principle to be applied we must make several assumptions:

1. No mutation of alleles takes place.
2. Random mating must occur. This means no one genotype has a particular advantage and every genotype is equally likely to mate with any other genotype in the population.
3. We are dealing with a large population so statistically our data is sound.
4. Immigration (species coming into the population) and emigration (species leaving the population) does not occur.
5. Natural selection is the rule. There is no selection for one genotype or another. All species have an equal chance of surviving and reproducing.

As you can see, the strictures are such the conditions of Hardy-Weinberg will almost never be met in real life. But let's assume the conditions can be met. That would mean the population in question is in Hardy-Weinberg equilibrium. A population in Hardy-Weinberg equilibrium (1) does not evolve because the allelic frequencies never change and (2) since the allelic frequencies never change, we can predict from that the genotypic frequencies.

If a population is at Hardy-Weinberg equilibrium where $p = A$ and $q = a$, then $AA = p^2$, $Aa = 2pq$, and $aa = q^2$. For example, let's say the allelic frequency of $p = 0.3$. From the equation $p + q = 1$, then q must equal 0.7. What is the genotypic frequency? $p^2 = 0.09$, $2pq = 2(0.3)(0.7)$ or 0.42, and $q^2 = .49$.

Since the only possible genotypes are AA, Aa, and aa, we can deduce the Hardy-Weinberg equation:

$$p^2 + 2pq + q^2 = 1.$$

The practical use of the Hardy-Weinberg equation is if we know the genotypic frequencies in a population (because we actually sampled it), these *observed* frequencies can be compared to the *expected* genotypic frequencies to determine if the population is at Hardy-Weinberg equilibrium. We can use chi square analysis to determine if any difference between the observed and expected is significant.

As you might guess, there are some things you can do with the Hardy-Weinberg equation and some things you cannot do.

1. If you know *all* the *genotypic* frequencies, you can calculate the allelic frequencies with the Hardy-Weinberg equation *regardless* of whether you assume Hardy-Weinberg equilibrium is met or

not.

2. It doesn't work the other way around. You can calculate genotypic frequencies from allelic frequencies only if you assume Hardy-Weinberg equilibrium.

3. If you know the fraction of homozygous recessives in a population, you can estimate the genotypic and allelic frequencies only if you assume Hardy-Weinberg equilibrium.

Exercise C: The Ability to Taste PTC

In 1931, a Dupont chemist by the name of Arthur Fox discovered an unusual effect with PTC (phenothiocarbamide) a synthetic chemical. Some of the chemical was accidentally released in the lab and another chemist working some distance away noted a very bitter taste in his mouth although Fox was closer and did not notice the taste (Wikipedia 2006). It has since been discovered that the ability to taste PTC is a simple, dominant trait and about 70% of the population as a whole are classified as "tasters." However, the ability to taste is different within specific groups. Approximately 58% of the aboriginal population of Australia and New Zealand are tasters and 98% of Native Americans are tasters (Wikipedia 2006). Helms and others (1994) state that 55% of the North American population are tasters.

Procedure

1. Obtain a strip of PTC paper (provided at your lab desk) and place on your tongue. Tasters will detect either an extremely bitter taste or a few of you may detect salty, sweet, or sour. Nontasters simply sense wet, soggy paper.
2. Your instructor will count the entire lab for tasters and nontasters by a show of hands.
3. Calculate the decimal number of tasters in lab by dividing by the total number of lab students present. _____ Do the same for nontasters. _____ Fill in the data table.
4. Calculate the allelic frequencies p and q from the data and using the Hardy-Weinberg equation.

5. Calculate chi square for the observed *versus* the expected results.

Data table 5: PTC tasters vs nontasters.

Population	Tasters ($p^2 + 2pq$)	Nontasters (q^2)	p	q
Lab Population				
North American Population	0.55			

Questions

1. Explain why tasters included the p^2 and $2pq$ variables but not q^2 . _____

2. Explain your chi square goodness of fit results. _____

Genetic Drift and the Founder Effect

Charles Darwin's study of the finches on the Galapagos let him to suppose the thirteen species of finches on the island evolved from a single species. The question was how 13 evolved from 1 and not even Darwin was able to answer that question. Ernst Walter Mayer (1904-2005) redefined the concept of species as individuals that can breed *only* among themselves and not with other species. If these species become isolated (as well they may on an island) subpopulations of these species may begin to differ in their allelic frequencies over time - the concept of genetic drift (Wikipedia 14 Jul 2006). Coupled with natural selection, genetic drift can allow for the evolution of new species from the initial species. When dealing with small populations the effect of genetic drift can be enhanced. The new species which evolved due to small populations is called the founder effect. A founder population is simply a small segment from a larger population which splinters off. Because of the small size of the splinter group, the gene pool may differ significantly from the parent population. Just think of how a small sample size can skew statistical results.

Exercise D: Simulation of the Founder Effect

In this exercise, you will simulate the founder effect by using different colored beans. There are two colors of beans and your instructor will tell you which color represents the recessive trait. You will be told of the actual number of each color. You will then calculate the frequency of each color of bean which represents p and q , the parent generation. Write the values for p and q in the space provided.

$$p = \underline{\hspace{2cm}} \quad q = \underline{\hspace{2cm}}$$

Procedure

1. To simulate the founder effect, you will now disperse the population randomly among 10 subpopulations (plastic cups) by randomly choosing 10 beans from the parent population and distributing them 1 of the 10 cups. An easy way to do the choosing randomly is to have one student draw out the beans without looking and shaking the parent container between each draw. Place 10 randomly chosen beans in each of 10 cups. Remember, the beans represent alleles, so each cup should have 5 individuals of 2 alleles each.
2. Count the number of rare (recessive) alleles in each cup and record your data in data table 6. Record the number of zero rare alleles also in data table 7.
3. Calculate the percentage of populations represented by the cups containing rare alleles. This percentage may be obtained by dividing the total number of cups in each column by the total number of cups in the class.

Questions

1. How many cups (populations) does your table have with zero rare alleles in the cup? _____
2. How many cups (populations) does your lab class have with zero rare alleles? _____
3. What is the percentage of all populations (lab class) is the rare allele missing? _____
4. Do you have any populations in the lab class with a higher proportion of rare alleles than the parental population? _____
5. What is the percentage where the parental population and the founder population are the same frequencies? _____
6. From your data, what conclusions can you make about allelic frequencies in founder populations? _____

Data Table 6: Bottleneck Effect - Rare Alleles.

Table 1	0 rare alleles	1 rare allele	2 rare alleles	3 rare alleles	4 rare alleles	5 rare alleles	6 rare alleles	7 rare alleles	8 rare alleles	9 rare alleles	10 rare alleles
Table 2											
Table 3											
Table 4											
Table 5											
Table 6											
Total Number of Cups with Specified Number of Rare Alleles.											
Percent of All Populations with Specified Number of Rare Alleles											

Procedure Continued

4. Now that you have established your founder populations, you will increase the size of the founder population to 10 individuals (each cup initially represents 5 individuals). To do so, randomly pair your 10 cups into groups of 5. **Caution! Don't mix the contents of the cups.**

5. Report the percentage of populations of 10 individuals that have zero rare alleles in data table seven.

Data table 7: Founder populations with zero rare alleles.

Number of Founder Populations with 0 Rare Alleles of	5 individuals	10 individuals	25 individuals
Table 1			
Table 2			
Table 3			
Table 4			
Table 5			
Table 6			
Total No. of Cups or Groups of Cups with Zero Rare Alleles			
Percent of All Populations with Zero Rare Alleles			

- Group your 10 cups into two founder populations containing 25 individuals each by pairing your cups as two sets of 5 cups.
- Record your number of zero rare alleles in data table 7.

Questions Continued

- Look at the percentages of zero rare alleles for 5, 10 and 25 individuals. How does your data relate to the size of your populations? _____
- How closely do any of the founder populations (5, 10, and 25 individuals) resemble the parent population? _____

Exercise E: Bottleneck Effect

You can think of this as bad luck, not bad genes. The bottleneck effect is when a population undergoes a severe reduction in the size as a result of bad luck, *e.g.* a tsunami, volcanic eruption, meteor event, etc. The term is derived from the idea of all the alleles in a population trying to pour out of a bottle and only a few make it through the neck. Those that make it through the neck of the bottle represent the survivors of the population.

Procedure

- Start with a population of 50 individuals with an allele frequency of 0.5 for each allele. Your instructor will tell you which color bean represents which allele. For 50 individuals, you should have 100 beans: 50 one color and 50 another.
- Randomly* select 10% of the population, 2 alleles at a time. Assume the other 90% of the population is wiped out by a meteorite. On data table 8 record the genotypes and the number of “A” and “a” alleles for this surviving population.
- Determine the numbers of each genotype and the numbers of each allele for your surviving population. From these data calculate the genotypic frequencies for AA, Aa, and aa and the allelic frequencies for these survivors. Record your data in data table 8 as observed values.
- From the observed values, calculate the expected values for p^2 , $2pq$, and q^2 and record them in data table 8.
- Re-establish the population to 50 individuals using the new allelic frequencies. As an example, let’s assume you have the following allelic frequencies in the survivor population.

$$A = 0.2$$

$$B = 0.8$$

You will need 100 beans and 20% need to be the color designated for A and 80% need to be the color designated for a.

- Repeat steps 2 through 4 and record your data in generation 2.
- Repeat the entire process again until you have accounted for 5 generations.
- Plot your results on a graph with the dependent variable on the x axis and the independent variable on the y axis. You should have two lines: one for “A” and one for “a”.

Questions

- Fixation occurs when the gene pool is composed of only one allele. Did you observe fixation in any of the generations? _____
- Explain the significance of bottleneck effect on your population. _____

Data table 8: Bottleneck Effect.

Generation	Observed AA	Observed Aa	Observed aa	Observed A (p)	Observed a (q)	Expected p^2	Expected $2pq$	Expected q^2
0	-	-	-	0.5	0.5	0.25	0.50	0.25
1								
2								
3								
4								
5								

Exercise F: Natural Selection and Lethal Genes

As stated previously, the conditions for Hardy-Weinberg equilibrium are almost never met. As a consequence, gene frequencies do change and evolution does take place. The Hardy-Weinberg equation allows us to measure changes in gene frequencies which do occur and theorize as to which of the five criteria for Hardy-Weinberg has been altered. Of these five criteria, natural selection is the most important. Natural selection may be defined as the process where individual organisms with favorable traits are more likely to survive, reproduce, and pass on those favorable genetic traits to their offspring. The definition is based on the phenotype.

Key to understanding natural selection is the idea of fitness. Natural selection acts on individual phenotypes, but its *average* effect on all individuals of a particular genotype is the fitness for that genotype. Fitness (W) can be measured as the proportion of progeny which survives, multiplied by the average fecundity (or the ability to reproduce), and is equivalent to the reproductive success of a genotype. If W is greater than one, it indicates the frequency of that genotype in the population increases, while a value of less than one indicates a decrease. When you compare the elimination of one genotype in a population to the elimination of a more successful genotype, you have a value called the selection coefficient (S). For example, say 0 is minimal elimination and 1.0 is maximum elimination. The larger the selection coefficient, the stronger natural selection will act against the genotype with the lowest fitness.

An extreme case of acting against the genotype is lethal homozygous recessive genes. Since selection against the genotype is 100% (1.0), the frequency of the recessive allele will drop rapidly. In theory, homozygous recessive lethal alleles would extinguish themselves over time but there is often a benefit for the heterozygous condition. Sickle cell anemia is an example. If you are a carrier for sickle cell (Ss) you don't get malaria - the largest killer of humans on the planet earth. Because you are artificially selected for protection from malaria, the recessive allele is maintained in the population.

In this exercise, we will simulate natural selection against the recessive genotype. You can relate this to the once lethal condition of sickle cell disease or to the lethality of cystic fibrosis in humans (Eberhard 1996).

Procedure

1. You will begin with a population of 50 individuals (100 alleles or beans). Your initial gene pool will have 75 dominant alleles and 25 recessive alleles. Your instructor will inform you as to which color is dominant and which is recessive.
2. Shake up the beans to simulate random mixing of gametes for the F1 generation.

- Designate someone in the group to randomly pull out two beans (alleles). This represents your first individual.
- Repeat the process 49 more times and arrange your "individuals" as to homozygous dominant, heterozygous, and homozygous recessive.
- You will now select against the recessive alleles by removing *all* homozygous recessive individuals.
- Count the number of "A" and "a" alleles left in the population and calculate the percentage and frequency of each.
- Record your data in data table 9.

Data table 9: First Draw, Natural Selection.

Initial Pool	75 alleles "A" 75% .75 (p)	25 alleles "a" 25% .25 (q)	100 Total 100% 1.00 ($p + q$)
First Draw: Selection: Survivors:	____ AA (-) ____ AA ____ AA	____ Aa (-) ____ Aa ____ Aa	____ aa (-) ____ aa ____ aa
Selected Gene Pool:	____ alleles AA ____ % ____ (p)	____ alleles Aa ____ % ____ (q)	____ Total alleles 100% 1.00 ($p + q$)
Add in: Replenished gene pool with:	(+) ____ ____ alleles AA	(+) ____ ____ alleles Aa	(+) ____ total ____ alleles total

- Begin your second draw by replenishing your alleles (beans) to 100 again with the same percentages you just calculated in data table 9. For example, say you calculated AA to be 80%, then 80 of the beans should be the dominant color.
- Repeat steps 1 through 4 and fill in your data in data table 10.

Data table 10: Second Draw, Natural Selection.

Second Draw: Selection: Survivors:	____ AA (-) ____ AA ____ AA	____ Aa (-) ____ Aa ____ Aa	____ aa (-) ____ aa ____ aa
Selected Gene Pool:	____ alleles AA ____ % ____ (p)	____ alleles Aa ____ % ____ (q)	____ Total alleles 100% 1.00 ($p + q$)
Add in: Replenished gene pool with:	(+) ____ ____ alleles AA	(+) ____ ____ alleles Aa	(+) ____ total ____ alleles total

10. Begin your third draw by replenishing your alleles to 100 again with the same percentages just calculated in data table 10.

11. Repeat steps 1 through 4 and fill in data table 11.

Data table 11: Third Draw, Natural Selection.

Third Draw:	___ AA	___ Aa	___ aa
Selection:	(-) ___ AA	(-) ___ Aa	(-) ___ aa
Survivors:	___ AA	___ Aa	___ aa
Selected Gene Pool:	___ alleles AA ___ % ___ (<i>p</i>)	___ alleles Aa ___ % ___ (<i>q</i>)	___ Total alleles 100% 1.00 (<i>p</i> + <i>q</i>)
Add in: Replenished gene pool with:	(+) ___ ___ alleles AA	(+) ___ ___ alleles Aa	(+) ___ total ___ alleles total

12. Continue the exercise until you have 5 generations. Fill in the appropriate data tables twelve and thirteen.

13. Plot your data for the 5 generations on a graph with the dependent variable on the x axis and the independent variable on the y axis.

Data table 12: Fourth Draw, Natural Selection.

Fourth Draw:	___ AA	___ Aa	___ aa
Selection:	(-) ___ AA	(-) ___ Aa	(-) ___ aa
Survivors:	___ AA	___ Aa	___ aa
Selected Gene Pool:	___ alleles AA ___ % ___ (<i>p</i>)	___ alleles Aa ___ % ___ (<i>q</i>)	___ Total alleles 100% 1.00 (<i>p</i> + <i>q</i>)
Add in: Replenished gene pool with:	(+) ___ ___ alleles AA	(+) ___ ___ alleles Aa	(+) ___ total ___ alleles total

Data table 13: Fifth Draw, Natural Selection.

Fifth Draw:	___ AA	___ Aa	___ aa
Selection:	(-) ___ AA	(-) ___ Aa	(-) ___ aa
Survivors:	___ AA	___ Aa	___ aa
Selected Gene Pool:	___ alleles AA ___ % ___ (<i>p</i>)	___ alleles Aa ___ % ___ (<i>q</i>)	___ Total alleles 100% 1.00 (<i>p</i> + <i>q</i>)
Add in: Replenished gene pool with:	(+) ___ ___ alleles AA	(+) ___ ___ alleles Aa	(+) ___ total ___ alleles total

Questions

1. What observations did you make about the frequency of the recessive allele through 5 generations? _____

2. How might the recessive allele be preserved in spite of the tendency to eliminate itself? _____

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