Name____________________________________Per_____
Lab Partner(s):

____

____

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Biology B

Essential Questions:

- Will allele frequencies in a simulated population change over time under various circumstances, and, if so, how will they change?
- What factors account for the changes, or lack thereof, in allele frequencies in the simulated populations?

Summary of Background:

In the space provided, give a concise summary of the relevant background information about the Hardy-Weinberg principle that you need to know to complete the lab activity.

Materials:

- 4 allele cards per student
- Supply of extra allele cards

Procedure:

The Hardy-Weinberg principle identifies the allele frequency of the dominant allele in the population as the variable p, and the allele frequency of the recessive allele in the population as the variable q.

The entire class will represent a breeding population of randomly mating heterozygous individuals with an initial gene frequency of 0.5 for the dominant allele *A* ($p = 0.5$) and 0.5 for the recessive allele *a*. ($q = 0.5$). Notice that $p + q = 1$. Does this make sense?

We will also assume, for the sake of simplicity, that the genotype frequencies in the population are 0.25 *AA,* 0.50 *Aa,* and 0.25 *aa* . In this simulation, we will assume that gender and genotype are irrelevant to mate selection.

Your initial genotype is *Aa*. Record this in the Data Collected section of the lab report.

Hardy-Weinberg Lab
Biology B

Each class member receives 4 cards. 2 cards will have *A* written on them, and 2 cards will have *a* written on them. The four cards represent the products of meiosis. Each "parent" contributes a haploid set of chromosomes to the next generation.

Case I – A Test of an Ideal Hardy-Weinberg Population

1. Turn the four cards over so that the letters do not show, shuffle them, and take the card on top to contribute to the production of the first offspring. Your partner should do the same.
2. Put the two cards together. The two cards represent the alleles of the first offspring. One of you should record the genotype of this offspring in the Case I section in the Data section. This will be this partner's genotype for the next round.
3. Each student must produce 2 offspring, so all four cards must be reshuffled and the process repeated to produce a second offspring. The other partner should record this genotype in the Data section. This will be the other partner's genotype for the next round.
4. The very short reproductive career of this generation is over. You and your partner now become the next generation by assuming the genotypes of the offspring.
5. Each student should obtain, if necessary, new cards representing the alleles in his or her respective gametes after the process of meiosis.
6. Each student should now *randomly* seek out a new person with which to mate in order to produce the offspring of the next generation. Remember, the sex of your mate does not matter, nor does the genotype.
7. Follow the same mating procedures as you did in steps 1 – 3. Record your new genotypes in the Data section.
8. Your teacher will collect class data on genotype frequencies at the end of 5 rounds.

Case II – Selection

In this Case you will modify the simulation to make it more realistic. In the natural world, not all genotypes have the same rate of survival. The environment might favor some genotypes while selecting against others. An example is the human condition of sickle-cell anemia, a disease caused by a recessive allele. Individuals who are homozygous recessive often do not survive to reproductive maturity.

For this simulation, you will assume that homozygous recessive individuals (*aa*) never survive and that homozygous dominant and heterozygous individuals survive 100% of the time.

1. The procedure is similar to that for Case I.
2. Start again with your initial genotype *Aa* and produce your "offspring" as you did for Case I.

3. An important difference in this Case is that every time your "offspring" is *aa*, it does not survive and reproduce. Since we maintain a constant population size, the same 2 parents must try again until they produce two surviving offspring.
4. Proceed through 5 generations, selecting against the homozygous recessive offspring 100% of the time.
5. Your teacher will collect class data on genotype frequencies at the end of 5 rounds.

Data Collected:

CASE I – Hardy-Weinberg Equilibrium

Initial Class Frequencies:

*AA*________ *Aa*_______ *aa*________

My initial genotype: ______

F_1 genotype:______

F_2 genotype: ______

F_3 genotype: ______

F_4 genotype: ______

F_5 genotype: ______

Final Class Frequencies:

*AA*________ *Aa*_______ *aa*

p________ q ________

CASE II – Selection

Initial Class Frequencies:

*AA*________ *Aa*_______ *aa*________

My initial genotype: ______

F_1 genotype:______

F_2 genotype: ______

F_3 genotype: ______

F_4 genotype: ______

F_5 genotype: ______

Final Class Frequencies:

*AA*________ *Aa*_______ *aa*

p________ q ________

Allele Frequency:

The allele frequencies, *p* and *q* should be calculated for the population after 5 generations of simulated random mating.

p = frequency of the dominant allele
q = frequency of the recessive allele

Hardy-Weinberg Lab
Biology B

Number of *A* alleles present at the 5th generation:

offspring with genotype *AA* ________ x 2 = ________ *A* alleles

offspring with genotype *Aa* ________ x 1 = ________*a* alleles

Total = ________ *A* alleles

***p* = Total # *A* alleles/Total # all alleles in population = ________**

Number of *a* alleles present at the 5th generation:

offspring with genotype *aa* ________ x 2 = ________ *a* alleles

offspring with genotype *Aa* ________ x 1 = ________*a* alleles

Total = ________ *a* alleles

***q* = Total # *a* alleles/Total # all alleles in population = ________**

Analysis and conclusions:

CASE I: Hardy-Weinberg Equilibrium

1. What were the values of *p* and *q* at the start of the simulation?

2. What does Hardy-Weinberg equilibrium predict for the values of *p* and *q* after 5 generations?

3. Do your results agree with the prediction above? If not, why do you think they do not?

4. What major assumption(s) of Hardy-Weinberg equilibrium were not strictly followed in this Case I simulation?

Hardy-Weinberg Lab
Biology B

CASE II: Selection

1. How do the new values for *p* and *q* compare to the initial values at the start of the simulation?

2. What major assumption(s) of Hardy-Weinberg equilibrium were not strictly followed in this Case II simulation?

3. Predict what would happen to the frequencies of *p* and *q* if you simulated another 5 generations.

4. In a large population, would it be possible to completely eliminate a deleterious *recessive* allele? Explain you answer. (Hint: does natural selection act on genotypes or phenotypes?)