

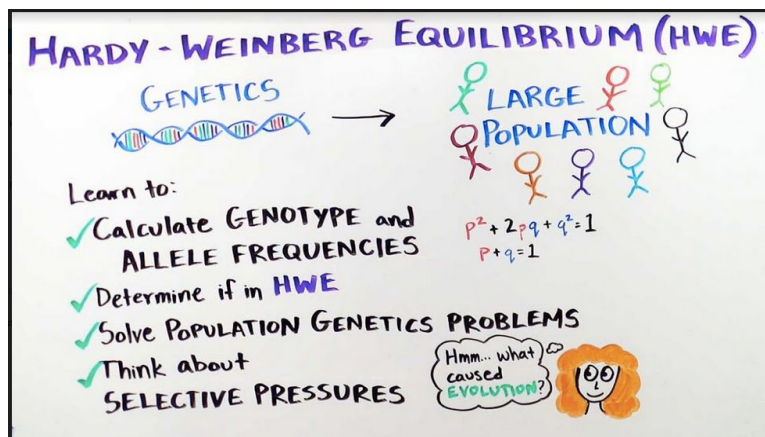
Session 4: How is Evolution Measured

Overview:

In this session, we investigate some of the methods used by scientists to measure evolution. A whiteboard animation introduces Hardy-Weinberg equilibrium (HWE) and explains how it can be used to calculate frequencies of specific alleles in a population. This whiteboard also suggests reasons why allele frequencies in a population may evolve or change over time. Three short video clips (from Drs. Hale, Tishkoff, and Newman) explain methods for generating phylogenetic trees and what they can tell us about the relatedness of species and how long ago they diverged. In our last video, David Haussler shares his excitement about the chance to compare multiple sequenced genomes and identify the genetic innovations that made us who we are today.

First video:

Title: Hardy-Weinberg Equilibrium



Questions for Part 1:

1. Assuming Hardy Weinberg Equilibrium, calculate the expected number of heterozygous individuals in a population of 500 individuals with an allele frequency of $p=0.3$ and $q=0.7$.
 - a. 45
 - b. 105
 - c. 210
 - d. 245
 - e. 490

2. Which term in the Hardy-Weinberg equation defines the frequency of individuals that carry a recessive genetic disorder but do not exhibit the disease?
 - a. q
 - b. p
 - c. q^2
 - d. p^2
 - e. $2pq$

3. By itself, which of the following is not likely to have a major impact on allele frequency?
 - a. Natural selection
 - b. Genetic drift
 - c. Mutation
 - d. Inbreeding
 - e. Both c and d

4. If a population is in Hardy-Weinberg equilibrium the population:
 - a. is not evolving.
 - b. is evolving at a constant rate.
 - c. is small.
 - d. is experiencing some selective pressure.
 - e. b and c only.

5. You are studying the eye-color gene in a population of mice that are in Hardy-Weinberg equilibrium. You analyze the **first** generation and determine that the frequency of the brown-eye (dominant) allele is 0.45. Given this information, what would be the frequency of the blue-eye (recessive) allele be in the **second** generation?
 - a. 0.45
 - b. 0.3025
 - c. 0.55
 - d. 0.495
 - e. The frequency of the recessive allele cannot be determined.

6. What are the assumptions of Hardy-Weinberg equilibrium?
 - a. Small population size, random mating, no selection, no migration, no mutation.
 - b. Large population size, random mating, no selection, no migration, no mutation.
 - c. Small population size, random mating, heterozygotes survive the best, no migration, no mutation.
 - d. Large population size, similar individuals mate, no selection, no migration, no mutation.
 - e. Large population size, random mating, no selection, migrants enter from other populations, no mutation.

7. Sickle cell anemia is a genetic disorder in which red blood cells have a “sickle” shape due to an abnormal allele (HbS) in the hemoglobin gene. Individuals who are homozygous recessive for this disorder are most severely affected, while heterozygous individuals do not manifest the disease. Researchers have found that the frequency of the HbS allele is high in African populations that are hard hit by malaria. Interestingly, individuals carrying the HbS allele are less easily infected with malaria. For this reason, the HbS allele is thought to be an adaptation to living in malaria endemic areas.

a. What type of natural selection is acting upon these African populations? Briefly explain.

b. Imagine that a large population of Africans from one of the areas affected by malaria moves to an island that does not have the mosquitoes that carry the malaria parasite. Would the type of natural selection remain the same as in malaria endemic areas? If not, what type of selection would now act upon this population? Briefly explain.

8. A population of coyotes was genotyped for the mitochondrial cytochrome b locus. The following results were recorded:

Genotype:	CC	Cc	cc
Number:	500	440	60

Calculate the genotype and allele frequencies of the cytochrome b locus for this population.

9. Name three conditions that can change allele frequencies in natural populations. How would allele frequencies change in the next generation in the absence of these processes? Briefly explain.

10. Just in time for Easter, you find a population of cute bunny rabbits in a local forest. You find that some individuals have large ears, while others have smaller ears, and that ear size is caused by one gene inherited in a Mendelian manner. The allele for large ears is dominant over the allele for smaller ears. You sequence this gene and find the following genotypes in 100 bunnies:

Genotype	Number of bunny rabbits
EE	10
Ee	40
ee	50

a. What is the frequency of both alleles in these bunny rabbits? Show your work.

b. What is the expected frequency of genotypes if the bunnies were able to mate and produce another generation of bunnies?

11. You have identified a population of 200 Monarch butterflies and genotyped all of the individuals for the glycoside hydrolase gene that is inherited in a Mendelian fashion. You find that the allele frequency of the p allele is 0.6.
- Assuming that the locus is in Hardy-Weinberg Equilibrium, calculate the expected genotype frequencies in the next generation.

 - How many heterozygous Monarch butterflies would you expect to find?

12. Voles (*Microtus ochrogaster*) were trapped in fields in southern Indiana and were genotyped for the transferrin locus. The following numbers of voles were recorded:

Genotype	TT	Tt	tt
Number	407	170	17

Calculate the allele frequencies of the transferrin locus for this population.

13. Monkeyflowers can have red, orange, or yellow flowers. Based on a model that flower color in these plants is caused by a single gene, with the AA genotype conferring red color, Aa orange color, and aa yellow color, calculate the allele frequency for each genotype in each region. 400 plants were collected from each of three regions, and the flower color of each recorded and listed in the table below.

Flower color	Coastal zone	Central zone	Desert
Red	64	16	125
Orange	192	200	150
Yellow	144	184	125

Second video (Review from Session 1):

Title: Introduction to Evolution

Speaker: Melina Hale

Please watch this video from time 14:54 to 17:53.



Third video:

Speaker: Diane Newman

Title: Phylogeny of Microbes



Fourth video (Review from Session 2):

Title: African Genomics: Human Evolution

Speaker: Sarah Tishkoff

Please watch this video from time 19:37 to 24:07.

Key Challenges in Human Genomics Research



How do ethnically diverse humans differ in regard to genomic and phenotypic variation?



Questions for Part 2, 3 and 4:

1. Which of the following is/are example(s) of methods that scientists use to build a phylogeny tree? Choose all of the answers that apply.
 - a. Studying mitochondrial DNA.
 - b. Studying ribosomal RNA.
 - c. Studying how bones connect.
 - d. Studying skin and/or coat color.
 - e. None of the above.

For questions 2-4, determine if the statement is true or false. If the statement is false, change one word to make it true.

2. It's likely that all species on Earth share microbes as their common ancestor.
3. Chloroplasts and lysosomes were originally bacterial cells, however, they were engulfed by another cell and became intracellular organelles.
4. Nuclear DNA is a great source to study evolutionary pressures.

5. Nina is studying two species of mice that have the same coat color, but they live thousands miles apart and breeding between these two species doesn't occur in nature. Given that these two species have the same coat color, Nina concludes that these two mice must have had a relatively recent common ancestor.
 - a. Is Nina's hypothesis correct? Briefly explain your answer.

 - b. Other than having a close common ancestor, is there any other way that these two species could have evolved to have the same coat color? Briefly explain.

6. As well as mitochondrial DNA, the Y chromosome can be used by scientists to build phylogenetic relationships between hominid species.
 - a. What properties of the Y chromosome allow scientists to use this as a genetic tool to study the relationship between hominid species?

 - b. Compare and contrast the information you could get from studying the Y chromosome vs mitochondrial DNA.

Fifth video:

Speaker: David Haussler

Title: What Can We Learn From Sequencing Our Genomes?



Questions for fifth video:

1. Which of the following is an inherited characteristic?
 - a. Cavities.
 - b. Dislike for horror movies.
 - c. Baldness.
 - d. A and C are correct.
 - e. A and B are correct.
 - f. None of the above.

For questions 2-3, determine if the statement is true or false. If the statement is false, change one word to make it true.

2. Studying nuclear DNA allows scientists to understand evolutionary pressures that shaped the history of the species.
3. Offspring can have genetic differences that are not found in DNA from either parent.
4. If you provide a sample of your DNA to a company, they can give you information about your ancestry and genetic predisposition to diseases. Which type of DNA are they likely using in order to give you these results? Briefly explain.
5. Scientists have found genes that have not changed since early eukaryotic cells evolved. Provide a hypothesis that explains this observation.

Answers for Session 4:

1. Assuming Hardy Weinberg Equilibrium, calculate the expected number of heterozygous individuals in a population of 500 individuals with an allele frequency of $p=0.3$ and $q=0.7$.
 - a. 45
 - b. 105
 - c. **210**
 - d. 245
 - e. 490
2. Which term in the Hardy-Weinberg equation defines the frequency of individuals that carry a recessive genetic disorder but do not exhibit the disease?
 - a. q
 - b. p
 - c. q^2
 - d. p^2
 - e. **$2pq$**
3. By itself, which of the following is not likely to have a major impact on allele frequency?
 - a. Natural selection
 - b. Genetic drift
 - c. Mutation
 - d. Inbreeding
 - e. **Both c and d**
4. If a population is in Hardy-Weinberg equilibrium the population:
 - a. **is not evolving.**
 - b. is evolving at a constant rate.
 - c. is small.
 - d. is experiencing some selective pressure.
 - e. b and c only.
5. You are studying the eye-color gene in a population of mice that are in Hardy-Weinberg equilibrium. You analyze the **first** generation and determine that the frequency of the brown-eye (dominant) allele is 0.45. Given this information, what would be the frequency of the blue-eye (recessive) allele be in the **second** generation?
 - a. 0.45
 - b. 0.3025
 - c. **0.55**
 - d. 0.495
 - e. The frequency of the recessive allele cannot be determined.

6. What are the assumptions of Hardy-Weinberg equilibrium?
- Small population size, random mating, no selection, no migration, no mutation.
 - Large population size, random mating, no selection, no migration, no mutation.**
 - Small population size, random mating, heterozygotes survive the best, no migration, no mutation.
 - Large population size, similar individuals mate, no selection, no migration, no mutation.
 - Large population size, random mating, no selection, migrants enter from other populations, no mutation.

7. Sickle cell anemia is a genetic disorder in which red blood cells have a “sickle” shape due to an abnormal allele (HbS) in the hemoglobin gene. Individuals who are homozygous recessive for this disorder are most severely affected, while heterozygous individuals do not manifest the disease. Researchers have found that the frequency of the HbS allele is high in African populations that are hard hit by malaria. Interestingly, individuals carrying the HbS allele are less easily infected with malaria. For this reason, the HbS allele is thought to be an adaptation to living in malaria endemic areas.

- What type of natural selection is acting upon these African populations? Briefly explain.

This is an example of stabilizing selection that would favor heterozygous individuals. Heterozygotes for HbS have an advantage over individuals who are HbS homozygous because they do not suffer from sickle cell disease, yet they are less likely to be infected by malaria than individuals who are homozygous for the normal hemoglobin gene.

- Imagine that a large population of Africans from one of the areas affected by malaria moves to an island that does not have the mosquitoes that carry the malaria parasite. Would the type of natural selection remain the same as in malaria endemic areas? If not, what type of selection would now act upon this population? Briefly explain.

Natural selection would change to divergent selection. It would start to favor individuals who are homozygous for the normal hemoglobin allele because they would not be affected by malaria or sickle cell anemia.

8. A population of coyotes was genotyped for the mitochondrial cytochrome b locus. The following results were recorded:

Genotype:	CC	Cc	cc
Number:	500	440	60

Calculate the genotype and allele frequencies of the cytochrome b locus for this population.

Total # of coyotes: 1000

Total of # of alleles: 2000 (2 alleles per individual)

of C allele = 500 (2) + 440 = 1440

(Each CC individual has two copies of the C allele & and each Cc individual has one copy of the C allele)

of c allele = 60 (2) + 440 = 560

(Each cc individual has two copies of the c allele & and each Cc individual has one copy of the c allele)

Allele frequency of C (dominant allele) = (# of C allele)/Total # alleles = 1440/2000 = 0.72

Allele frequency of c (recessive allele) = 1 - C = 1 - 0.72 = 0.28

Genotype frequency of CC (homozygous dominant) = #CC individuals/Total = 500/1000 = 0.5

Genotype frequency of Cc (heterozygous) = #Cc individuals/ Total = 440/1000 = 0.44

Genotype frequency of cc (homozygous recessive) = # cc individuals/total = 60/1000 = 0.06

NOTE: If this population was in Hardy-Weinberg equilibrium, you could use the $p^2 + 2pq + q^2 = 1$ equation to solve these problems.

9. Name three conditions that can change allele frequencies in natural populations. How would allele frequencies change in the next generation in the absence of these processes? Briefly explain.

All of the possible processes:

- a. **Small population sizes**
- b. **Mutation**
- c. **Natural selection**
- d. **Migration (gene flow)**
- e. **Nonrandom mating**

Allele frequencies should remain the same in each generation if these processes are not acting on the population. The population is in Hardy-Weinberg Equilibrium and is thus not evolving.

10. Just in time for Easter, you find a population of cute bunny rabbits in a local forest. You find that some individuals have large ears, while others have smaller ears, and that ear size is caused by one gene inherited in a Mendelian manner. The allele for large ears is dominant over the allele for smaller ears. You sequence this gene and find the following genotypes in 100 bunnies:

Genotype	Number of bunny rabbits
EE	10
Ee	40
ee	50

- a. What is the frequency of both alleles in these bunny rabbits? Show your work.

$$p (E) = (20 + 40)/200 = 0.3$$

$$q (e) = (100 + 40)/200 = 0.7$$

- b. What is the expected frequency of genotypes if the bunnies were able to mate and produce another generation of bunnies?

$$p^2 = 0.3^2 = 0.09$$

$$2 pq = 2(.3)(0.7) = .42$$

$$q^2 = 0.7^2 = 0.49$$

11. You have identified a population of 200 Monarch butterflies and genotyped all of the individuals for the glycoside hydrolase gene that is inherited in a Mendelian fashion. You find that the allele frequency of the p allele is 0.6.
- a. Assuming that the locus is in Hardy-Weinberg Equilibrium, calculate the expected genotype frequencies in the next generation.

**Frequency of the p allele = 0.6, therefore the frequency of the q allele is 0.4.
To find the genotype frequency, use $p^2 + 2pq + q^2 = 1$**

$$p^2 = 0.6^2 = 0.36$$

$$2pq = 2(0.6)(0.4) = 0.48$$

$$q^2 = 0.4^2 = 0.16$$

- b. How many heterozygous Monarch butterflies would you expect to find?

**Frequency of heterozygotes = $2pq = 2(0.6)(0.4) = 0.48$
Number of heterozygotes = $0.48 \times 200 = 96$**

12. Voles (*Microtus ochrogaster*) were trapped in fields in southern Indiana and were genotyped for the transferrin locus. The following numbers of voles were recorded:

Genotype	TT	Tt	tt
Number	407	170	17

Calculate the allele frequencies of the transferrin locus for this population.

The total number of voles is 594.

Allele frequencies:

$$p (T) = (814 + 170)/1188 = 0.83$$

$$q (t) = (34 + 170)/1188 = 0.17$$

NOTE: you can also find the allele frequency of q by remembering that $p + q = 1$, so $q = 1 - p$.

13. Monkeyflowers can have red, orange, or yellow flowers. Based on a model that flower color in these plants is caused by a single gene, with the AA genotype conferring red color, Aa orange color, and aa yellow color, calculate the allele frequency for each genotype in each region. 400 plants were collected from each of three regions, and the flower color of each recorded and listed in the table below.

Flower color	Coastal zone	Central zone	Desert
Red	64	16	125
Orange	192	200	150
Yellow	144	184	125
Frequency of A	0.4	0.58	0.5
Frequency of a	0.6	0.42	0.5

Questions for Part 2, 3 and 4:

1. Which of the following is/are example(s) of methods that scientists use to build a phylogeny tree? Choose all of the answers that apply.
 - a. **Studying mitochondrial DNA.**
 - b. **Studying ribosomal RNA.**
 - c. **Studying how bones connect.**
 - d. Studying skin and/or coat color.
 - e. None of the above.

For questions 2-4, determine if the statement is true or false. If the statement is false, change one word to make it true.

2. It's likely that all species on Earth share microbes as their common ancestor.
True.
3. Chloroplasts and lysosomes were originally bacterial cells, however, they were engulfed by another cell and became intracellular organelles.
False; Lysosome mitochondria
4. Nuclear DNA is a great source to study evolutionary pressures.
True.

5. Nina is studying two species of mice that have the same coat color, but they live thousands miles apart and breeding between these two species doesn't occur in nature. Given that these two species have the same coat color, Nina concludes that these two mice must have had a relatively recent common ancestor.
- Is Nina's hypothesis correct? Briefly explain your answer.
Her hypothesis is incorrect. Phenotype does not provide enough evidence to conclude that these two species are related by a common ancestor. She needs to compare their genomes determine their relatedness.
 - Other than having a close common ancestor, is there any other way that these two species could have evolved to have the same coat color? Briefly explain.
Convergent evolution. If these two mice populations live in similar environments, the same selective pressure could have led both species to evolve the same coat color.
6. As well as mitochondrial DNA, the Y chromosome can be used by scientists to build phylogenetic relationships between hominid species.
- What properties of the Y chromosome allow scientists to use this as a genetic tool to study the relationship between hominid species?
Similar to mitochondrial DNA, the Y chromosome is inherited without recombination.
 - Compare and contrast the information you could get from studying the Y chromosome vs mitochondrial DNA.
Mitochondrial DNA traces the female lineage, while the Y chromosome traces male lineage. Migration patterns between females and males are sometime different, and therefore they show a different side of the hominid evolutionary history.

Questions for fifth video:

- Which of the following is an inherited characteristic?
 - Cavities.
 - Dislike for horror movies.
 - Baldness.**
 - A and C are correct.
 - A and B are correct.
 - None of the above.

For questions 2-3, determine if the statement is true or false. If the statement is false, change one word to make it true.

2. Studying nuclear DNA allows scientists to understand evolutionary pressures that shaped the history of the species.

True.

3. Offspring can have genetic differences that are not found in DNA from either parent.

True.

4. If you provide a sample of your DNA to a company, they can give you information about your ancestry and genetic predisposition to diseases. Which type of DNA are they likely using in order to give you these results? Briefly explain.

Genetic predisposition: For this they are likely using nuclear DNA. Most disease predisposition is encoded in the nuclear DNA.

Ancestry: For this they are likely using mitochondrial DNA, although they could use the Y chromosome for male individuals.

5. Scientists have found genes that have not changed since early eukaryotic cells evolved. Provide a hypothesis that explains this observation.

Genes that are essential for the cell function are unlikely to change through evolution. Any mutation to an essential gene would have encountered strong negative selective pressure.