Population Genetics and Evolution Lab/AP Biology   Name _______________________

Introduction: In 1908, G.H.Hardy and W. Weinberg independently suggested a scheme whereby evolution could be viewed as changes in frequency of alleles in a population of organisms. In this scheme, if **A** and **a** are alleles for a particular gene locus and each diploid individual has two such loci, then **p** can be designated as the frequency of the A allele and **q** as the frequency of the a allele. For example, in a population of 100 individuals (each with two loci) in which 40% of the alleles are A, **p** would be 0.40. The rest of the alleles would be (60%) would be a and **q** would be equal to 0.60. **p + q = 1** These are referred to as **allele frequencies**. The frequency of the possible diploid combinations of these alleles (AA, Aa, aa) is expressed as $p^2 + 2pq + q^2 = 1.0$. Hardy and Weinberg also argued that if 5 conditions are met, the population's alleles and genotype frequencies will remain constant from generation to generation. These conditions are as follows:

- **The breeding population is large.** (Reduces the problem of genetic drift.)
- **Mating is random.** (Individual show no preference for a particular mating type.)
- **There is no mutation of the alleles.**
- **No differential migration occurs.** (No immigration or emigration.)
- **There is no selection**. (All genotypes have an equal chance of surviving and reproducing.)

The Hardy-Weinberg equation describes an existing situation. Of what value is such a rule? It provides a yardstick by which changes in allelic frequencies can be measured. If a population's allelic frequencies change it is undergoing evolution.

Estimating Allele Frequencies for a Specific Trait within a Sample Population

Using the class as a sample population, the allele frequency of a gene controlling the ability to roll their tongue could be estimated. An ability to roll the tongue is evidence of the presence of a dominant allele in either a homozygous (TT) or heterozygous (Tt) condition. The inability to roll the tongue is dependent on the presence of the two recessive alleles (tt).

Procedure

1. Survey a number of individuals indicated by your teacher for tongue rolling which is a dominant trait and non-rolling which is a recessive trait.

2. A decimal number representing the frequency of rollers **(p^2+2pq)** should be calculated by dividing the number of rollers in the class by the total number of individuals sampled.
A decimal number representing the frequency of the non rollers (q2) can be obtained by dividing the number of non rollers by the total number of students. You should then record these numbers in the table below..

3. Use the Hardy-Weinberg equation to determine the frequencies (p and q) of the two alleles. The frequency q can be calculated by taking the square root of q^2. Once q has been determined, p can be determined because **1-q=p**.

Phenotypic Proportions of Rollers and Non-rollers and Frequencies of the Determining Alleles

	Phenotypes				**Allele Frequency Based on the H-W Equation**	
	Rollers (p^2+2pq)		**Non Roller(q^2)**		**p**	**q**
Class Population	#=	%=	#=	%=		

Questions

1. What is the percentage of homozygous and heterozygous rollers in the class sample? Show your work.

Solve showing all work neatly using a pencil.

2. Obtain the predicted value of rollers and non-rollers from your teacher and do a chi-square calculation of the values you obtained both individually and as a class.

Solve showing all work neatly using a pencil.

Case Studies

Case 1 (Test of an Ideal Hardy-Weinberg Community)

The entire class will represent a breeding population, so find a large open space for its simulation. In order to ensure random mating, choose another student at random. In this simulation, we will assume that gender and genotype are irrelevant to mate selection.

The class will simulate a population of randomly mating heterozygous individuals with an initial gene frequency of 0.5 for the dominant allele **A** and the recessive allele **a** and genotype frequencies of 0.25**AA**, 0.50**Aa**, and 0.25**aa**. Record this on the **Data page** at the end of the lab. Each member of the class will receive four cards. Two cards will have **A** and two cards will have **a**. The four cars represent the products of meiosis. Each "parent" will contribute a haploid set of chromosomes to the next generation.

Procedure

1. Turn the four cards over so the letters are not showing, shuffle them, and take the card on top to contribute to the production of the first offspring. Your partner should do the same. Put the cards together. The two cards represent the alleles of the first offspring. One of you should record the genotype of this offspring in the data table which follows. Each student pair must produce two offspring, so all four cards must be reshuffled and the process repeated to produce a second offspring.

2. The other partner should then record the genotype of the second offspring in the data table which follows. Using the genotypes produced from the matings, you and your partner will mate again using the genotypes of the two offspring. That is , student 1 assumes the genotype of the first offspring, and student 2 assumes the genotype of the second offspring.

3. Each student should obtain, if necessary, new cards representing their alleles in his or her respective gametes after the process of meiosis. For example, student 1 becomes the genotype **Aa** and obtains cards **A,A,a,a;** student 2 becomes **aa** and obtains cards,**a,a,a,a**. Each participant should **randomly** seek out another person with whom to mate in order to produce offspring of the next generation. You should follow the same mating procedure as for the first generation, being sure you record your new genotype after each generation in the **Case 1** section. Class data should be collected after each generation for five generations. At the end of each generation, remember to record the genotype that you have assumed. Your teacher will collect class data after each generation by asking you to raise your hand to report your genotype.

Complete the table below: For the population (class data), what are the **theoretical allele & genotype frequencies** in the initial parental generation? Based on the Hardy-Weinberg theorem, what would the **theoretical allele & genotype frequencies** be for the 5th generation? What are the **actual allele & genotype frequencies** at the end of the 5th generation?

A. Individual Data

	Initial	F1	F2	F3	F4	F5
My Genotype						

B. Class Data

	Surviving genotypes				Surviving alleles		
Generation #	AA	Aa	aa	Total Individuals	A	a	Total alleles
Parental							
F1							
F2							
F3							
F4							
F5							

	Frequency of genotypes			Frequency of alleles	
Generation #	p^2 (AA)	2pq (Aa)	q^2 (aa)	p (A)	q (a)
Parental (H-W theoretical)					
F5 (H-W theoretical)					
F5 (actual)					

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Questions

1. Do the class results for the p and q values of the 5th generation agree with the predicted values? ________________________________

2. What does this mean about the population? ____________________________________

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3. What major assumption(s) were not strictly followed in this simulation for a population in Hardy-Weinberg equilibrium?

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4. What do these results indicate about the importance of population size as an evolutionary force?

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5. How is the concept of genetic drift significant in reference to endangered species conservation?

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(Case II Selection)

In this case you will modify the simulation to make it more realistic. in the natural environment , not all genotypes have the same rate of survival; that is, the environment might favor some genotypes while selecting against others. An example is the human condition sickle-celled anemia. It is a condition caused by a mutation on one allele, in which a homozygous recessive does not survive to reproduce. For this simulation you will assume that the **homozygous recessive** individuals **never survive**. Heterozygous and homozygous dominant individuals always survive.

The procedure is similar to that for **Case 1**. Start again with your initial genotype, and produce your "offspring" as in **Case 1**. This time, However, there is one important difference. Every time your offspring is **aa** it **does not reproduce**. Since we want to maintain a constant population size, the same two parents must try again until they produce two surviving offspring. You may need to get new allele cards from the pool. Proceed through five generations, selecting against the homozygous offspring 100% of the time. Then add up the genotype frequencies that exist in the population and calculate the new p and q frequencies in the same way as it was done in **Case 1**.

Allele frequency: The allele frequencies, p and q, should be calculated for the parental generation and for the offspring after 5 generations of simulated matings.

Complete the table below: For the population (class data), what are the **theoretical allele & genotype frequencies** in the initial parental generation? Based on the Hardy-Weinberg theorem, what would the **theoretical allele & genotype frequencies** be for the 5th generation? What are the **actual allele & genotype frequencies** at the end of the 5th generation?

A. Individual Data

	Initial	F1	F2	F3	F4	F5
My Genotype						

B. Class Data

	Surviving genotypes					Surviving alleles		
Generation #	AA	Aa	aa	Total Individuals		A	a	Total alleles
Parental								
F1								
F2								
F3								
F4								
F5								

	Frequency of genotypes				Frequency of alleles	
Generation #	p^2 (AA)	2pq (Aa)	q^2 (aa)		p (A)	q (a)
Parental (H-W theoretical)						
F5 (H-W theoretical)						
F5 (actual)						

6. Do the class results for the p and q values of the 5th generation agree with the predicted values? ______________________________________

7. How do the new p and q frequencies compare to the parental frequencies?

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8. How do the new fifth generation frequencies of p and q compare to the fifth generation frequencies in Case 1?

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9. Predict what would happen to the p and q frequencies if you simulated another five generations?

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10.. Since homozygous recessives are strongly selected against, would you expect the recessive (a) allele to be completely removed from the population? In other words, in a large population would it be possible to completely eliminate a deleterious (or even lethal) recessive allele. Explain.

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11. Describe a real-life example of selection against a homozygous recessive genotype.

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12. Explain how heterozygote superiority could work against selection against an dominant or recessive phenotype. State an example of this in human populations and explain why the extreme phenotype is selected against, while the heterozygous phenotype is favored for survival.

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Hardy-Weinberg Problems

1. In *Drosophilia*, the allele for normal length wings is dominant over the allele for vestigial wings. In a population of 1,000 individuals, 360 show the recessive phenotype. How many individuals would you expect to be homozygous dominant and heterozygous for this trait?

Choose the letters you will use to represent the alleles & genotypes:

Dominant allele	
recessive allele	

Homozygous Dominant	
Heterozygous	
Homozygous recessive	

Translate to known frequencies:

p (Dominant allele)	
q (recessive allele)	

p^2 (Homozygous Dominant)	
2pq (Heterozygous)	
q^2 (Homozygous recessive)	

Solve showing all work neatly using a pencil.

2. The allele for the ability to roll one's tongue is dominant over the allele for the lack of this ability. In a population of 500 individuals, 25% show the recessive phenotype. How many individuals would you expect to be homozygous dominant and heterozygous for this trait?

Choose the letters you will use to represent the alleles & genotypes:

Dominant allele	
recessive allele	

Homozygous Dominant	
Heterozygous	
Homozygous recessive	

Translate to known frequencies:

p (Dominant allele)	
q (recessive allele)	

p^2 (Homozygous Dominant)	
2pq (Heterozygous)	
q^2 (Homozygous recessive)	

Solve showing all work neatly using a pencil.

3. The allele for the hair pattern called "widow's peak" is dominant over the allele for no "widow's peak." In a population of 1,000 individuals, 510 show the dominant phenotype. How many individuals would you expect of each of the possible three genotypes for this trait?

Choose the letters you will use to represent the alleles & genotypes:

Dominant allele	
recessive allele	

Homozygous Dominant	
Heterozygous	
Homozygous recessive	

Translate to known frequencies:

p (Dominant allele)	
q (recessive allele)	

p^2 (Homozygous Dominant)	
2pq (Heterozygous)	
q^2 (Homozygous recessive)	

Solve showing all work neatly using a pencil.

4. In a certain population, the dominant phenotype of a certain trait occurs 91 % of the time. What is the frequency of the dominant allele?

Choose the letters you will use to represent the alleles & genotypes:

Dominant allele	
recessive allele	

Homozygous Dominant	
Heterozygous	
Homozygous recessive	

Translate to known frequencies:

p (Dominant allele)	
q (recessive allele)	

p^2 (Homozygous Dominant)	
2pq (Heterozygous)	
q^2 (Homozygous recessive)	

Solve showing all work neatly using a pencil.