

Unit 7 BILL

Activity log:

Activities

- Natural Selection and Evolution of Rock Pocket Mouse Populations (HHMI)

1 - Natural Selection

| Mc1r Gene Missense Mutation | | Pinacate Light Mouse Population | Pinacate Dark Mouse Population | Kenzin Dark Mouse Population | Armendaris Dark Mouse Population | Carrizozo Dark Mouse Population |
|-----------------------------|------------|---------------------------------|--------------------------------|------------------------------|----------------------------------|---------------------------------|
| 018 | mRNA | CGC | UGC | CGC | CGC | CGC |
| | Amino Acid | Arg | Cys | Arg | Arg | Arg |
| 109 | mRNA | CGG | UGG | CGG | CGG | CGG |
| | Amino Acid | Arg | Trp | Arg | Arg | Arg |
| 160 | mRNA | CGG | UGG | CGG | CGG | CGG |
| | Amino Acid | Arg | Trp | Arg | Arg | Arg |
| 233 | mRNA | CAA | CAC | CAA | CAA | CAA |
| | Amino Acid | Gln | His | Gln | Gln | Gln |

Questions

- Having color-matched fur with mice and their environment gives them an environmental advantage as they are harder to prey on when harder to spot. Light fur on light sand is an advantage and dark on dark is too, but a mismatch of colors will make them stick out in their environment.
2.
 - It contains four mutations
 - They do not have the mutation and the amino acid sequence is the same as the light color's, yet they still display dark fur.
 - This shows that they have evolved the same phenotype through different genetic mutations. This also shows that some mutations or evolution are repeatable.
- This is a theory that says the mutations that give a certain population an environmental or reproductive advantage will be more likely to survive to the next generation and will grow in proportion to the non-carriers. This means that "good" traits will be more likely to survive and will overtake the population.
- Gene flow: literally just a fancy word for migration
Genetic drift: When the population is small enough that it could just change by chance

- Mutation: A random change in the DNA of something, making new genes available to the population.
- Non-random mating: a trait or factor that increases likelihood that a particular specimen will reproduce
5. Gene flow could increase and decrease the population of dark haired mouse within these two populations, as there is a pathway of rocks between the two.
2. Developing an Explanation for Mouse Fur Color (HHMI)

2 - Mouse Fur Color

Procedure

1. •

2. 2

- I. Since we have previously established that melanism is quite a common mutation, it is also likely to have happened to at least some of the population of rock pocket mice in this area, meaning that a dark fur phenotype exists in this population. Melanism is also a genetically inherited trait, meaning that such mutations can be passed down to children. Since there is a nearby environment with dark surroundings (the dark rocks) the dark fur of the dark fur mutation mice will have a higher chance of surviving in the area because they will be harder to spot and predate upon. This will give a natural selective pressure towards the darker furred mice. Over time, with this selective pressure, most of the mice living on the dark rocks will have the dark fur.
- II. Needed to, they don't really have influence on whether they want dark fur or not, unless it is seen as a reproductive advantage to these mice and would lead them to increase likelihood of mating. But in this example, mice probably would not know that they should be self breeding to produce black mice, and instead natural pressures such as predation are more likely to push the population to have darker fur.

3. Table 1

aa

aa

Condition

Description

Evidence

Variation

Individuals in a population or group differ in some trait of interest.

- Melanism is a common mutation across many animals
- Larger populations probably have some dark colored mice due to the common-ness of melanism
- Black mice likely exist in the population

| | | |
|--|--|--|
| Inheritance | The variation in the trait of interest is at least partially inherited (passed from parents to offspring). The variation stems from random mutations and the recombination that accompanies sexual reproduction. The genetic variation may have arisen many generations in the past. | <ul style="list-style-type: none"> • Melanism is a genetic mutation, meaning it is genetically inheritable • Fur color is governed by genetics • Mutations in genetics are inheritable |
| Differential survival and reproduction | <p>More offspring are born than can survive, resulting in competition among individuals within a population. Some individuals with a particular trait are more likely to survive and/or have relatively more offspring compared to individuals that do not have that trait.</p> <p>Selection depends on the specific context of a species.</p> <p>Traits that are beneficial in one environment may cause problems in another environment.</p> | <ul style="list-style-type: none"> • Mice likely do not have a sexual preference when it comes to fur color • Dark mice are more likely to survive in a dark environment as they blend in to their environment, making it hard to predate on them • Dark mice have a natural environmental pressure favoring them |

Adaption

The frequency of the trait that helps individuals survive or leave more offspring will increase in the population over time, as will the alleles that affect the trait. This process can take many generations and extend over very long periods of time.

- Dark mice are more likely to survive in dark areas
- Since dark fur is inheritable, its increased fitness will be more likely to pass on to the next generation
- Over time, more mice will be dark furred as they are more fit for the environment

4. •
5. •
6. •
7. 7

I.

Table 2

| Population | Christmas Pass | Tule Well | Lava (West) | Lava (Mid) | Lava (East) | O'Neill Pass |
|------------------------|----------------|-----------|-------------|------------|-------------|--------------|
| Soil color | Light | Light | Dark | Dark | Dark | Light |
| Number of tan mice | 6 | 80 | 0 | 0 | 3 | 34 |
| Number of dark mice | 0 | 5 | 7 | 5 | 42 | 43 |
| Total number of mice | 6 | 85 | 7 | 5 | 45 | 77 |
| Percentage of tan mice | 100% | 94.1% | 0% | 0% | 6.67% | 44.2% |

- II. Only the Tule Well, Lava (East), and the O'Neill Pass. this is more likely because the sample size for these populations are larger
- III. Variation, this shows that in a larger population there will likely be genetic variation within the population. Additionally, this shows the effects of natural selection through selective fitness, because similar skinned furs hold a higher percentage in their respective environments.
8. Fur color is effected by the genotype of the MC1R gene. Additionally, the more of allele 2 there are, the more likely the mouse is to have dark fur. Heterozygous mice tend to have fur inbetween light and dark on average.
- I. Yes, since there is a significant difference between the strata, this shows that the fur color is in part governed by this gene and is therefore inherited. The spread of

each strata is minuscule compared to the differences in percent reflectance across strata.

9. *Figure 4* shows a correlation between the frequency of the MC1R allele 2 and frequency of black mice in a population by comparing it to *Figure 2*. Their visual similarities - the similar peaks in dark mice with peaks in allele 2 frequency show that there is a correlation between the two. Since we know that having dark fur cannot influence the genetic information of the mice, we can say that the MC1R gene causes in part the dark fur of the mice. This contributes to natural selection because the MC1R allele 2 is inheritable through its genetic code.

10. • (see above)

Apply what you learned

1. We would need to collect evidence that proves the claim that light fur is more prevalent in light areas and that dark fur is more prevalent in dark areas. Then we can look for variation across the two populations to see if the other variant exists in their non-respective environment. This will prove that there is variation across the population. Then, we will need to prove that fur color for these mice is inheritable. This can either be proven by finding a gene that governs fur color within these mice, which will by definition be inheritable through its genetic information. Alternatively, experiments on the breeding of these mice can be conducted to see the probability of dark fur amongst offspring. If dark furred mice have a statistically significant more amount of dark mice than light mice do, then with a large enough sample size, we can conclude with high certainty that the fur color is indeed inherited. After that, to prove differential survival, we can either conduct an observational study to watch and see the likelihood of different colored mice in each environment and note the predation rates, death rates, and reproductive rates amongst others. If different colored furs have different survival rates, then we can conclude that the environment has a natural selection for a certain fur color with a relatively low certainty, noting that the experiment is merely observational. Alternatively, we can prove differential survival by placing different colored mice in different environments and noting if they die, reproduce, etc. If there is statistical significance between these data across the different colored furs, we can conclude that there is natural selection across the fur colors with relatively high certainty. Lastly, to prove adaptation we can conclude a similar experiment to watch as the proportions of different furred mice change over generations.

2. Basically the same data as above ^

3. We have to be more ethical when dealing with humans, so we cannot conduct controlled experiments and rather only observational, which means we cannot prove causation, but only correlation.

I. Ethics

II. Humans live much longer, meaning the generational gap will be much larger

III. Humans don't really have predators or impacted chances of survivals from nature

3. Allele and Phenotype Frequencies in Rock Pocket Mouse Populations (HHMI)

3 - Allele and Phenotype Frequencies in Rock Pocket Mouse

Procedure

1. 1

I. Fur color through melanism

II. Dark are more likely to survive in a dark environment and the same is true for light in light

III. Frequencies in dark colored mice are in part governed by the MC1R gene

2. •

Part 1

1. $q = 0.5$ because $q^2 = 4/16 = 0.25$ therefore $q = 0.5$
2. $q = 0.4$ because $p + q = 1$ and $p = 0.6$
3. $p^2 = 0.04$ because $q^2 = 640/1000 = 0.64 \therefore q = 0.8$ and $p + q = 1 \therefore p = 0.2$

Part 2

1. Light = $120/168 = 71\%$ and Dark = $48/169 = 20\%$
2. Light = $3/57 = 5\%$ and Dark = $54/57 = 95\%$
3.
 - I. $dd = 71\%$
 - II. $Dd = 26\%$
 - III. $DD = 3\%$
4.
 - I. $dd = 5\%$
 - II. $Dd = 34\%$
 - III. $DD = 61\%$
5. Dark colored, as on the light colored ground, there is still a whole 20% of dark colored mice, whilst on the dark ground, there is only 5% light colored mice. This likely means that dark ground has a higher pressure to have dark colored fur
6. Their visibility to predators and therefore survival before reproduction
7. This shows that natural selection is nonrandom and can indeed happen similarly in two separate places individually. Similar factors will likely produce similar results through evolution and natural selection.
8. We need to see how the color changes over time to see if any adaptation is actually happening. If it does not change then there is no pressure acting upon the population and it should stay in Hardy-Weinburg Equilibrium

Part 3

1. As s increases, p increases more aggressively over each generation, as q inversely directly decreases. When s is 0, there is no change as there is no pressure.
2. The selection constant s is related to natural selection because it represents the amount of selective pressure upon a certain population, pushing to change the phenotypic ratios. The higher the selection constant is, the more the environment favors a certain phenotype, and pushes the population to have that phenotype.
3.
 - I. About 936 generations
 - II. About 100 generations
 - III. About 0.22
4. Making Cladograms
4 - Making Cladograms

Data Table

| TRAITS | Kangaroo | Lamprey | Rhesus Monkey | Bullfrog | Human | Snapping Turtle | Tuna |
|-------------------|----------|---------|---------------|----------|-------|-----------------|------|
| Dorsal Nerve Cord | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ |

| TRAITS | Kangaroo | Lamprey | Rhesus Monkey | Bullfrog | Human | Snapping Turtle | Tuna |
|--|----------|---------|---------------|----------|-------|-----------------|------|
| Notochord | | | | | | | |
| Paired Appendages Vertebral Column | ✓ | | ✓ | ✓ | ✓ | ✓ | ✓ |
| Paired Legs | ✓ | | ✓ | ✓ | ✓ | ✓ | |
| Amnion | ✓ | | ✓ | | ✓ | ✓ | |
| Mammary Glands | ✓ | | ✓ | | ✓ | | |
| Placenta | | | ✓ | | ✓ | | |
| Canine teeth short Foramen magnum fwd | | | | | | ✓ | |

Reordered Table

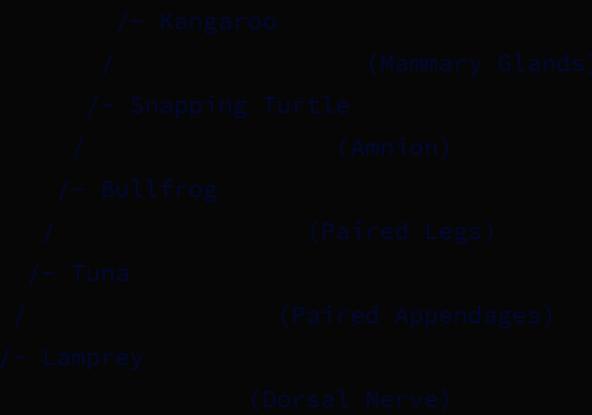
| TRAITS | Human | Rhesus Monkey | Kangaroo | Snapping Turtle | Bullfrog | Tuna | Lamprey |
|--|-------|---------------|----------|-----------------|----------|------|---------|
| Dorsal Nerve Cord Notochord | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ |
| Paired Appendages Vertebral Column | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | |
| Paired Legs | ✓ | ✓ | ✓ | ✓ | ✓ | | |
| Amnion | ✓ | ✓ | ✓ | ✓ | | | |
| Mammary Glands | ✓ | ✓ | ✓ | | | | |
| Placenta | ✓ | ✓ | | | | | |
| Canine teeth short Foramen magnum fwd | | ✓ | | | | | |

Claydogram

```

/- Human
/
/- Rhesus Monkey
/
(Foramen magnum fwd)
(Placenta)

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Summary

Shows

1. Likely relationships
2. Possible common ancestors and origins of characteristic
3. Shared characteristics

Application

1. Iguana: near the turtle as they share prior characteristics
2. Rat: Near the monkey
3. Goldfish: Near the tuna

Article Reading

1. Artificial Selection

Bell Ringers

1. Natural Selection in Giraffes
 - 1 - Natural Selection in Giraffes
 1. Pressure to get food from tall trees, short giraffes will be restricted from eating from tall trees and will be more likely to starve.
 2. It would select for tall giraffes as the short ones cannot eat
 3. Short ones cannot eat, so they will starve
 4. Over time, as the tall ones are more likely to survive, the tall phenotype will be inherited and its frequency amongst the population will increase
2. Evolutionary Scientists
 - 2 - Evolutionary Scientists
 1. Charles Darwin: Theory of natural selection, proven to be right
 2. Alfred Wallace: Also theory of natural selection, also proven right
 3. Jean Baptiste de Lamarck: Theory of selection through use and disuse, proven wrong
 4. Charles Lyell: Theory of Uniformitarianism - slow steady pressures, proven right and aided in proving the earth to be old
 5. Georges Cuvier: Theory of catastrophism - large violent changes caused changes in organisms, proven in part wrong
3. Survival of the Fittest
 - 3 - Survival of the Fittest

1. (d) - Learned Behavior
2. Mosquitoes evolved to become DDT resistant. They are more common, because without it they would be more likely to die and not reproduce (an environmental pressure)
4. Furry Evolution FRQ
 - 4 - Furry Evolution FRQ
 1. The left bump (light color) would likely move to the right over time and decrease as the non-mutated would die out until the graph would no longer look bimodal. This would happen because the environment that pressured for light colored fur would no longer exist and would turn rocky over time, pressuring the mice to have dark colored fur instead
 2. (Just chop off the left bump)
 3. It selects for darker fur color. The allelic frequencies would tend towards dark fur in the population over time

5. Constructing a Phylogenetic Tree
 - 5 - Constructing a Phylogenetic Tree
 1. Gene flow - they literally leave or enter the population; Natural Selection - the environment favors a particular phenotype, so it would slowly lead to that over time
 2. Table 1



The Penguin, because there are only 7 genomic differences compares to 20 to Donkey and more to the rest.

6. Mechanisms of Evolution
 - 6 - Mechanisms of Evolution

| Term | Definition |
|----------------------|--|
| Bottleneck effect | Small populations are at higher risk for random genetic factors |
| Genetic drift | Cheetahs have little genetic variation due to dwindling populations |
| Founder effect | Dutch-descended S. Africans have a high rate of Huntington's disease |
| Natural selection | Differential reproductive success; 'survival of the fittest' |
| Disruptive selection | Medium-sized beaks of finches are a poor fit for the environment |

| Term | Definition |
|-----------------------|--|
| Directional selection | The tendency for larger individuals to survive |
| Artificial selection | Brassica oleracea can be bred to create a host of vegetable types such as broccoli, cauliflower and Brussels sprouts |
| Stabilizing selection | A tendency for a population mean to also become the mode |
| Gene flow | New individuals migrate to an island bringing their own genes |

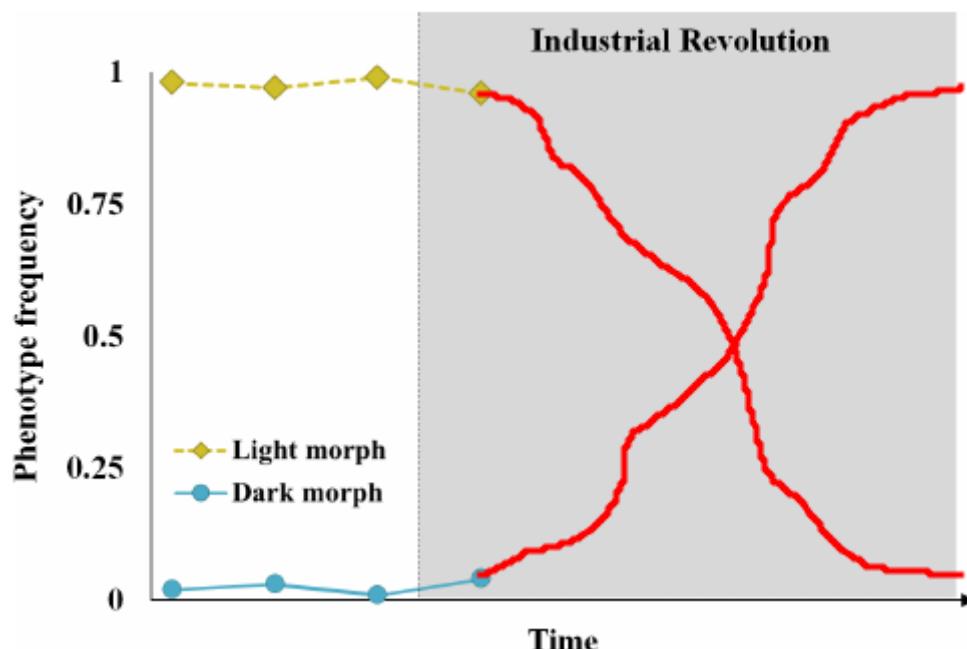
Case Studies

1. Peppered Moth

1 - Peppered Moth

Part 1

1. If the Industrial Revolution led to changes in the moth population through a change in the environment, then the phenotypic ratios of the moth population would change to fit the environment and bow to selective pressures



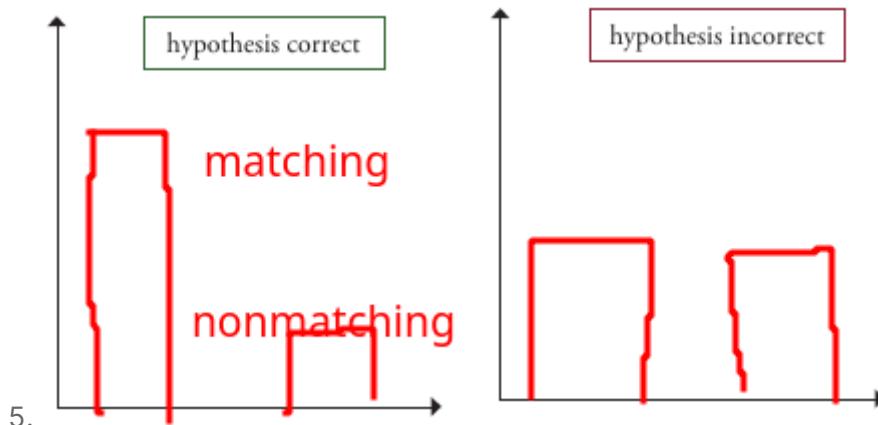
- 2.

Part 2

1. Table 1

| Environment | Phenotype | Predicted number recaptured |
|-------------------------|-----------|-----------------------------|
| unpolluted / light bark | light | 80 |
| unpolluted / light bark | dark | 10 |
| polluted / dark bark | light | 20 |
| polluted / dark bark | dark | 70 |

- Predation from other species, like animals that do not rely on sight for food and instead use things like sound, temperature, or echolocation.
- Force them to perch on a certain tree trunk by releasing them in an area the only has those trees for a long distance and is isolated from trees of other types.
- The exact same experiment will be conducted, but in a more remote testing area



Part 3

- Non-matching moth and tree bark would attract more attention from birds
- Non-matching moth and tree bark would attract more attention from humans
- No, because the way birds see and experience vision is very different from humans, and they also are not at a standstill and looking for moths whom are told exist
- Its non-independent since the same birds are used across different times, and may have a memory of the previous trials
- Place fake light and dark moths on both light and dark trees, with cameras recording them. Count the number of times birds visit or look at each fake sample and compare the occurrences.

Part 4

- Table 2

| Year | Light morphs released | Light morphs eaten | w_{light} | s_{light} | Dark morphs released | Dark morphs eaten | w_{dark} | s_{dark} |
|------|-----------------------|--------------------|-------------|-------------|----------------------|-------------------|------------|------------|
| 2002 | 706 | 162 | 1 | 0 | 101 | 32 | 0.90 | 0.10 |
| 2003 | 731 | 204 | 1 | 0 | 82 | 24 | 0.99 | 0.01 |
| 2004 | 751 | 128 | 1 | 0 | 53 | 17 | 0.82 | 0.18 |
| 2005 | 763 | 166 | 1 | 0 | 58 | 18 | 0.88 | 0.12 |

- $500 * (1 - 0.18) = 410$
- Yes, it should have some evidence that light moths are being selected for after seeing the data.

Part 5

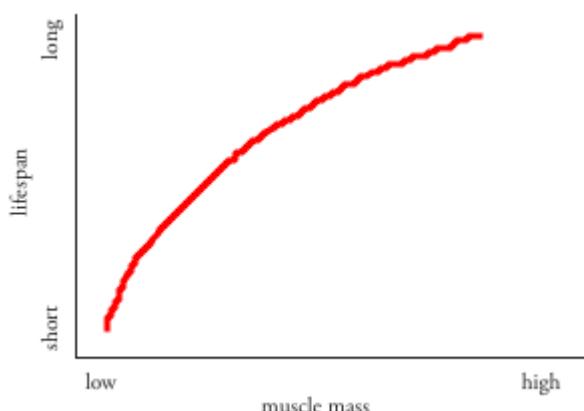
- Birds with shorter wings probably can move faster, and avoid cars coming at them, leading them to have a selective advantage, which can be seen in the population at large
- Watch birds with cameras to see if there is car avoidance from short winged birds.

2. Fish out of salt water

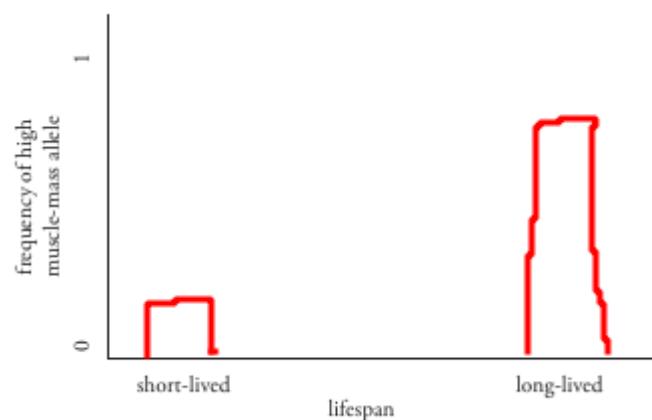
2 - Fish out of salt water

Part 1

1. It must be variable across the population, have selective pressure towards a certain size of muscle mass, and be heritable



2.



3.

4. Yes, like energy efficiency, proportions, coat color

Part 2

1. maybe like 7, because most things should remain similar across the same species but some things would be different due to different environmental pressures

2. Table 1

| Trial | Number of different alleles |
|-------|-----------------------------|
| 1 | 7 |
| 2 | 6 |
| 3 | 5 |
| 4 | 7 |
| 5 | 6 |
| 6 | 7 |
| 7 | 7 |
| 8 | 6 |
| 9 | 8 |

| Trial | Number of different alleles |
|-------|-----------------------------|
| 10 | 7 |
| Avg | 6.6 |

3. 6.6, no not really
4. about 20
5. I would say it is quite close as it would all tend towards similar phenotypes in a similar environment anyway
6. Less natural selection would happen because there are less things to select from

Part 3

1. Organelles within the cells of the respective fish, since they may be required to work at different pH levels
2. The genome that would code for the cell walls, or proteins that would aid moving molecules across it, as they may differ in the way they deal with high or low pH molecules
3. There are some abnormally high differences in chromosomes 1, 4, 8, 14, 15, and 28
4. It most likely correlates to differences in genomes to respond to their respective environments (freshwater and saltwater)

Part 4

1. High F_{ST} likely means that there is a difference in those genes
2. Maybe the way that solutes around the cell would be different from saltwater to freshwater fish, as there will likely be more solutes in the saltwater fish, meaning they need to be transported out of the cell more often more likely

Part 5

1. The F_{ST} would likely decrease as it readapts to the new environment, choosing alleles that would be better for this environment through natural selection
2. Its unlikely, but maybe they got flushed out of a river into the ocean. They would likely die because it takes generations to acclimate to such a different environment without easing into it.

Doodle Notes

1. Natural Selection
 - 1 - Natural Selection

How does Natural Selection happen?

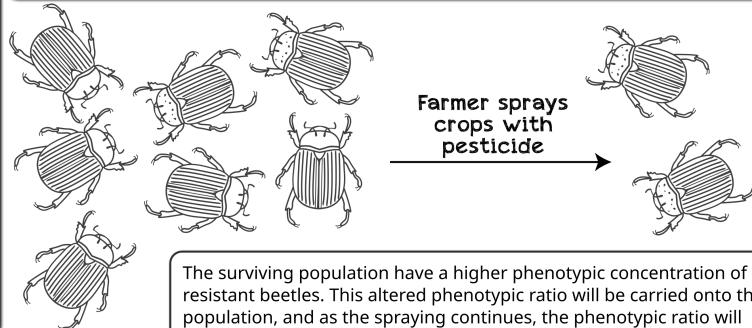
Natural Selection Happens when:

1. There is variation in the phenotypes in a certain population
2. One phenotype has a particular advantage over another either environmentally or reproductively
3. The trait is heritable, or has influence on offspring

The Colorado potato beetle is a pest that eats crops all over the US. There is a portion of the population that are resistant to pesticides (and those that aren't). Resistant beetles have a particular protein that enables them to break down the toxic pesticide quickly, allowing them to survive and pass on the trait.



When beetle populations are sprayed with the pesticide, the resistant beetles have an environmental advantage as they have a higher chance of surviving the spraying. They therefore have an greater fitness in this environment and will be selected for.



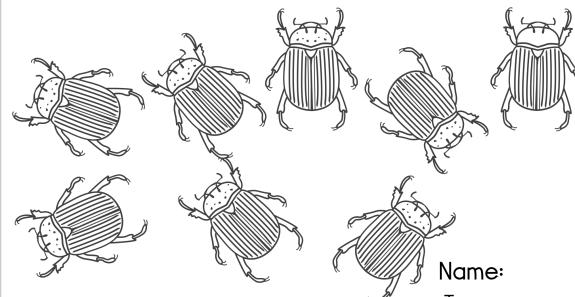
Types of natural selection

In this example, we are seeing Negative Natural Selection, as it gives a consequence to a particular phenotype / multiple phenotypes, instead of giving (a) particular phenotype(s) an advantage against the others.

When an average/middle allele gets selected for, this is called a Balancing Natural Selection as it pulls more of the population towards the mean, instead of pushing the entire mean higher or lower. The average allele tends to be closest to the heterozygote genotype.

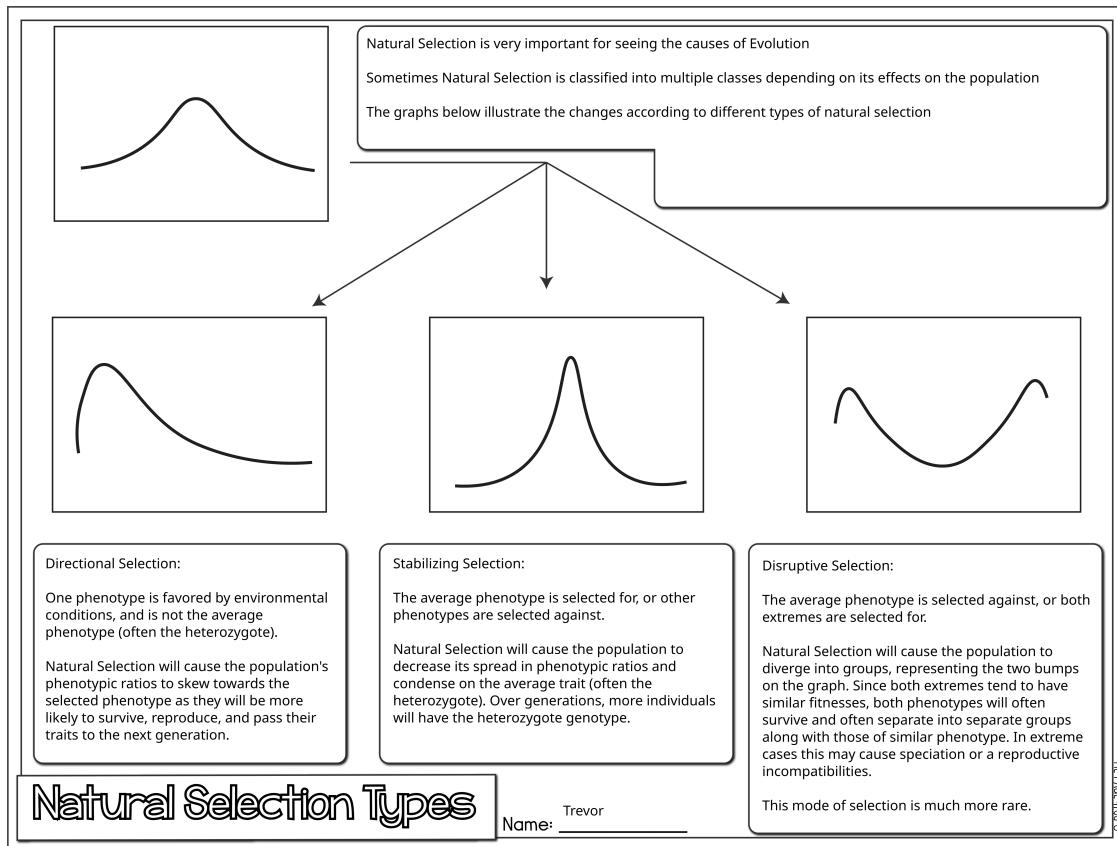
The surviving population have a higher phenotypic concentration of resistant beetles. This altered phenotypic ratio will be carried onto the population, and as the spraying continues, the phenotypic ratio will continue to tend towards having more resistant beetles.

The next generation of Colorado potato beetles



Natural Selection

2. Natural Selection Types
2 - Natural Selection Types



3. Population Genetics
 3 - Population Genetics

Population Genetics:

Scientists use population statistics to figure out how common certain alleles are in a population and how often there are population changes

Peppered Moth Population:

There are two alleles in the English peppered moth population: dark (D) and light (d)

In the early 1800s, there were a lot more light colored moths than dark ones

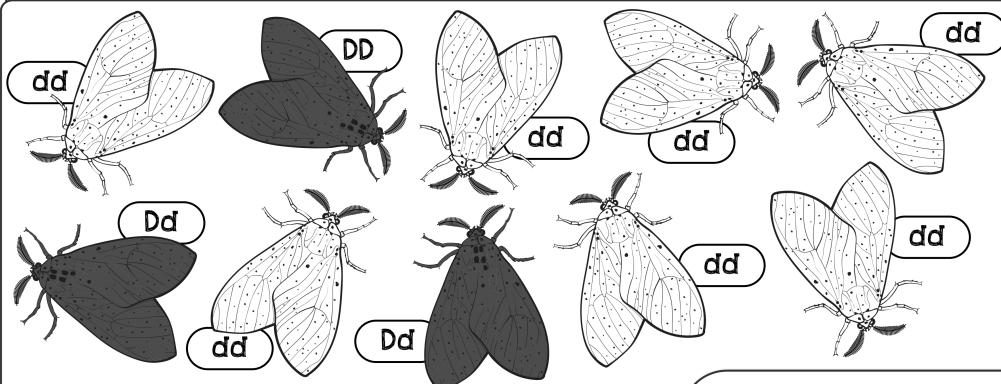
Phenotype Frequencies:

$F(d)$ = light moths / total moths

$$\Rightarrow 7/10$$

$F(D)$ = dark moths / total moths

$$\Rightarrow 3/10$$



Population Sample
~ 1820

Genotype Frequencies:

$F(DD)$ = DD moths / Total Moths

$$\Rightarrow 1/10$$

$F(Dd)$ = Dd moths / Total Moths

$$\Rightarrow 2/10$$

$F(dd)$ = dd moths / Total Moths

$$\Rightarrow 7/10$$

Allele Frequencies:

Allele frequencies are used to measure how population genetics change over time

p is used for the dominant frequency, and q is for recessive in the alleles

$p = D \text{ alleles} / \text{total alleles}$

$$\Rightarrow 4/10 = 1/5$$

$q = d \text{ alleles} / \text{total alleles}$

$$\Rightarrow 16/20 = 4/5$$

Name:
Trevor

Population Genetics

Before the Industrial Revolution

In the early 1800s most of the moths were light in color

Predators were more likely to see dark colored moths, so the dark ones were more frequently predated upon, leading to an increase in the light colored moth phenotype

Light colored moths were hence more likely to survive and reproduce, leading the phenotypic ratios to tend towards the light phenotype over generations

Then the Industrial Revolution happened...

In the late 1800s, soot and sulfur dioxide gas greatly increased in the atmosphere around the moths. This made the trees darker in color

When the trees became darker, the selective advantage the light moths had had fully reversed to favoring the dark moths instead.

Since then, the environment has been selecting for dark colored moths and the phenotypic rates show that.

Population Sample
~ 1890

Allele Frequencies:

$p = D/20 = 11/20$

$q = d/20 = 9/20$

When p and q are changing, this is defined as evolution

Evolution is the change in allele frequency within a population over time

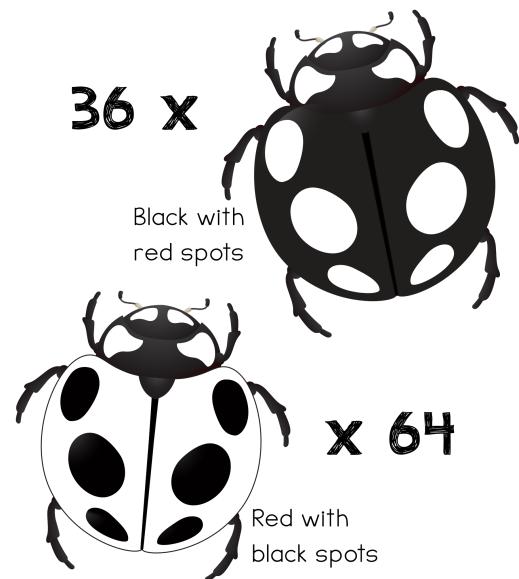
Natural Selection due to a change in the environment is causing the moths to evolve

Natural Selection is one mechanism driving evolution

4. Hardy-Weinberg Equilibrium
4 - Hardy-Weinberg

This is a population in HW equilibrium.

This means that the phenotypic ratios are not changing over time



HW equilibrium is defined as when a population:

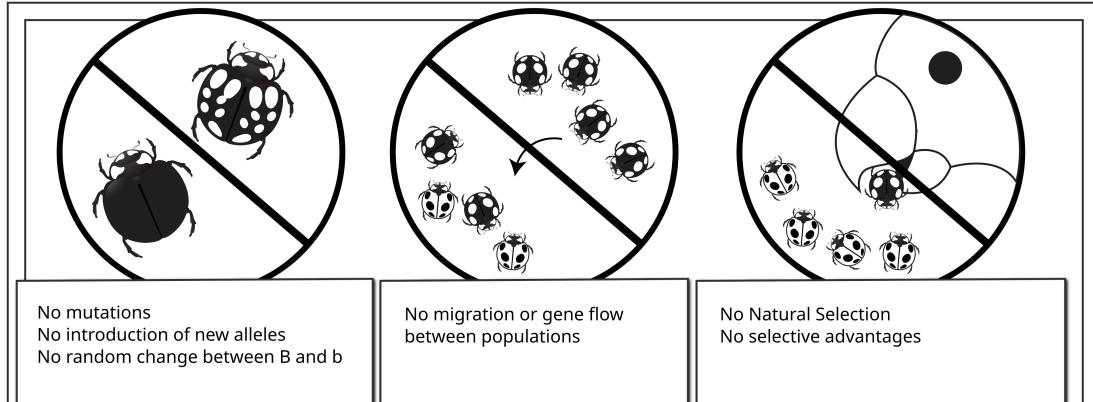
1. Has two alleles of an autosomal diploid gene being studied
2. Has allele frequencies that do not change over time
3. Population is considered non-evolving (no change in phenotypic ratios)
4. Follows the ratios of p and q due to being in equilibrium

| Population Statistic | Formula | Calculate |
|-------------------------------|-------------|--------------------------------|
| Dominant allele frequency | p | $1-0.8 = 0.2$ |
| Recessive allele frequency | q | $\sqrt{0.64} = 0.8$ |
| F(BB) | p^2 | $0.2^2 = 0.04$ |
| F(Bb) | $2pq$ | $2 \cdot 0.2 \cdot 0.8 = 0.32$ |
| F(bb) | q^2 | 0.64 |
| Dominant phenotype frequency | $p^2 + 2pq$ | 0.36 |
| Recessive phenotype frequency | q^2 | 0.64 |

This only works when a population is in HW equilibrium

Name:
Trevor

Hardy-Weinberg Equilibrium



A Population in HW Equilibrium Must Have:

| | |
|--|---|
| X | X |
| ✓ | X |
| A large or infinite size to prevent genetic drift, which causes allele frequencies to change due to random chance. | Random mating Allele frequencies dont change |

5. Mechanisms of Evolution 1
5 - Mechanisms of Evolution 1

Mechanisms of Evolution:

Evolution takes place when the allele frequencies (often abbreviated as p and q) change over time in a population

There are many factors that influence evolution in a population

| | Definition | Effects on Genetic Variation | Effects on Population's Overall Fitness |
|--|--|--------------------------------------|--|
| Genetic Drift | Random fluctuation in allele frequency | Lowers genetic variation | Usually lowers population fitness as populations are less able to adapt to environmental change |
| Nonrandom mating (inbreeding) | Mating occurs between similar individuals | Lowers genetic variation | Usually lowers population fitness, due to higher incidence of lethal alleles |
| Mutation | New mutations arise in a population | Increase genetic variation | Can increase fitness if variety helps the population in the event of an environmental change |
| Gene Flow | A population gets individuals from another population | Normally increases genetic variation | Can increase fitness if variety helps the population in the event of an environmental change |
| Natural Selection (Negative selection) | Natural Selection selects against one phenotype / allele | Lowers genetic variation | Can increase fitness of population in that environment (but may be less able to adapt to change in the future) |
| Natural Selection (Balancing Selection) | Natural Selection supports both phenotypes/alleles | Increases genetic variation | Can increase fitness of population in that environment and help it adapt to future changes |

If allele frequencies change a lot, what can happen?

Speciation may occur, where part of a population becomes so different that they can no longer reproduce with the old population.

Name:
Trevor

Mechanisms of Evolution

6. Mechanisms of Evolution 2
6 - Mechanisms of Evolution 2

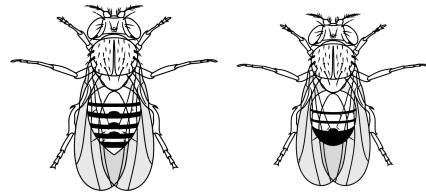
Genetic Drift in the Lab

In the 1950s, Peter Burl performed an experiment with Drosophila to test whether in small populations, genetic drift could cause large changes in allele frequency.

He used flies in his experiment, recording the eye color allele

When those flies had offspring, he removed the first 8 new males and 8 new females to start the next generation, in order to keep the population low

He repeated this experiment multiple times and found that within 19 generations, one allele became extinct



Orange female (Rr) Orange male (Rr)

x 8 x 8

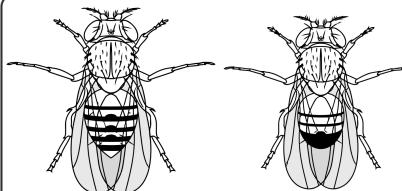
$$p = 8/16 = 0.5$$

$$q = 8/16 = 0.5$$

Founder effect:

Genetic drift coming from small founder populations, often from moving to a new place

Some trials



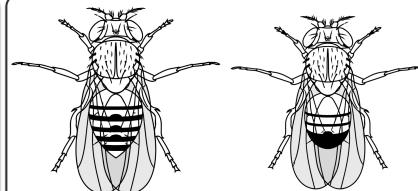
Red female (RR)
x 8

Red male (RR)
x 8

$$p = 16/16 = 1$$

$$q = 0/16 = 0$$

Some trials



White female (rr)
x 8 White male (rr)
x 8

$$p = 0/16 = 0$$

$$q = 16/16 = 1$$

Genetic drift is for when allele frequencies change due to having a small population
This particularly strikes small populations

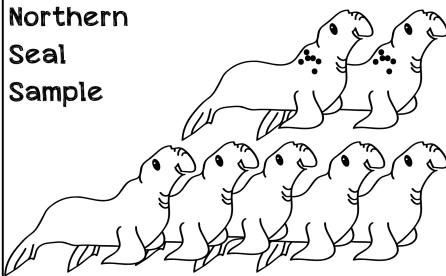
Name:
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Genetic Drift

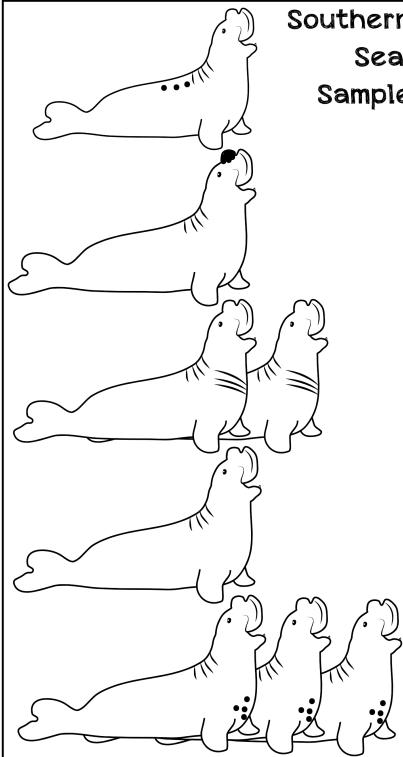
Today's Northern Elephant Seal:

Smaller body size
9 years average lifespan
Many more birth defects
Much less genetic variation in the population

Northern
Seal
Sample



Southern
Seal
Sample



Elephant Seal Example:

Intense hunting of the elephant seal lead to dwindling populations
There are the northern and southern seals, they are different species
At one point there were only 20 nothern seals left, when the southern ones are believed to have over 1000 at all times

Name: _____



Today's Southern Elephant Seal:

Larger body
20-25 years avg
lifespan
Less birth defects

Bottleneck Effect:

This is when a population quickly decreases in size and can easily suffer from genetic drift
After a bottleneck event, the population will increase in size but will have less genetic diversity

Bottleneck Effect

Nonrandom Mating

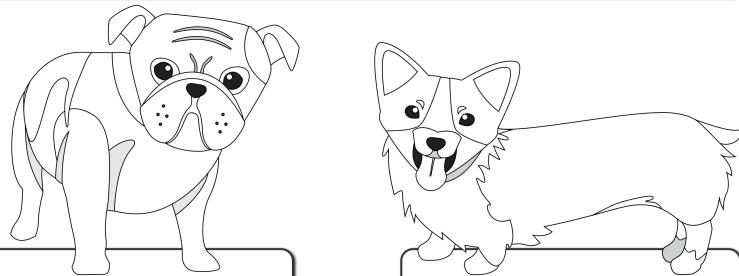
Nonrandom mating by itself does not cause allele frequencies to change in a population

In a small population, it can essentuate genetic drift and cause the overall fitness to decrease faster

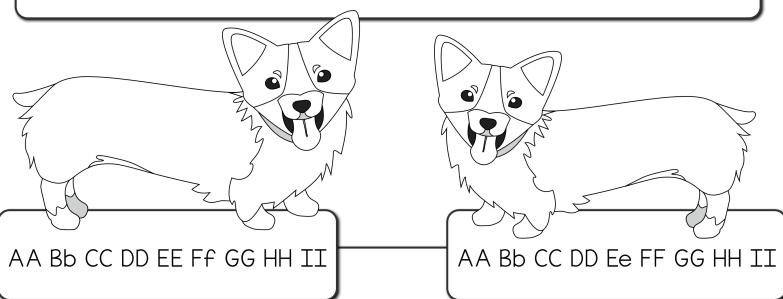
Inbreeding is a form of nonrandom mating. When it happens, homozygotes increase in frequency and heterozygotes decrease

Inbreeding depression is a term scientists use for when inbreeding within a population reduces the average fitness or health of a population

Say there is a recessive allele that leads to negative effects on a species, if these organisms only breed with each other, all of them will have the negative effect



If two unrelated gods mate, they have a low chance of having the same genes



If two related organisms mate, they likely have similar genes already, so negative effects will be continued to the next generations

Name:
Trevor

Nonrandom Mating

7. Evidence for Evolution
7 - Evidence for Evolution

Evidence of common descent

Scientists researching many disciplines accept that many pieces of evidence support the idea that life on Earth comes from a single common ancestor

Evidence that supports a universal common ancestor

| | |
|---|---|
| Natural Selection and Sexual Selection | <p>Natural Selection is one of the driving forces of evolution and can be observed in populations and experiments</p> <p>Natural Selection can cause two populations of the same species to diverge over time in different environments</p> <p>Sexual selection causes changes in populations over time due to reproduction preferences</p> |
| Comparative Anatomy and Adaptations | <p>Species with different lineages but with similar roles in an ecosystem community often develop analogous features, giving evidence of natural selection</p> <p>Species with the same lineage often have homologous features that may have different functions but will maintain a similarity to their common ancestor</p> |
| Comparative Genomics | <p>Almost all organisms share genetic code</p> <p>Higer degree of similarity in DNA between different species</p> <p>Hox genes are shared across many species, using shared DNA for similar functions</p> |
| Fossils | <p>The fossil record shows some organisms that do not exist in the modern age</p> <p>Shows development of complex organisms over time, with semi-smooth changes</p> |
| Biogeography | It's the easiest way to explain the difference and spread of species across the Earth |
| Speciation | <p>Over time new species have arisen</p> <p>Artificial speciation is possible, proving that it can also happen naturally</p> <p>Populations have been observed speciating in the wild</p> |

Name:

Trevor

Evidence For Evolution

8. Comparative Genomics
8 - Comparative Genomics

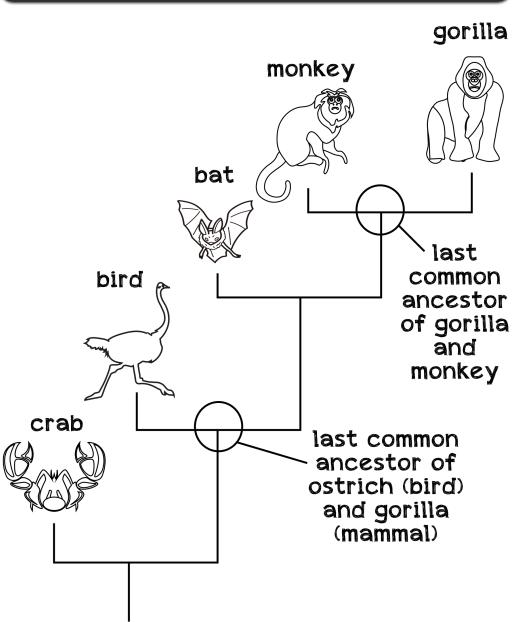
| | U | C | A | G | | |
|---|-----|-----|------------|------------|-------------|--------|
| U | UUU | Phe | UCU UAC | UAU UGC | UGU UGC | U C |
| | UUC | | | Tyr | Cys | A |
| | UUA | Leu | UCA | UAA UAG | STOP Trp | G |
| C | UUG | | UCG | | | |
| | CUU | Leu | CCU CCC | CAU CAC | CGU CGC | U C |
| | CUC | | CCA | CAA | CGA | A |
| | CUA | | CCG | CAG | CGG | G |
| A | CUG | | | | | |
| | AUU | Ile | ACU ACC | AAU AAC | AGU AGC | U C |
| | AUC | | ACA | AAA | AGA | A |
| | AUA | | ACG | AAG | AGG | G |
| G | AUG | Met | Ala | | | |
| | GUU | Val | GCU GCC | GAU GAC | GGU GGC | U C |
| | GUC | | GCA | | GGA | A |
| | GUA | | GCG | GAA GAG | Gly | G |
| | GUG | | | | GGG | |

Universal Genetic Code

- In almost all organisms on earth, the same codons are used to code for the same amino acids!
- This is evidence that there is a Last Universal Common Ancestor that used this coding system in its RNA or DNA to produce its proteins and ribosomes to do the translation process.
- It is thought that organisms that try to deviate from this universal code must have a big disadvantage, which is why very few species today are known to deviate from this code. Scientists don't yet understand why species haven't evolved away from using this code.

Similarity of Genomes

- As scientists sequence more and more genomes of organisms, they find that all organisms on earth share a certain degree of genetic similarity, suggesting they have a universal common ancestor.
- One of the genes that is highly conserved is the sequence of the ribosome. The ribosome seems to be a necessity for life.
- Scientists often take the genetic sequence of the ribosome in different organisms and compare how similar they are to each other.
- The similarity of the gene sequences in two species can be defined in a calculated value called genetic distance. The larger the genetic distance, the further back in time was the split in their ancestry that eventually produced the two species.
- Scientists can use phylogenetic tree diagrams to display their findings in their studies of genetic distance between different organisms.



Name: _____

Comparative Genomics

Coding Regions • Coding regions in the genome are symbolized by arrows. These are the regions in the genome that are transcribed into RNA and those RNAs are in turn translated into a protein. Coding regions are often conserved between different related species.

- In less complex organisms, a high percentage of the genome is made of coding regions. In more complex organisms, a low percentage of the genome is made of coding regions.
- In humans, coding regions are estimated to take up only 2% of the human genome.

Noncoding regions

- Noncoding regions are shown on genome diagrams as lines in between the arrows.
- Some noncoding DNA is transcribed into functional RNA molecules (like transfer RNA, ribosomal RNA, and regulatory RNAs)
- In the human genome, 98% of DNA is noncoding. Scientists don't know how much of that 98% is useful or 'junk DNA'.
- Pseudogenes are also present in noncoding DNA. These are the nonfunctional remnants of genes that scientists think used to function in our ancestors.
- Introns are noncoding regions that are found inside of genes and are cut out (spliced) at the mRNA modification stage.
- Noncoding regions tend to be less conserved between different species.

Name: _____

Parts of a Genome

©Barbara J. Illig

9. Antibiotic Resistance

9 - Antibiotic Resistance Evolution in the Lab

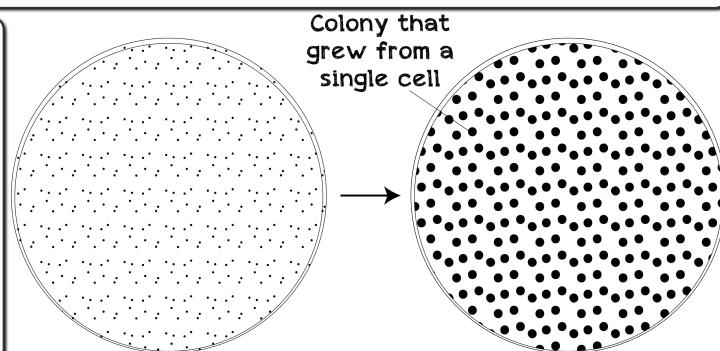
Scientists can demonstrate how natural selection and mutation can cause evolution on a micro-scale

If bacteria is spread across a dish, the bacteria will spread over the dish, with the descendants of a single cell covering the whole dish

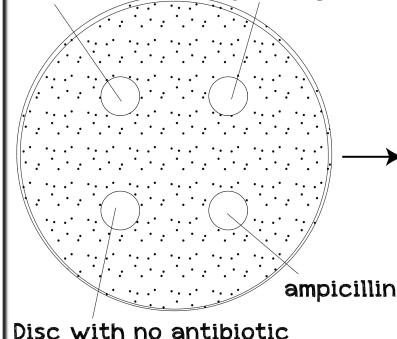
If antibiotic is spread in certain areas, those bacteria will die

If the bacteria around the antibiotic survive, they likely have immunity to that antibiotic

Then, a new lawn will be made with this resistant bacteria and tested with the antibiotic again



Discs placed on top of lawn
tetracycline gentamycin



Zones of inhibition

Colony that grew
from a survivor
while exposed to
antibiotic

Name: Trevor

Effects on Human Health

Antibiotic resistance is a big problem. Overuse of antibiotics could just lead to more resistant bacteria

Antibiotic bacteria can infect people and cause fatal sicknesses

Research is done into finding new antibiotics to kill bacteria effectively. And antibiotic use is often restricted to when necessary

© richarday.au

Antibiotic Resistance: Evolution in the Lab

10. Speciation

10 - Comparison Genomics

Universal Genetic Code

In almost all organisms, the same codons code for the same amino acids

This also acts as evidence that there is a common ancestor

It is believed that organisms that deviate from the code have a severe disadvantage

| | U | C | A | G | |
|---|---------|-----|----------|----------|---|
| U | UUU Phe | UCU | UAU Tyr | UGU Cys | U |
| | UUC | UCC | UAC | UGC | C |
| | UUA Leu | Ser | UAA STOP | UGA STOP | A |
| | UUG | | UAG STOP | UGG Trp | G |
| C | CUU | CCU | CAU His | CGU | U |
| | CUC | CCC | CAC | CGC | C |
| | CUA | Leu | CCA | CGA Arg | A |
| | CUG | | CAG Gln | CGG | G |
| A | AUU Ile | ACU | AAU Asn | AGU | U |
| | AUC | ACC | AAC | AGC Ser | C |
| | AUA | Thr | ACA | AGA Lys | A |
| | AUG Met | | ACG | AGG Arg | G |
| G | GUU | GCU | GAU Asp | GGU | U |
| | GUC | GCC | GAC | GGC | C |
| | GUA | Val | GCA | GGA Gly | A |
| | GUG | | GCG | GGG | G |

Similarity of Genomes

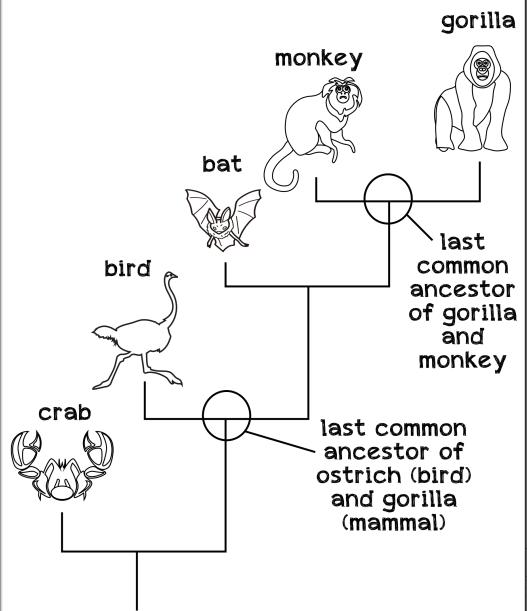
As more genomes are sequenced, we find that more organisms share genetic information, suggesting a common ancestor

One gene that is highly similar across all organisms is the ribosome, a necessity of life

Scientists often take the genetic sequence of the ribosome in different organisms and compare to find how similar they are

The similarity of gene sequences can be calculated to find the genetic difference between the two

Phylogenetic trees are used to visualize this difference



Name:
Trevor

Comparative Genomics

Coding Regions

Coding regions in the genome are symbolized by arrows. These are regions that are transcribed into RNA, which gets translated into proteins.

In less complex organisms, most of the genome is coding, for more complex it is less.

In humans, coding regions are estimated to take up only 2% of the genome.

Noncoding regions

Noncoding regions are shown on the genome as the space between the arrows.

Some noncoding DNA is transcribed into functional RNA molecules, like tRNA, rRNA, etc.

Pseudogenes are also present in noncoding DNA; these are genes that are likely passed from ancestors but aren't used anymore.

Introns are portions of genes that are cut out when being made into proteins.

Noncoding regions vary greatly across organisms, more so than coding regions.

Name: Trevor

Parts of a Genome

Hox Genes

Hox genes are highly conserved across all organisms.

Hox genes code from DNA binding proteins, to activate and turn up transcription factors.

In all animals with bilateral body structures, there is a Hox gene that regulates body structure development.

They are so similar that they can be interchanged across different species and still produce functioning organisms.

Name: _____

Diagram adapted (and simplified/modified for learning purposes) from: Improving Hox Protein Classification across the Major Model Organisms. PLOS ONE. 2010. © Battaglia et al.

POGILs

1. Selection and Speciation

1 - Selection and Speciation

1. Body size and number of Individuals

2. Directional, Disruptive, and Stabilizing

3. This could be due to random mutation, or having multiple selective environments across the population

4. 4

I. They are on average heavier

II. The heavier ones, since they are being selected for

III. Perhaps the heavier ones have more muscle mass, allowing them to run faster and evade predators or aid in predation

5. 5

I. The new population will be larger or smaller than the old average, but not the old average

II. Either heavier ones or lighter ones, but not average ones

III. Heavier ones could have more muscle mass and aid in running away or chasing prey, while lighter ones may be smaller and harder to spot, providing more camo and surprise over prey

6. 6

I. The new population is closer to the average, meaning the spread of the weight is less

II. Those of average weight

III. This could be because heavier ones would be easier to spot and predate upon, and too small would not have muscle mass and cannot evade predators

7. 7

I. Directional selection means that over time and generations, a particular phenotypic trait - more or less than the current average of that trait - of the population will be selected for as they are more well fit for the environment they fit in.

II. Disruptive selection means that over time and generations, a particular phenotypic trait of the population will be selected against as they are unfit for the environment they fit in, so phenotypes displaying either more or less of that trait would be selected for instead.

III. Directional selection means that over time and generations, the current average phenotypic trait of the population will be selected for as they are more well fit for the environment they fit in.

8. 8

I. Directional, it will select for larger beaks

II. Stabilizing, as both large and small are unfavorable, so the average will thrive

III. Disruptive, as there is no "best" for the average, but benefits for those on the outskirts of the trait

IV. Directional, as larger salmons are more likely to be predated upon, so only the smaller ones reproduce

9. AB, CD, EF

10. AB

11. Unable to produce fertile offspring

12. No, all mules are unable to reproduce so their parents - the horse and donkey - are not of the same species

13. No, as they are highly unlikely to mate at all so would likely undergo divergent speciation and at some point be unable to produce fertile offspring
14. Possibly, if a particular population of a species is being directionally selected upon, then those of that species in a different population would be diverging from this population. Over time, they could diverge far enough that they would no longer be able to mate with each other anymore due to custom, environment, or infertility
15. Yes, it would split the population into two groups, those above average and those below. These two populations may be selecting for separate things and may be unlikely to mate. For example, if some of them are selected for colder temperatures, and the other for hotter temperatures, they would likely migrate away, undergo more selective pressures, diverge, and likely never mate or produce fertile offspring due to environmental factors
16. No, because all it does is make the most common traits even more common, which would not change anything about the population in comparison to other populations

17. Table 1

| | 1st Generation | 2nd Generation | 3rd Generation | 4th Generation |
|--------|----------------|----------------|----------------|----------------|
| Light | 4 | 2 | 1 | 0 |
| Medium | 4 | 5 | 5 | 6 |
| Dark | 4 | 5 | 6 | 6 |

18. They are all of equal frequency
19. This is considered a bottleneck situation, as it is a small population and by chance the phenotypic ratios were changed by random chance (the death of two of the same phenotype) This means that the phenotypic frequency of the light phenotype will be lower for coming generations, and will be even more susceptible for random change in future generations
20. Since there is significantly less light phenotype in this population due to small population size, that phenotype will become less likely to be passed on to the next generation. And in such a small population it is not uncommon that it will be completely lost from the population by random events.
21. No, you can only inherit phenotypes that are already present within the population. It has a low chance of reappearing through random mutation if being selected for by the environment.
22. No, in a larger population, losing two individuals of a particular allele would be easily stabilized over time, as the impact on a larger population is minuscule.

Worksheets

1. Hardy-Weinberg Equilibrium
1 - Hardy-Weinberg Equilibrium

1. 1

$$\text{I. } 2Aa = 2(0.19)(0.81) = 30.78\%$$

$$\text{II. } a^2 = (0.81)^2 = 65.61\%$$

$$2. q^2 = 9/900 = 0.01$$

$$q = 0.1$$

$$p = 0.9$$

$$3. q^2 = 0.09$$

$$q = 0.3$$

$$p = 0.7$$

$$p^2 = 0.49 = 49\%$$

$$4. q^2 = 0.38$$

$$q = 0.6164$$

$$p = 0.3836$$

$$p^2 = 0.1471 = 14.71\%$$

$$2pq = 0.4729 = 47.2\%$$

$$5. q^2 = 65/400$$

$$q = 0.4$$

$$p = 0.6$$

$$2pq = 0.48 = 48\%$$

$$6. q^2 = 40/200$$

$$rh : q = 0.447 = 44.7\%$$

$$Rh^+ : p = 0.553 = 55.3\%$$

7. 7

$$\text{I. } w^2 = 9/100 = 0.09$$

$$w = 0.3$$

$$W = 0.7$$

$$\text{II. } 2(0.3)(0.7) = 0.42 = 42\%$$

$$8. a^2 = 1/1,000,000$$

$$a = 0.001$$

$$p = 0.999$$

$$2pq = 2(0.999)(0.001)(14,000) = 27.972$$

$$q^2 = (0.001)^2(14,000) = 0.014$$

$$27.972 + 0.014 = 27.986 \approx 28 \text{ people}$$