SI Genetics- Full Discipline Demo

Phylogenetics

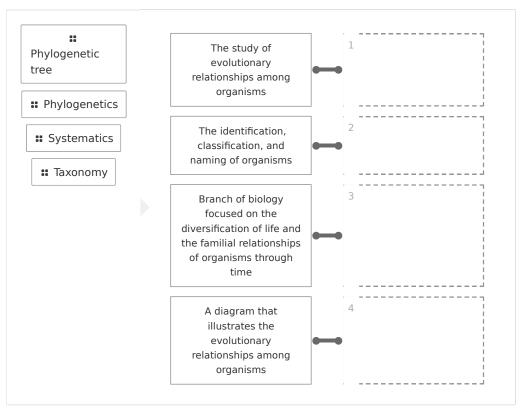
Final Report - Answer Guide

InstitutionScience Interactive UniversitySessionSI Genetics - Full Discipline DemoCourseSI Genetics- Full Discipline Demo

Instructor Sales SI Demo

Test Your Knowledge

Match each term with the best description.

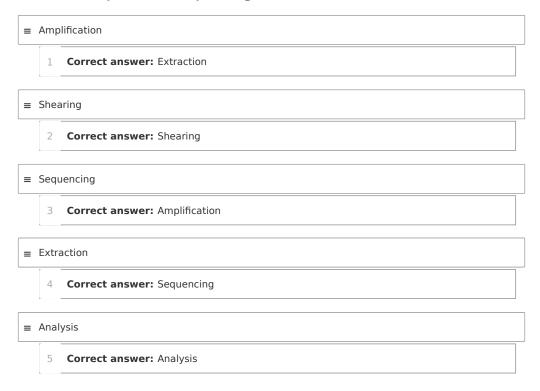


Correct answers:

1 Phylogenetics 2 Taxonomy 3 Systematics 4 Phylogenetic tree



Order the steps of DNA sequencing from first to last.



Exploration

The pattern of branching in a phylogenetic tree suggests how organisms evolved from common ancestors.

	True False	~
Ove	er time, shared DNA sequences accumulate differences through	
	extinction	
0	mutation	~
C	attenuation	
	senescence	



Closely related species have similar DNA sequences.		
│ ○ True		
□ False		
Exercise 1		
Why are DNA sequence reads used to determine the relatedness of organisms?		
Related organisms share DNA sequences that were present in a common ancestor. Over time, the shared DNA sequences accumulate differences through mutation. Distantly related organisms have more differences in their shared DNA sequences because more time has elapsed since they shared a common ancestor. Closely related species have had little time to accumulate mutations and therefore have similar DNA sequences.		
What do your results recorded in Data Table 1 suggest about the relationship between rainbow trout, brown trout, and common carp? Explain your answer by referencing the number of nucleotide differences between each species.		
The results recorded in Data Table 1 indicate that brown trout are more closely related to rainbow trout than to common carp. Only five nucleotides differ in the 840-940 section of the sequenced 12S gene between brown and rainbow trout. Conversely, over 80 nucleotides differ in the same section of the gene between rainbow trout and common carp.		
What does the phylogenetic tree uploaded into Photo 2 suggest about the evolutionary history of common carp, brown trout, and rainbow trout?		
The phylogenetic tree uploaded into Photo 2 suggests that brown and rainbow trout share a more recent ancestor with each other than is shared with common carp.		



Photo 1: DNA Sequence Read Comparison

(SAMPLE ANSWER BELOW)



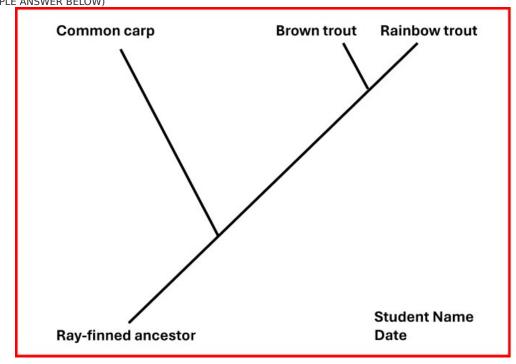
Data Table 1: Gene Sequence Comparison (SAMPLE ANSWER BELOW)

Species Nucleotide differences from rainbow trout



Brown trout	5
Common carp	80

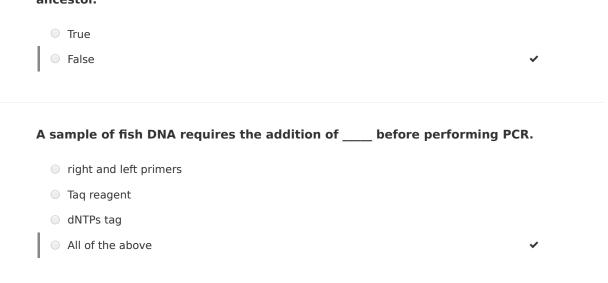
Photo 2: Phylogenetic Tree (SAMPLE ANSWER BELOW)



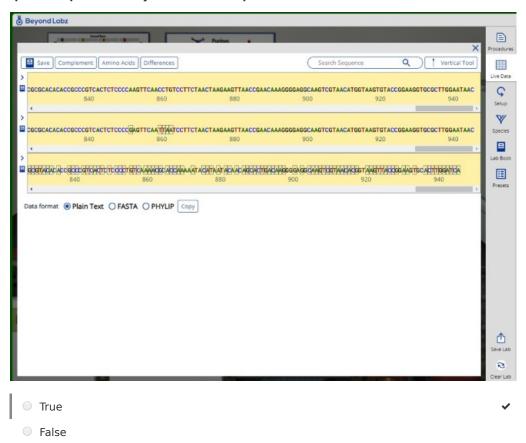
Competency Review is the study of evolutionary history and relationships of organisms. Phylogenetics Taxonomy Systematics Phenetics Organisms with a more recent common ancestor are more closely related than organisms with a less recent common ancestor. True False Molecular phylogenetics utilizes modern laboratory techniques to compare and analyze ____ from organisms. body length total mass DNA sequences gut flora The amplification step of DNA sequencing is performed using ____ techniques. capillary gel electrophoresis polymerase chain reaction paper chromatography restriction enzyme



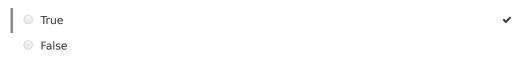
Distantly related organisms have more similarities in their shared DNA sequences because more time has elapsed since they shared a common ancestor.



The DNA read comparison below indicates that the species represented by the middle sequence is more closely related to the reference sequence than the species represented by the bottom sequence.



Rainbow trout and brown trout share a more recent common ancestor with each other than either species shares with common carp.



Extension Questions

A pharmacology researcher has identified a medically important compound from a newly discovered, but endangered, plant species. Apply your knowledge of the principles of phylogenetics to suggest how the researcher could locate other sources for the compound to avoid extirpating the newly discovered plant species.

(SAMPLE ANSWER BELOW)

The pharmacology researcher could extract DNA from the endangered plant and sequence a DNA fragment shared with more abundant plant species. The sequence could then be compared to sequences from abundant plant species to determine which are most like the endangered species. Abundant species with the most similar sequences should be considered to share the most recent common ancestor and therefore are most likely to have genes associated with the medically important compound.