**Salmon Natural Selection/Evolution Simulation

Name:\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_**

In this activity we will simulate how genetic variability, a changing environment, and natural selection affect the evolutionary success of a population of Pacific salmonids (that’s you by the way!). Our salmon will face a series of events that will test them and we can witness first-hand how the genetic makeup of an individual allows it to meet (or not meet) environmental pressures and what that means in terms of long-term evolutionary trends. May the fittest survive!

**Part 1: Establish your salmon**
We will choose, as a class, one of the five species of Pacific salmon. Everyone must be the same species: remember, we are a population! We will be doing a bit of research on this species natural habitat, life cycle, niche in the environment, and environmental challenges that it faces. Choose wisely!

**Species:\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_**

**Part 2: Genetic “make-up”**
Each individual in a population of salmon has its own unique genetic mix. While all members of a population have the same general traits (fins, scales, teeth, ability to smolt, etc.) each individual has small differences from other members of the population. For example, one fish may have slightly longer pectoral fins that any other member of the population. It is still a salmon, just as people with blue eyes are just as human as those with brown. Both have eyes, just slightly different versions. We will discuss this in much greater detail in the coming days.

It is impossible to model all of the potential traits (in the tens of thousands!) that a complex multicellular organisms possesses. Instead we will be using eight salmonid “genes” which you will establish much like in role-playing games like Dungeons and Dragons. By establishing your individual salmon’s “genetic make-up”, we can simplify some of the evolutionary processes that are occurring.

In order to determine your genetic make-up, you will roll a twenty-sided die to determine each allele for each gene. The number on the die will determine which alleles you inherit.

*The “Genes”*
*ABP1 – related to surface area of the gills.* Two alleles: A and a
 Genotypes (Phenotypes): AA (above average gill surface area), Aa (above average gill surface area),
 aa (below average gill surface area)

**Roll: 1-10 = A 11-20 = a Your genotype:\_\_\_\_\_\_\_\_\_\_\_\_**

 *SEN3 – related to sensory cells in the nose.* Two alleles: S and s
 Genotypes (Phenotypes): SS (Above average number of food related sensory cells), Ss (Average
 number of food related sensory cells), aa (Below average number of food
 related sensory cells)

**Roll: 1-10 = S Your genotype:\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_
 11-20= s**

*ADG4 – related to muscle structure.* Three alleles: A, F and S
 Genotypes (Phenotypes): AA (Strong swimmer, average turning ability), AF (Strong swimmer, above
 average turning ability), AS (Average swimmer, below average turning ability), FF (Average
 swimmer, strong turning ability), FS (Below average swimmer, average turning ability),
 SS (Weak swimmer, below average turning ability)

**Roll: 1-7 = A Your genotype: \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_
 8-13= F
 14-20 = S**
*SEN1 – related to sensory cells in the nose.* Two alleles: M and m
 Genotypes (Phenotypes): MM (Average chemical sensing cells), Mm (Average chemical sensing cells),
 mm (Above average chemical sensing cells)

**Roll: 1-10 = M Your genotype:\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_
 11-20 = m**
*CAM2 – related to skin cell pigmentation.* Three alleles: G, B, and w
 Genotypes (Phenotypes): GG (Greenish belly color), GB (Blue-green belly color), Gw (Light green belly
 color), BB (Bluish belly color), Bw (light blue belly color), ww (White belly
 color)

**Roll: 1-7 = G Your genotype:\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_
 8-13 = B
 14-20 = w**
 *TOL9 – related to temperature tolerance.* Two alleles: T and t
 Genotypes (Phenotypes): TT (Low temperature tolerance), Tt (Average temperature tolerance), tt
 (high temperature tolerance)

**Roll: 1-10 = T Your genotype:\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_
 11-20 = t**

*LPG5 – related to tail muscle structure.* Two alleles: L and l
 Genotype (Phenotypes): LL (Strong leaping ability), Ll (Strong leaping ability), ll (Weak leaping abiligy)

**Roll: 1-10 = L Your genotype:\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_
 11-20 = l**
*SCL3 – related to scale toughness.* Two alleles: X and x
 Genotype (Phenotypes): XX (Average scale toughness), Xx (Average scale toughness), xx (Strong scale
 toughness)

**Roll: 1-10 = X Your genotype:\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_
 11-20 = x**

*Question:*  Examine the genotypes and phenotypes of other salmon around you. Do they have the same genotypes as you for each gene? Does anybody have *all* the same genotypes? Does this agree or disagree with your understanding of population genetics? Why or why not?

**Part 3: Hardy-Weinberg**

One way that biologists can demonstrate that evolution is occurring is through analyzing the ratio of alleles for a particular gene. Since some genotypes produce advantageous traits, while others produce traits of no or negative value, it can be expected that over time advantageous alleles will accumulate as those with more unsuccessful traits die off. The Hardy-Weinberg equation is one way to measure the ratio of alleles for a particular gene. If, between one generation and the next, one allele is passed on at a greater rate than another allele for the same gene, then we can assume that having that particular allele was advantageous and that the population has evolved to be more likely to have that phenotype.

*Hardy-Weinburg equation:* ***p2+2pq+q2 = 1*
\***In this equation ***p*** represents one of the alleles and ***q*** represents the other allele. Also ***p+q=1***

In Hardy-Weinburg, ***p2***is the percentage of homozygous dominant individuals, ***2pq*** is the percentage of heterozygous individuals and ***q2*** is the percentage of homozygous recessive individuals.

We will record the starting ratio for two of our eight genes (*SEN1* and *LPG5*). At the end of the simulation we will see if the ratio has changed due to natural selection!

 **Gene 1 (*SEN1*)**
How many homozygous dominant individuals in our population?

How many heterozygous individuals?

How many homozygous recessive individuals?

p value \_\_\_\_\_\_\_\_\_ q value \_\_\_\_\_\_\_\_\_\_\_

***Gene 2 (LPG5*):**

How many homozygous dominant individuals in our population?

How many heterozygous individuals?

How many homozygous recessive individuals?

p value \_\_\_\_\_\_\_\_\_ q value \_\_\_\_\_\_\_\_\_\_\_

*Question*: For each gene, which allele is more abundant? Does this match your expectations based on the traits controlled by each gene and their phenotypes? Why or why not?

**Step 3: Scenarios**

Your salmon will face a series of scenarios much like a real salmon would face out in the environment. Each scenario will relate to at least one gene. The particular genotype of your fish will determine the evolutionary score that your fish receives. Your cumulative score at the end of the simulation will determine how “successful” your fish was and what the gene pool of the next generation looks like!

Since not all fish will successfully spawn, or even survive to spawn, only a few individuals will provide the genetic material for the next generation. In this simulation we have a population of around 20 fish. Only the top 25% will be evolutionarily “fit” enough to spawn. This means that only the top 4-5 scores will get to reproduce!

**Salmon Natural Selection/Evolution Simulation Data Sheet**

**Name:\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_**

|  |  |  |
| --- | --- | --- |
| ***Genes*** | ***Genotype*** | ***Phenotype*** |
| *ABP1* |  |  |
| *SEN3* |  |  |
| *ADG4* |  |  |
| *SEN1* |  |  |
| *CAM2* |  |  |
| *TOL9* |  |  |
| *LPG5* |  |  |
| *SCL3* |  |  |

**Scenario scoresheet**

|  |  |  |  |
| --- | --- | --- | --- |
| ***Date*** | ***Brief scenario description*** | ***Statistic affected*** | ***Scenario Score*** |
|  |  |  |  |
|  |  |  |  |
|  |  |  |  |
|  |  |  |  |
|  |  |  |  |
|  |  |  |  |
|  |  |  |  |
|  |  |  |  |
|  |  | **Total Score** |  |

**Part 4: Reproduction**

Only the most evolutionarily fit individuals are likely to successfully reproduce. These few individuals will provide the majority of the genetic material for the next generation of salmon. In our simulation, only the fish with the score in the top 25% (the best 4-5 fish) will be considered fit enough to reproduce. Each lab group will be assigned the genetic profile of two of the top 4-5 fish and will use this to produce a new generation of salmon.

Each person in a lab group is responsible for making one new fish from the genetic profile of the parents. In order to determine the genotypes for the new fish you will need to randomly select one allele from each parent for that particular gene.

Using the twenty-sided die roll for the allele from parent #1. If your roll is **1-10**, you will choose the first allele in the genotype of parent #1. If your roll is **11-20**, you will choose the second allele in the genotype of parent #1. Repeat this process for parent #2. Note that for each gene, you will end up with *two* alleles, one from each parent. Following this method, you will determine and record below the genotype (and phenotype) for each of our eight gene for your new fish.

**Second Generation Genome**

|  |  |  |
| --- | --- | --- |
| ***Genes*** | ***Genotype*** | ***Phenotype*** |
| *ABP1* |  |  |
| *SEN3* |  |  |
| *ADG4* |  |  |
| *SEN1* |  |  |
| *CAM2* |  |  |
| *TOL9* |  |  |
| *LPG5* |  |  |
| *SCL3* |  |  |

**Part 5: Hardy Weinberg revisited**

Now we can determine if our population of salmon has evolved! With our new population of fish, each with its own unique genetic make-up, we can check the ratio of alleles for our two genes and see if there has been any changes.

**Gene 1 (*SEN1*)**
How many homozygous dominant individuals in our population?

How many heterozygous individuals?

How many homozygous recessive individuals?

p value \_\_\_\_\_\_\_\_\_ q value \_\_\_\_\_\_\_\_\_\_\_

*Question:* Are the p and q values different in this generation of fish? If so, what conclusions can you draw from the differences?

**Gene 2 *(LPG5*):**

How many homozygous dominant individuals in our population?

How many heterozygous individuals?

How many homozygous recessive individuals?

p value \_\_\_\_\_\_\_\_\_ q value \_\_\_\_\_\_\_\_\_\_\_

*Question:* Are the p and q values different in this generation of fish? If so, what conclusions can you draw from the differences?

**Final Questions**
1. How does natural selection work to change the gene pool of a species? Use specific examples from this simulation to support your answer.

2. This simulation is designed to mimic many real aspects of a living population. Like all simulations, however, there are parts that don’t mimic the real world. Identify two details about this simulation that doesn’t accurately reflect what would occur in a natural salmonid population.

3. Which aspects of this simulation are non-random? What aspects are random? Does this agree with your understanding of evolution by natural selection? Why or why not?

4. Climate change will have a larger and larger impact on species like salmon. Choose two
 genes from our salmon population and explain (specifically!) how climate change could
 impact the future gene pool of our fish. *Hint: Which phenotypes would be more
 advantageous!*