



Natural Selection Bunny Simulation

<http://phet.colorado.edu/en/simulation/natural-selection>



Background Information:

In the mid 1800's a scientist named Charles Darwin discovered and developed a mechanism for evolution that he called natural selection. Natural selection simply stated that within any population with variation there would be a struggle for existence that would ultimately lead to the survival of the fittest. Darwin then went on to say that those traits that were the most fit would be passed on to the next generation more frequently. This continual selection for certain traits and against others over billions of years led to what Darwin called descent with modification. Descent with modification says that different environments selecting for certain traits over long periods of time could have caused an ancient ancestor of all life to be modified over and over again until it had evolved from a single species into all of the species that have lived on Earth since.

While Darwin defined the mechanism of evolution fairly accurately, there were two major components he was missing. Darwin had little to no idea what caused the variation he saw in nature and he could not explain how the variations he saw were passed from parent to offspring. It was not until the Hershey-Chase experiment in 1952, which showed DNA to be the hereditary molecule, and the discovery of the structure of DNA by Watson and Crick in 1953 that these questions could be answered. This discovery would change the way science studied evolution. Now that science knew it was DNA that caused the variation seen in nature and DNA that caused those traits to be passed from parent to offspring, they could focus on it as the root of evolution by natural selection. This meant that instead of approaching evolution by looking at how an organism's phenotype (physical features) changed over time, scientists could study the evolution of an organism's genotype (allele combinations). This leads to our modern definition of evolution: The increase or decrease in the frequency of an allele over time.

In today's simulation you will be studying how mutations in the DNA of an organism can lead directly to the evolution of the population it is a part of. This will be done by tracking how allele frequency is dependent upon the core principles of natural selection.

Pre simulation: Do this before you log on and start the simulation.

1. Define the following terms—

Mutation:

Allele:

Allele frequency:

2. In your own words explain how you think that DNA, mutation, genotype, phenotype, and natural selection interconnect to cause evolution.

The simulation: Today you will be using the simulation software to run three experiments. Follow the directions below to collect the required data then use that data to answer the discussion questions that follow.

Experiment 1:

In this experiment you will be examining the effect of a recessive mutation that changes the color of the organism and alters how it avoids predators. The original population of white bunnies live in an arid, equatorial environment and are preyed upon by wolves. A mutation arises in the gene for fur color that results in a recessive gene for brown fur color. In the space below write your hypothesis about how this change in DNA will affect the evolution of this population over the next 10 generations. (Remember... if, then, because)

Hypothesis 1:

Experiment 1 Procedure:

1. Open the Phet Natural Selection simulation. You will need Java and/or Flash Player installed on your computer. You can select either, “run now” or “download” to start.
2. Take a few minutes to familiarize yourself with the page. Be sure to notice the following:

The population graph under the environment. This is where you will get the number of each type of rabbit. You can zoom in or out to get a more accurate reading of population size.

The generation bar, play, and pause buttons. These give you a time before each breeding period. The pause button allows you to stop the simulation so you can read the graph and take your data.

3. When you are ready to start your first experiment make sure the environment is set to “equator” then click on the “add a friend” button in the lower left hand corner of the environment. This will start the simulation. Watch the generation bar and let it run twice, then hit pause. Record the data from the graph for generation two in data table 1.
4. Once you’ve recorded the data, click on “Brown fur” in the add mutation section of the simulator. Using the edit genes section of the simulator change brown fur to a **recessive** trait.
5. Start the simulation and let it run for two more generations. At this point pause the simulation and use the graph to fill in generation 4 data in data table 1.
6. Now add **wolves** as a selection factor and start the simulation. Let the simulation run for three more generations. Hit pause and collect the data for generation 7 on data table 1.
7. Click play and let the simulation run for three more generations. Pause the simulation and record the data for generation 10 in data table 1 then answer the associated analysis questions below the table.

Data table 1	Graphical Data			Percentage calculations	
Generation number	Number of Brown	Number of White	Total	% Brown Rabbits	% White Rabbits
2					
4					
7					
10					

Analysis:

1. Calculate the percentage of each color of rabbit using the following method:

% Brown rabbit = (Brown rabbits / Total rabbits) X 100

% White rabbit = 100% - % brown rabbits.

2. Briefly explain how this change in DNA affected the allele frequency of the population. Be sure to use your data in this explanation.
3. Use the data in an explanation of why the data does or does not support your hypothesis.

Experiment 2: In this experiment you will be examining the effect of a dominant mutation that changes how the organism obtains food. The mutation results in longer teeth and the selection pressure is a limited amount of food. In the space below hypothesize how this change in DNA will affect the evolution of this population over the next 10 generations. (Remember... if, then, because).

Hypothesis 2:

Experiment 2 Procedure:

1. Click the reset all button in the lower right hand corner of the simulator
2. When you are ready to start your second experiment click on the “add a friend” button in the lower left hand corner of the environment. This will start the simulation. Watch the generation bar, let it run twice, then hit pause. Record the data from the graph for generation two in data table 2.
3. Once you’ve recorded the data click on “long teeth” in the add mutation section of the simulator. This mutation should already be designated as the **dominant** trait but check the edit genes section of the simulator to be sure.

4. Start the simulation and let it run for two more generations. At this point pause the simulation and use the graph to fill in generation 4 data in data table 2.
5. Now add **food** as a selection factor and start the simulation. Let the simulation run for three more generations. Hit pause and collect the data for generation 7 on data table 2.
6. Click play and let the simulation run for three more generations. Pause the simulation and record the data for generation 10 in data table 2 then answer the associated analysis questions below the table.

Data table 2	Graphical Data			Percentage calculations	
Generation number	Number of Normal teeth	Number of Long teeth	Total	% Normal Tooth Rabbits	% Long Tooth Rabbits
2					
4					
7					
10					

Analysis:

1. Calculate the percentage of each tooth type using the following method:

% Long tooth rabbit = (Long tooth rabbits / Total rabbits) X 100

% Normal tooth rabbit = 100% - % Long tooth rabbits.

2. Briefly explain how this change in DNA affected the allele frequency of the population. Be sure to use your data in this explanation.
3. Does the data in the table above support the hypothesis for this experiment? Be sure to use your data in an explanation of why the data does or does not support your hypothesis.

Experiment 3: In this experiment you will be examining the effect of a dominant mutation that changes the length of the rabbit's tail. Your job in this simulation is to determine whether or not having a longer tail gives the rabbits an advantage when trying to escape predators. In the space below, hypothesize how this change in DNA will affect the evolution of this population over the next 10 generations. (Remember... if, then, because)

1. Click the reset all button in the lower right hand corner of the simulator.
2. When you are ready to start your third experiment click on the "add a friend" button in the lower left hand corner of the environment. This will start the simulation. Watch the generation bar, let it run twice, then hit pause. Record the data from the graph for generation two in data table 3.
3. Once you've recorded the data click on "long tail" in the add mutation section of the simulator. This mutation should already be designated as the **dominant** trait but check the edit genes section of the simulator to be sure.
4. Start the simulation and let it run for two more generations. At this point pause the simulation and use the graph to fill in generation 4 data in data table 3.
5. Now add **wolves** as a selection factor and start the simulation. Let the simulation run for three more generations. Hit pause and collect the data for generation 7 on data table 3.
6. Click play and let the simulation run for three more generations. Pause the simulation and record the data for generation 10 in data table 3 then answer the associated analysis questions below the table.

Data table 3	Graphical Data			Percentage calculations	
Generation number	Number of Short Tail	Number of Long Tail	Total	% Short Tail Rabbits	% Long tail Rabbits
2					
4					
7					
10					

Analysis:

1. Calculate the percentage of each tail type using the following method:

$$\% \text{ Short tail rabbit} = (\text{Short tail rabbits} / \text{Total rabbits}) \times 100$$

$$\% \text{ Long tail rabbit} = 100\% - \% \text{ brown rabbits.}$$
2. Briefly explain how this change in DNA affected the allele frequency of the population. Be sure to use your data in this explanation.

3. Does the data in the table above support the hypothesis for this experiment? Be sure to use your data in an explanation of why the data does or does not support your hypothesis.
4. Run this experiment one more time (or if you have time two more times). How can you explain the fact that the results are not the same?

Discussion Questions: Use your data, your knowledge of evolution, and genetics to answer the questions that follow.

1. Given the current definition of evolution being a change in allele frequency in a population over time (The species must survive and change. Extinction is not an example of evolution), did any of the mutations above fail to cause the population to evolve? If so which one? Use your data to explain how you know.
2. Predict what would have happened in simulation 1 if you had started with the environment set to arctic rather than equator. Do you think the brown rabbits could have been completely and forever bred out of the population like the white ones may have been in simulation 1? Why or Why not?
3. In simulation three there should have been very little change in the percentage of each type of rabbit (in the generations before extinction). Why did the allele frequencies not change as drastically in this simulation as they did in the other two?

4. Compare your data from simulation 1 and simulation 2. Both mutations were successful but in simulation 1 the mutation was recessive; in simulation 2 the mutation was dominant. What was different about how these two populations evolved after the mutation?

5. Does being the dominant form of the trait insure that it will be selected for?

6. The mutations you made were in reality small changes in the DNA. Briefly explain how a small change in DNA can cause such a huge evolutionary shift within a population.