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### **Mystery #3: Cold Snap Genetic Drift Simulation**

**Objective:** Students will understand one type of genetic drift, the bottleneck effect, using the example of a cold snap die off of spotted seatrout. Students will understand how drastic environmental events can impact the genetics of a population over generations.

**Materials:**

- 2 different colored marbles or counting cubes (ex. blue and red)
- Computer w/ internet
- Data sheet

**Background:** Genetic drift is one way evolution can occur in a population and involves random changes in gene frequency over time (unlike natural selection which is non-random). Two types of genetic drift that are easier to detect are the bottleneck effect and the founder effect. This activity will focus on impacts of the bottleneck effect which occurs when a species goes through an event that suddenly and significantly reduces its population size. The individuals that survive will have a greatly reduced genetic diversity compared to the original larger population (fewer individuals means fewer genotypes). Bottlenecks are selective events because the organisms that survive are more well suited to the change, but genetic drift is a neutral process. So we are modeling a neutral process in RESPONSE to a heavy selection event.

**KEY TERMS**

**Gene** – a region of DNA that encodes an RNA and/or protein and is the molecular unit of heredity

**Allele** – a mutational variant of a gene

**Genotype** – an individual's genetic makeup; the particular alleles inherited for a gene

**Phenotype** – an individual's physical appearance

**Neutral gene** – gene at which mutational changes do not change the adaptive fitness of the organism (i.e., selectively neutral)

**Fixation** – increase of the frequency of an allele in a population until it is present in 100% of individuals

**Extinction** – decrease in the frequency of an allele until it is present in 0% of individuals (absent)

**Bottleneck event** – sharp reduction in the size of a population; generally results in the loss of a subset of alleles present in the original population (a decrease in local genetic variation)

**Colonization** – process by which a species spreads (migrates) to new geographic areas

**Genetic drift** – process that changes allele frequencies over time due to random sampling

What are some applications of DNA and genetic analysis that you know of? (medicine: vaccines and insulin, forensics: identify individuals, and agriculture: selective breeding dogs, modify food)

Genetic analysis is an important aspect of wildlife conservation and can give scientists a better idea of how species are doing in an area. Every plant and animal on earth has a unique genetic code stored in their DNA. DNA strands are made up of a series of four nucleotide bases; Adenine, Thymine, Guanine, and Cytosine. The DNA sequence of a species can be written like this: Periwinkle Snail (AGTCCAG) although in reality they are millions or billions of bases long. The bases pair up with each other to create two connected strands held together in the middle like a ladder. The complementary base pairs are A-T and G-C. Knowing the sequence of one strand automatically tells you the sequence of the other!

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Biologists at the South Carolina Department of Natural Resources use genetic analysis for multiple reasons. They use it for population health/genetic diversity, species distribution and abundance, genetic identification, and population structure. Here we are going to see how these tools can be used to determine the genetic diversity of the spotted seatrout population.

In this activity, we will simulate a bottleneck event by selecting 10 spotted seatrouts randomly from a large original population and deeming them the survivors of a cold snap event. We will monitor the change in allele frequency of a neutral gene (represented by marbles, either blue or red) through time. In this activity, you and your group will explore, as scientists, how genetic drift acts within this small population of spotted seatrout to change the relative frequency of an allele over time. Make sure students are familiar with the terms from the glossary.

**Pre-Activity Engagement:** Read this [post](#) and look up the water temperature graphs during January 2018 by going to this [site](#). Choose the ACE Basin NERR, water temperature, January 2018. What dates do you think the cold kill of spotted seatrout occurred? Use this [document](#) to find out what we have learned about spotted seatrout's ability to tolerate cold temperatures.

**Mystery 3:** Spotted seatrout (*Cynoscion nebulosus*) are a common estuarine fish inhabiting shallow waters during spring and summer. They primarily feed on crustaceans and prefer to stay near oyster beds and seagrass beds. They are also a popular sport fish. Males reach an average of 19 inches in length and females can get up to 25 inches. As water temperatures decline during the fall, spotted seatrout move into deeper waters and return to shallow estuaries when temperatures warm again in the spring. During the winter of 2019, water and air temperatures dropped drastically during a cold snap period. The spotted seatrout population of Charleston Harbor didn't have enough time to move into deeper waters and a significant percentage of the population died off. This drastic environmental change caused a bottleneck effect in the population. It is your job to figure out what will happen to the genetic variation in the surviving group of spotted seatrout as a result of genetic drift following the bottleneck event.

**Instructions:**

1. Open the online model and read through the introduction page about genetic drift.  
[https://www.whfreeman.com/BrainHoney/Resource/6716/SitebuilderUploads/Hillis2e/Student%20Resources/Animated%20Tutorials/pol2e\\_at\\_1502\\_genetic\\_drift\\_simulation/pol2e\\_at\\_1502\\_genetic\\_drift\\_simulation.html#](https://www.whfreeman.com/BrainHoney/Resource/6716/SitebuilderUploads/Hillis2e/Student%20Resources/Animated%20Tutorials/pol2e_at_1502_genetic_drift_simulation/pol2e_at_1502_genetic_drift_simulation.html#)
2. Calculate Original Allele Frequency:
  - There is a large pile of marbles representing alleles in the original population of spotted seatrout before the cold snap. Draw a random sample of 10 marbles from this pool.  
*NOTE: In the unlikely case that you happen to draw 10 of the same color, put them all back and repeat the random draw until you get at least 1 of each color represented in your sample of 10.*
  - Calculate the proportion of blue marbles/cubes in your sample (e.g., if you drew 6 blue marbles/cubes and 4 red marbles, this would be 0.6). This will determine the frequency of the Allele A (on the y-axis) at the start of the simulation.
  - Enter your frequency in the online model where it says "Original Allele Frequency".

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3. Set the “Number of Generations” to 500. This will determine the length of time/number of generations for which the simulation will run (displayed on the x-axis).

4. Set the “Population Size” to 1,000 or less.

5. Click the “Plot” button and observe the results. The graph should now be displaying a red line, representing the proportion of Allele A (blue cubes) over time.

6. Record the final allele frequency of the 1<sup>st</sup> simulation (the proportion of Allele A at the end of 500 generations) in the results table provided on the next page. To get this number, find where the red line ends and follow it across to the y-axis. Estimate the allele frequency between 0-1.0.

7. Click “Plot”, once again, to repeat the simulation (DO NOT CLICK CLEAR YET). A second line should now be displayed in a different color. Observe and record the results of this 2<sup>nd</sup> simulation in the table.

8. Repeat until you have completed 10 simulations.

*NOTE: If the graph starts to look too cluttered, you can clear them before running the rest of your simulations. Just be sure to record all results of prior simulation runs before hitting “Clear”.*

**Discussion:**

What do you notice about your 10 simulations? Were they all similar?

How many times was your ending allele frequency similar to your initial allele frequency ( $p_0$ )?

How many times was it higher? Lower? Enter these numbers in the table.

How many times did it go to fixation (1) or extinction (0)? Enter these numbers in the table.

How might you explain the fact that the same input produced different outcomes over your 10 sims?

What if the presence of this allele determined the spotted seatrout’s phenotype? What effect could it have on the population?

**Follow up activity:**

*As the instructor(s) collect and compile the results from all of the groups, complete the following steps to explore how the effects of genetic drift change as the number of generations increases or decreases.*

1. After completing all of Part A, click “Clear” to clear your results.

2. Set the “Number of generations” to a smaller amount (e.g. 100-500). Leave your  $p_0$  unchanged.

3. Run a few simulations at this lower # of generations.

-How did your results this time compare to your prior results (at 500 generations)? What does this suggest to you about the effects of genetic drift over time?

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**Mystery 3  
Cold Snap  
Data Sheet**

**Initial allele frequency ( $p_0$ )/proportion (circle one):**

0.1 0.2 0.3 0.4 0.5 0.6 0.7 0.8 0.9

	<b>Final allele frequency (after 500 generations)</b>
Simulation 1	
Simulation 2	
Simulation 3	
Simulation 4	
Simulation 5	
Simulation 6	
Simulation 7	
Simulation 8	
Simulation 9	
Simulation 10	
<b># of simulation results lower than <math>p_0</math></b>	
<b># of simulation results higher than <math>p_0</math></b>	
<b># of fixations (1s)</b>	
<b># of extinctions (0s)</b>	

**Now that you have completed PART A, and viewed other groups' results, please reflect on the following:**

1. How does  $p_0$  compare to the proportion of times that your simulation resulted in fixation of the allele? How about extinction?
2. Why do you think the results may have differed from group to group?