**Shoebox Lab: Hardy Weinberg Simulations**

**Background**

Understanding natural selection can be difficult for some students. Many people often think that animals consciously adapt to their environment - that the rock pocket mouse can change its color, the giraffe can permanently stretch its neck, the polar bear can turn itself white - all so that they can better survive in their environments. In this activity you will use two types of goldfish crackers to help further your understanding of natural selection and the role of genetics and gene frequencies in evolution.

This activity demonstrates the effects of selective predation on a small population. Predators (you!) selectively and non-selectively prey upon (eat) fish (Goldfish crackers) in a small population. Prey are replaced with fish randomly selected from an ocean (a mixing bowl full of Goldfish crackers) to create the next generation. You will then calculate genotype frequencies for each generation using the Hardy-Weinberg rule and examine your data to determine whether the genotype frequencies have shifted as a result of selective predation.

To review, the Hardy-Weinberg rule for a population at genetic equilibrium assumes the following:

1. No genetic mutation is occurring within the population.

2. The breeding population is large.

3. The population is isolated from other populations of the species 🡺No gene flow occurs.

4. There is no natural selection 🡺All members of the population survive and reproduce.

5. Mating is random within the population.

Genotype frequencies for a population in Hardy-Weinberg equilibrium are as follows:

p2+2pq+q2=1

where: p2 = the frequency of *BB* 2pq = the frequency of *Bb* q2 = the frequency of *bb*

This means that the fraction of homozygous dominant (or *BB*) individuals plus the fraction of heterozygous (or *Bb*) individuals plus the fraction of homozygous recessive (*bb*) individuals equals 1. The pq is multiplied by 2 because there are two ways to get that combination; you can get *B* from the male and *b* from the female OR *b* from the male and *B* from female.

**Hints for calculating genotype frequencies**

If you know that 16% of the fish in a population express the recessive allele (*bb*), then the q2 value is 0.16, and q equals the square root of 0.16 (0.4). Thus, the frequency of the *b* allele is 0.4. Since the sum of the *B* and *b* alleles must be 1, the frequency of the *B* allele must be 0.6. Using Hardy-Weinberg, you can assume that in the population there are 0.36 *BB* (0.6 x 0.6), 0.48 *Bb* (2 x 0.4 x 0.6), and 0.16 *bb*.

**Remember:** p2 + 2pq + q2 =1 and p + q= 1

**Materials:**

* A large mixing bowl
* Paper towels
* A package of cheese-flavored Pepperidge Farm Goldfish crackers
* A package of pretzel-flavored Pepperidge Farm Goldfish crackers

**Procedure (WITHOUT selection):**

*Remember: Gold fish (cheese-flavored Goldfish) express the recessive allele (b) and brown fish (pretzel-flavored Goldfish) express the dominant allele (B).*

1. Empty both packages of Goldfish crackers into the bowl and mix thoroughly.
2. Take a random population of 10 fish (crackers) from the ocean (mixing bowl).
3. In Table 1 under “Generation 1” record the number of gold fish and brown fish in the random population. You can calculate frequencies later.
4. Choose 3 fish from the first generation and eat them.
5. Randomly choose 3 fish from the ocean- one fish for each one that died (*i.e.,* consumed by you) - and add them to your population.
6. In Table 1 under “Generation 2” record the number of gold fish and brown fish in the random population.
7. Choose 3 fish from the second generation and eat them.
8. Randomly choose 3 fish from the ocean and add them to your population.
9. In Table 1 under “Generation 3” record the number of gold fish and brown fish in the random population.
10. Choose 3 fish from the third generation and eat them.
11. Randomly choose 3 fish from the ocean and add them to your population.
12. In Table 1 under “Generation 4” record the number of gold fish and brown fish
13. Choose 3 fish from the fourth generation and eat them.
14. Randomly choose 3 fish from the ocean and add them to your population.
15. In Table 1 under “Generation 5” record the number of gold fish and brown fish.
16. Complete Table 1 by calculating the allele and genotype frequencies for each generation using the data you recorded.
17. Calculate the sum of the gold and brown fish counts of each generation for at least **FIVE** other groups, record them in Table 2, and then calculate the allele and genotype frequencies of the aggregate data for each generation.

**Table 1 (Group Data)**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Generation** | **Gold**  **(bb)** | **Brown**  **(B\_\_)** | **q2** | **q** | **p** | **p2** | **2pq** |
| **1** |  |  |  |  |  |  |  |
| **2** |  |  |  |  |  |  |  |
| **3** |  |  |  |  |  |  |  |
| **4** |  |  |  |  |  |  |  |
| **5** |  |  |  |  |  |  |  |

**Table 2 (Class Data)**

**Group Names:\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Generation** | **Gold**  **(bb)** | **Brown**  **(B\_\_)** | **q2** | **q** | **p** | **p2** | **2pq** |
| **1** |  |  |  |  |  |  |  |
| **2** |  |  |  |  |  |  |  |
| **3** |  |  |  |  |  |  |  |
| **4** |  |  |  |  |  |  |  |
| **5** |  |  |  |  |  |  |  |

**Procedure (WITH selection):**

1. Empty both packages of Goldfish crackers into the bowl and mix thoroughly.
2. Take a random population of 10 fish (crackers) from the ocean (mixing bowl).
3. In Table 3 under “Generation 1” record the number of gold fish and brown fish in the random population. You can calculate frequencies later. Gold fish (cheese-flavored Goldfish) express the recessive allele (*b*) and brown fish (pretzel-flavored Goldfish) express the dominant allele (*B*).
4. Choose 3 gold fish from the first generation and eat them; if you do not have 3 gold fish, fill in the missing number by eating brown fish.
5. Randomly choose 3 fish from the ocean—one fish for each one that died (was consumed by you)—and add them to your population. Do not use artificial selection.
6. In Table 3 under “Generation 2” record the number of gold fish and brown fish.
7. Choose 3 gold fish from the second generation and eat them; if you do not have 3 gold fish, fill in the missing number by eating brown fish.
8. Randomly choose 3 fish from the ocean and add them to your population. Do not use artificial selection.
9. In Table 3 under “Generation 3” record the number of gold fish and brown fish.
10. Choose 3 gold fish from the third generation and eat them; if you do not have 3 gold fish, fill in the missing number by eating brown fish.
11. Randomly choose 3 fish from the ocean and add them to your population. Do not use artificial selection.
12. In Table under “Generation 4” record the number of gold fish and brown fish
13. Choose 3 gold fish from the fourth generation and eat them; if you do not have 3 gold fish, fill in the missing number by eating brown fish.
14. Randomly choose 3 fish from the ocean and add them to your population. Do not use artificial selection.
15. In Table 3 under “Generation 5” record the number of gold fish and brown fish
16. Complete Table 3 by calculating the allele and genotype frequencies for each generation using the data you recorded.
17. Calculate the sum of the gold and brown fish counts of each generation for at least **FIVE** other groups, record them in Table 4, and then calculate the allele and genotype frequencies of the aggregate data for each generation.

**Table 3 (Group Data)**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Generation** | **Gold**  **(bb)** | **Brown**  **(B\_\_)** | **q2** | **q** | **p** | **p2** | **2pq** |
| **1** |  |  |  |  |  |  |  |
| **2** |  |  |  |  |  |  |  |
| **3** |  |  |  |  |  |  |  |
| **4** |  |  |  |  |  |  |  |
| **5** |  |  |  |  |  |  |  |

**Table 4 (Class Data)**

**Group Names:\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Generation** | **Gold**  **(bb)** | **Brown**  **(B\_\_)** | **q2** | **q** | **p** | **p2** | **2pq** |
| **1** |  |  |  |  |  |  |  |
| **2** |  |  |  |  |  |  |  |
| **3** |  |  |  |  |  |  |  |
| **4** |  |  |  |  |  |  |  |
| **5** |  |  |  |  |  |  |  |

**Analysis:**

You and your partner will create a digital presentation that will illustrate your results. You need to include the following items in your presentation before submitting it through Google Classroom.

1. **Partner Names**
2. **Picture of you conducting your lab**
3. **Tables 1 – 4**
4. **Analysis Questions including Graph**
5. Create a graph of frequency vs. time for selection and no selection of each allele in your population of fish. On the x- axis put generations 1-5 and, on the y-axis, put frequency (0-1). Plot both the q and p for your group data and your class data. Label lines clearly (group data and class data).
6. In either situation (selection or no selection), did your allele frequencies stay approximately the same over time? If yes, which situation?
7. Was your group data different from the class data? How? Why is it important to collect class data?
8. What conditions would have to exist for the frequencies to stay the same over time?
9. With selection, what happens to the allele frequencies from generation 1 to generation 5? Which phenotype is NOT favorable to the fish and why?
10. What process is occurring when there is a change in allele frequencies over a long period of time?
11. What would happen if it were more advantageous to be heterozygous (*Bb*)? Would there still be homozygous fish? Explain.
12. What happens to the recessive alleles over successive generations and why? Why don’t the recessive alleles disappear from the population?
13. Explain what would happen if selective pressure changed and the recessive allele was selected FOR?

**Extension Question:**

1. In a habitat of new animals often come into the habitat (immigrate), and others leave the area (emigrate). How might emigration real and immigration affect the gene frequency of *F* and *f* in this population of rabbits? How might you simulate this effect if you were to repeat this activity?

**Conclusion**

The Hardy-Weinberg rule is an important tool for detecting changes in the genotype frequencies of a population. Applying the Hardy-Weinberg rule to the data shows that selective predation of the gold fish results in the frequency of the *b* allele’s decreasing in subsequent generations. It is important to recognize that gold fish and the *b* allele will not totally disappear from the population.

Although individuals expressing the *bb* genotype may die because of selective predation before they reproduce, surviving individuals that do not express the *b* allele still carry it. If the pressure of selective predation is removed, individuals expressing the *bb* genotype survive, reproduce, and the population expressing the *bb* genotype increases, as does the frequency of the *b* allele.