Study Guide
Introduction to Evolution
Lecture 5: Molecular Phylogenies

Important Terms and Concepts

Agarose Gel
Alignment
Allozymes
Annealing DNA
Antibodies
Antigen
Capillary DNA Sequencer
Chloroplast DNA
Clustal
Coding DNA Region
Codon
Contig Assembly
Cytochrome C Protein
Deletion
Denature DNA
Dideoxy-nucleotides
DNA-DNA Hybridization
Exon
FastA Format
Gaps
Gap Penalty
Genes
Genetic Code
Genome
Homoplasy
Immunology
InDel
Insertion
Intron
Kary Mullis
Macromolecules
Melting DNA
Microsatellites
Micromolecules
Mitochondrial DNA
Multiple Sequence Alignment
Next Generation Sequencing
Non-coding DNA Region
Nuclear Genome
Nucleotide

Polymerase Chain Reaction
Purine
Primer
Pyrimidine
Repetitive DNA
Restriction Enzyme
Restriction Site
RFLP
Sanger Sequencing Method
Serology
Single Copy Genes
Spacer Region
Starch Gel Electrophoresis
Taq Polymerase
Transcription
Transition
Translation
Transversion
Voucher Specimen

Study Questions

1. What are the advantages of using molecular data to determine phylogenies as opposed to using morphological data?

2. How do researchers use antigens-antibody reactions in making phylogenetic determinations? Explain the basic procedure for DNA-DNA hybridization studies.

3. What is the basis for using gel electrophoresis to separate DNA or proteins? What kind of information can be obtained from allozymes and how can it be used?

4. What are restriction enzymes and how can they be used to generate data for phylogenetic analysis?

5. How does the polymerase chain reaction work? What are its advantages? What are primers?

6. What are the components of a PCR reaction? Diagram a typical thermal cycle that takes place in PCR. What happens in each temperature?

7. What factors do you have to consider when choosing a gene region for phylogenetic comparison?

8. What is the difference between coding and non-coding DNA regions, and why is this significant for phylogenetic studies?

9. What three genomes are found in organisms? How do they compare?

10. Why is sequence alignment such a crucial step in preparing and analyzing a matrix if DNA sequences for phylogenetic analysis?

11. Can one find homoplasy in aligned DNA sequences? In phylogeny reconstruction, why are homoplasious traits not useful?

12. Outline the steps one goes through from planning a study and collecting material through the sequencing and analysis?

13. What is the basis for the Sanger dideoxynucleotide sequencing reaction? How are the sequences generated and visualized?

14. What are the differences between Sanger sequencing and Next Generation Sequencing in terms of generating DNA sequence data?