## Evolution and Gene Frequencies:

## A Game of Survival and Reproductive Success



## Introduction:

In this population of Bengal tigers, alleles exist as either dominant or recessive. Bengal tigers live high in the mountains of India where the temperature is very cold. The presence of fur is dominant to the absence of fur, which is recessive. Because of this, the homozygous recessive trait is lethal. [Remember, an individual has TWO alleles!\}
Purpose:
To determine the effect of random mating in a population of tigers possessing a recessive gene.
Hypothesis:
State a hypothesis to predict what will happen to the lethal recessive gene after 10 generations in a closed population.

## Materials:

- 50 red M \& M candies (or a color of similar candies)
- 50 green $M \& M$ candies (or a color of similar candies)
- 1 paper bag
- A student with a sweet tooth


## Procedure:

1. Let 50 M \& M's represent the allele for fur and 50 M \& M 's represent the allele for no fur in a Bengal tiger population.
2. Let the paper bag represent the deep dark jungles of India where random mating occurs unwitnessed by biology students.
3. Label one paper towel 'H' for the dominant allele. Label a second towel ' h ' for the recessive allele. Label the third towel 'RIP' for those were not naturally selected to survive the cold environment.
4. Place the 50 red and 50 green alleles ( $\mathrm{M} \& \mathrm{M}$ 's) in the dark jungle bag and shake up (mate) the tigers. DON'T LOOK!
5. Select two alleles (genotype for ONE baby tiger) at a time and record in your chart next to generation \#1 each individual (combination of alleles or genotype) tiger produced. Sort the dominant and recessive alleles resulting from HH an Hh genotypes onto towels \#1 and \#2. All homozygous recessive tiger cubs unfortunately get placed on towel \#3 of the RIP Graveyard. Continue this procedure until all alleles have been counted and sorted. (for each generation, you must mate the entire population)
*** Once in the RIP Graveyard these alleles are no longer able to be passed on to the next generation and become available to the sweet-toothed Homo sapiens. ENJOY!!
6. Count and record the ' H ' and ' h ' alleles obtained and place in the chart. Total the number of ' H ' an ' h ' for the first generation and record this number also.
7. Place the alleles of the surviving tigers (which have grown, survived and reached reproductive age) back into the dark jungle and mate them again to get the F2 generation.
8. Repeat steps 5, 6, and 7 to obtain generations \#2-10.

Remember: all 'hh' individuals become part of the RIP Graveyard and therefore cannot reproduce. Because some die each generation, the TOTAL population changes and must be recalculated.
9. Determine the gene frequency of 'H' (p) and ' h ' $(q)$ for each generation and record in the chart.

- \# of 'hh'/Total = $q^{2}$ Take the square root of this number to find $q$
- The frequency of ' $H$ ' and ' $h$ ' = 1 (all the alleles for fur in the population) ( $1-q=p$ )

10. Plot your frequency of ' H ' and ' $h$ ' on one full page graph using a solid line for ' H ' and a dotted line for ' h '. Plot the class data on the same graph using the same symbols but a different color. Be sure to include all three titles, a key, and all four lines.
$\qquad$ Hour
Evolution And Gene Frequencies Game/Simulation : DATA SHEET
Hypothesis: $\qquad$
$\qquad$

Describe natural selective pressures on each genotype:

|  | Alleles | Phenotype | Environment | Fertility |
| :--- | :--- | :--- | :--- | :--- |
| Homozygous |  |  |  |  |
| Heterozygous |  |  |  |  |
| Homozygous |  |  |  |  |

(Class Data)

| Generation | Gene Frequencies <br> q | Gene Frequencies <br> $p$ |
| :---: | :---: | :---: |
| Initial | 0.50 | 0.50 |
| $\mathbf{1}$ |  |  |
| $\mathbf{2}$ |  |  |
| $\mathbf{3}$ |  |  |
| $\mathbf{4}$ |  |  |
| 5 |  |  |
| $\mathbf{6}$ |  |  |
| $\mathbf{8}$ |  |  |
| $\mathbf{9}$ |  |  |
| 10 |  |  |

Partner Data

| Generation | Number of <br> Individuals <br> HH | Number of <br> Individuals <br> Hh | Number of <br> Individuals <br> hh | Number of <br> Alleles <br> Total H | Number of <br> Alleles <br> Total h | Gene <br> Frequencies <br> q | Gene <br> Frequencies <br> p |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| 1 |  |  |  |  |  |  |  |
| 2 |  |  |  |  |  |  |  |
| 3 |  |  |  |  |  |  |  |
| 4 |  |  |  |  |  |  |  |
| 5 |  |  |  |  |  |  |  |
| 6 |  |  |  |  |  |  |  |
| 7 |  |  |  |  |  |  |  |
| $\mathbf{8}$ |  |  |  |  |  |  |  |
| $\mathbf{9}$ |  |  |  |  |  |  |  |
| $\mathbf{1 0}$ |  |  |  |  |  |  |  |

Set up a graph of Evolution in Bengal Tigers. See \# 10 in instructions


## Analysis Questions: Answer with support from your graph.

1. Do your results support, refute, or render inconclusive your hypothesis? Explain. $\qquad$
2. (a) What happened to the appearance of the dominant trait from one generation to the next? (b) What happened to its allele frequency? (c) Account for any change.
$\qquad$
$\qquad$
3. (a) What happened to the appearance of the recessive gene from one generation to the next?
(b) What happened to its frequency? (c) Account for any changes from generation to generation.
$\qquad$
$\qquad$
$\qquad$

4 How would emigration and immigration affect the gene frequency of ' H ' and ' h ' in this population of tigers?
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5. Compare your data with the class data. What are some sources of error?
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6. Define evolution in terms of Hardy-Weinberg. Are the results of this game/simulation an example of evolution? Explain your answer.
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$\qquad$
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