

Upon completion of *Domesticating Dogs (WB)*, students should be able to:

1. Describe mutation in the context of a DNA sequence.
2. Explain how random genetic drift can affect the frequency of a mutation in a population.
3. Predict that, on average, a new neutral mutation in one individual is unlikely to spread through a population over many generations.
4. Define what it means for a mutation to become "fixed" in a population.
5. Describe how the number of DNA sequence differences between two related populations correlates with the amount of time since the populations split.
6. Given three related populations, predict which two are likely to be more closely related, based on the number of DNA sequence differences between each pair of populations.
7. Understand that the number of neutral DNA sequence differences between two populations increases linearly over time.
8. Use the number of DNA sequence differences between multiple related populations to reconstruct an evolutionary tree of those populations using UPGMA.
9. Given an evolutionary tree of populations or species, answer questions about the evolutionary relationship among those populations.