Population Genetics – Natural Selection

INTRODUCTION

Charles Darwin (1859) proposed a mechanism for change through **natural selection** which as a result of differential survival and reproductive fitness leads to **evolution** of populations. In the early twentieth century, naturalists and geneticists were not in agreement on the importance of the influence of small variations in populations on the processes of natural selection and evolution. It is now accepted "doctrine" that **populations** and their **gene pools** are what evolve and not individuals.

It was in 1908 that this concern for the impact of gene variation on populations was first addressed by G. W. Hardy in England and W. Weinberg in Germany. They both proposed that the process of heredity (as described by Mendel in 1865) operating in isolation would not alter the genetic makeup of a population. The **Hardy-Weinberg Theory of Genetic Equilibrium**, as it came to be called, says that the proportions of alleles in a population will stay the same forever. However, this equilibrium of allele frequencies will be maintained only if the following conditions are met:

1. Mating is completely random
2. Populations are large
3. Mutations are in equilibrium, i.e. forward events = backward events
4. There is no migration into or out of the population
5. All genotypes have equal reproductive fitness (no selection)

In examining the above list, we immediately recognize that any population that meets these criteria is NOT going to evolve. Thus, the Hardy-Weinberg conditions listed above provide guidelines for examining those circumstances or conditions that lead to changes in allele frequencies and ultimately to evolution of the population.

HARDY-WEINBERG IN ACTION

Because populations evolve due to changes in the gene pool, we can think of the act of producing the next generation as being the same as taking all the male and female gametes of the population and stirring them together in a big tub and then handing a certain number of the newly formed zygotes out to each pair of parents in the population. By doing this, the pairing of gametes is a purely random chance set of events that obey the basic laws of probability. This approach is similar to the thinking of Hardy and Weinberg.

It is rare that a population in nature ever meets all of the Hardy-Weinberg criteria in any given generation. How often do you think that mating is completely random like our "make believe" of collecting all the gametes and stirring them together in a tub? ____

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Are all populations large? ____
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Do all alleles of any gene have the same survival value? _________________
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EVOLUTIONARY CHANGE THROUGH NATURAL SELECTION

Under conditions of natural selection, one phenotype may be favored for survival over another. In our simulation, one phenotype will be totally selected against in each generation. Recall the sad plight of the naked bunnies. Breeders of rabbits have long been familiar with a variety of genetic traits that affect the survivability of rabbits in the wild, as well as in breeding populations. One such trait is the trait for furless rabbits (naked bunnies). This trait was first discovered in England by W.E. Castle in 1933. The furless rabbit is found rarely in the wild because the cold English winters are a definite selective force against it. The trait for fur is dominant to the trait for furless. A bunny that is born homozygous for this serious recessive condition will die because it will not survive the English winters. (There are many such hereditary lethal alleles in the human genome.)

PROCEDURE

1. The white beads will represent the dominant allele for fur (*A*). The red beads will represent the recessive allele for furless (*a*). The cup will represent the English countryside, where the rabbits randomly mate.

2. We will imagine that we are setting 50 heterozygous rabbits (*Aa*) that are furred loose in the English countryside. That means that we will have 50 *A* alleles and 50 *a* alleles.

3. To represent this, we will begin the exercise with 50 white beads (*A*) and 50 red beads (*a*) in the cup. This means that we are beginning with an allele frequency of 0.5 (50%) *A* and 0.5 (50%) *a*. Record this data in the “Allele and Genotype Frequency Changes Due to Natural Selection” for Generation 0.

4. Place the beads in the cup and shake up (mate) the rabbits. You will be producing Generation 1.

5. Without looking at the beads, select two at a time to represent a zygote. You will record this result on the table in the Generation 2 row. If you draw two white beads, you need to make a tick mark under “White / White”. If you draw a white bead and a red bead, you need to make a tick mark under “White / Red”. If you draw two red beads, you need to make a tick mark under “Red / Red”. **We are sampling with replacement, so you will need to return the beads to your “breeding” cup or gene pool.**

6. Shake the cup again. Without looking, draw two more beads & record your result on the table. You will continue this process until you have 50 bead pairs (or baby bunnies).

7. The *aa* (or red/red bunnies) are born furless. The cold weather kills them before they reach reproductive age, so they can't pass on their genes. These alleles are lost to the next generation.

8. We now need to calculate the frequency of alleles in the survivors of generation #1. That is the total of the *A* (white – furred) alleles among all the *AA* and *Aa* individuals and the total of the *a* (red – furless) among the *Aa* individuals. (Recall, all of the *aa* individuals were killed by the winter temperatures.)

Example: Let us imagine that you drew 14 *AA* bunnies, 34 *Aa* bunnies, and 2 *aa* bunnies.

Number of *AA* individuals = 14 (contains 28 *A* alleles)
Number of *Aa* individuals = 34 (containing 34 *A* alleles and 34 *a* alleles)
Number of *aa* individuals = 2 (contains 4 *aa* alleles that are lost due to death)

The total surviving population contains 28 + 34 *A* alleles, or 62 *A* alleles, and 34 *a* alleles for a total of 96 alleles. The new allele frequencies for Generation 1 will be the progenitors of Generation 2. This frequency is calculated as…

Frequency of *A* alleles = 62 / 96 or 65% which = 0.65
Frequency of *a* alleles = 34 / 96 or 35% which = 0.35

9. Adjust your container by counting out enough red & white beads to represent the *A* and *a* frequency. In our example, you would count out 65 white beads (for 0.65 frequency of *A*) and 35 red beads (for 0.35 frequency of *a*).

10. Repeat the selection procedure for another 50 bead pairs to produce Generation 2. Again, record your new frequencies in the table below.

11. Adjust the frequency of the alleles in the container on the basis of the outcome of the **surviving fraction** of the Generation 2 and repeat the procedure again.

12. You will continue this exercise until one of two things happen…

1) You produce the ninth, and final, generation of bunnies, OR
2) Gene fixation occurs. Gene fixation is the loss of one of your genes (in other words, you have no more red beads).

Allele and Genotype Frequency Changes Due to Natural Selection

	White / White *AA* (Furred)	White / Red *Aa* (Furred)	Red / Red *aa* (Naked)	Total Beads Remaining	Frequency of *A* (White)	White Bead Change	Frequency of *a* (Red)	Red Bead Change
Formulas				100 – 2(aa)	$\frac{\text{2(AA) + Aa}}{\text{Total Beads}}$		$\frac{\text{Number of Aa}}{\text{Total Beads}}$	
Generation 0	0	50	0	100 – 2(0)= 100 – 0 = 100	$\frac{2(0) + 50}{100}$ 50%	NA	$\frac{50}{100}$ 50%	NA
Generation 1								
Generation 2								
Generation 3								
Generation 4								
Generation 5								
Generation 6								
Generation 7								
Generation 8								
Generation 9								
Generation 10								

DISCUSSION OF THE RESULTS OF THE NATURAL SELECTION SIMULATION

1. What did you expect to happen to the frequency of the two alleles *A* and *a* as a consequence of selection removing the furless offspring?

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2. On the provided graph paper, graph the change in frequency of the alleles over the generations and answer the following questions about the graphed results.
a) Did the frequency change for the two alleles occur at a constant rate over time?

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b) Was the change as rapid as you would have predicted? _____ If not, how would you describe or explain the observed change in frequency that did occur over time?

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c) Based on your results, what could be postulated about the loss of a deleterious gene from a population by the process of natural selection?

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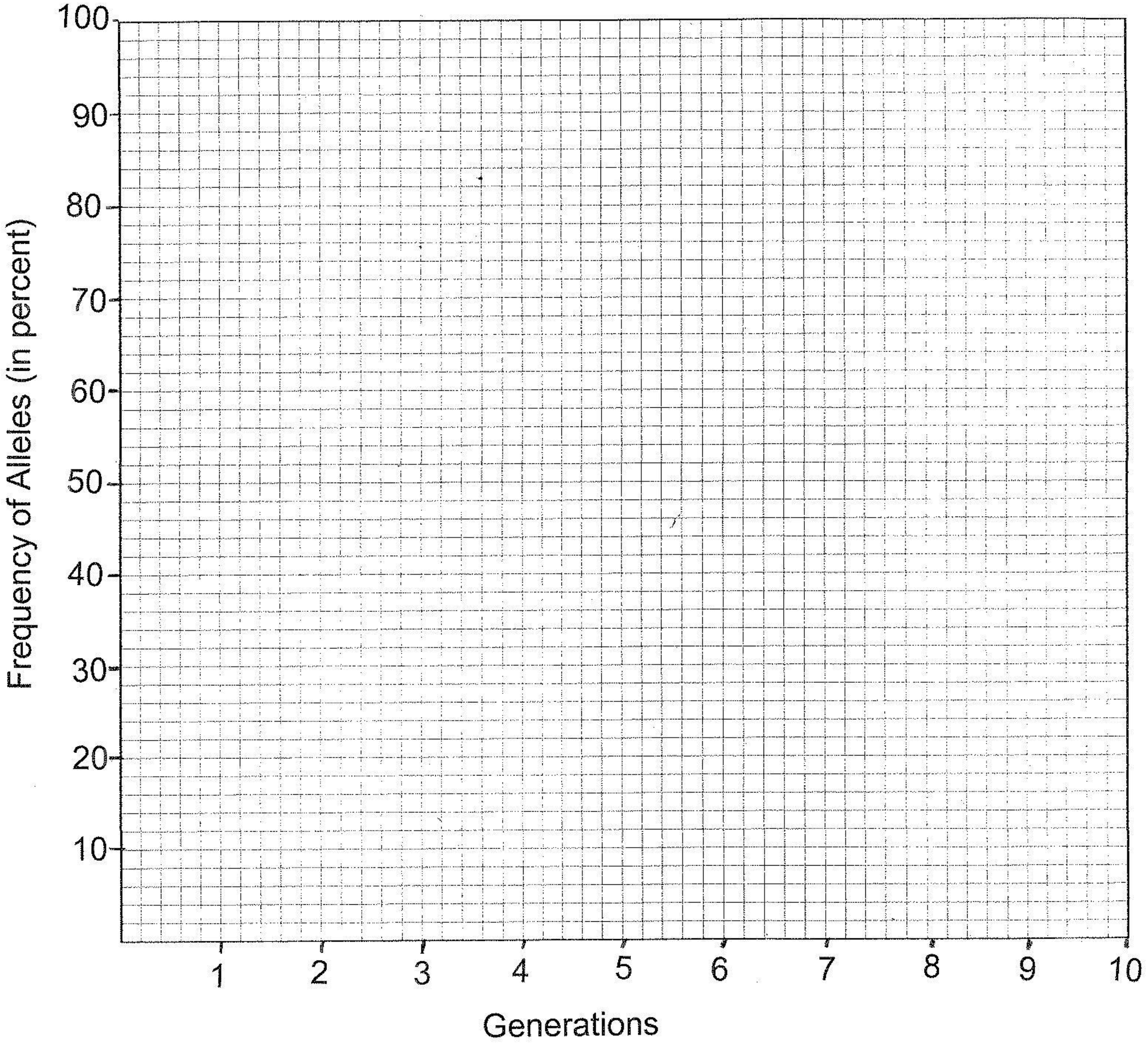
Natural Selection Among Furred and Furless Rabbits



x = Frequency of A (White bead = Furred allele)
o = Frequency of a (Red bead = Furless allele)