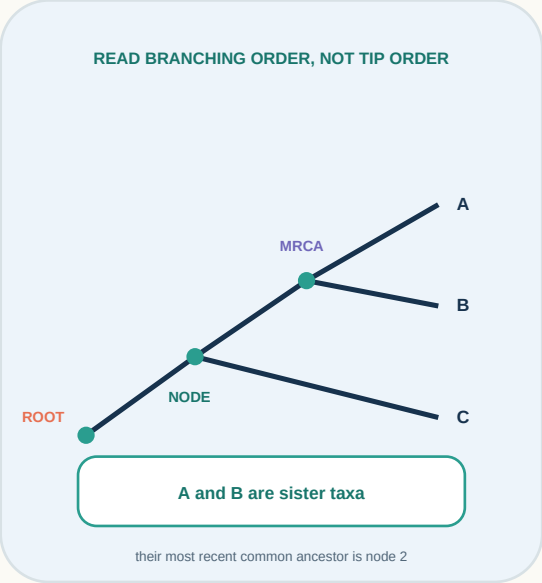
AP BIOLOGY | UNIT 7

TOPIC 7.9

Phylogeny

Phylogenetic trees are testable models that use branching patterns to represent hypotheses about evolutionary relationships.



THE CORE CAUSAL CHAIN

CHARACTERS → collect evidence

COMPARE → find shared traits

BRANCH → infer ancestors

REVISE → test with new data

BY THE END, YOU SHOULD BE ABLE TO...

1. Identify tips, branches, nodes, roots, and clades.
2. Compare relatedness using the most recent common ancestor.
3. Use shared derived characters and an out-group to infer a tree.

CENTRAL IDEA

Relatedness is determined by the recency of shared ancestry. The left-to-right order of the tips does not determine which taxa are closest.

1 Read topology, not visual placement

The meaningful information is the branching pattern: which lineages share a node and how recently that common ancestor occurred.

TREE ANATOMY

TIP / LINEAGE

A sampled taxon or line of descent.

NODE

The most recent common ancestor of branches.

ROOT

The ancestral lineage before all shown splits.

SISTER TAXA

Lineages sharing an immediate common ancestor.

CLADE

An ancestor and all of its descendants.

BRANCH

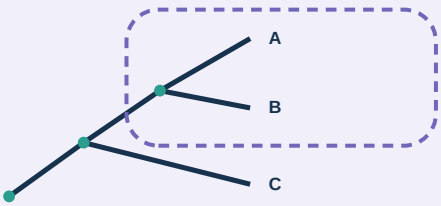
A lineage connecting ancestors and descendants.

ROTATING A NODE DOES NOT CHANGE THE RELATIONSHIPS



The branches can swivel around a node like a mobile; the ancestor-descendant connections stay the same.

A CLADE INCLUDES AN ANCESTOR AND ALL DESCENDANTS



The highlighted group begins at node 2 and includes both descendant tips. Leaving one descendant out would make the group incomplete.

DO NOT READ A LADDER OF PROGRESS

No living tip is the ancestor of another living tip, and a lineage drawn farther right is not automatically more advanced or more recently evolved.

2 Characters generate testable relationship models

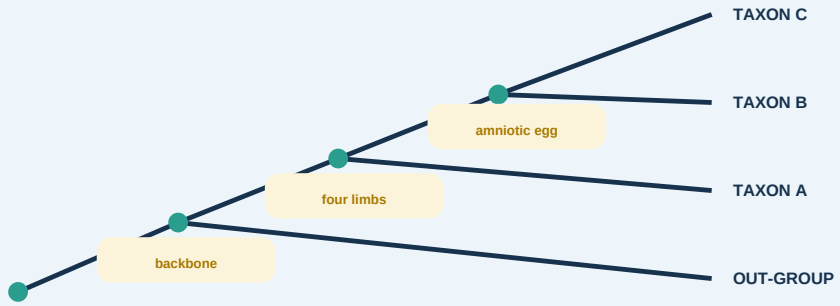
Shared derived characters identify nested groups, while an out-group helps determine which character states are ancestral or derived.

CHARACTER MATRIX

TAXON	BACKBONE	FOUR LIMBS	AMNIOTIC EGG
OUT-GROUP	0	0	0
TAXON A	1	0	0
TAXON B	1	1	0
TAXON C	1	1	1

1 = trait present 0 = trait absent

INFER THE MOST PARSIMONIOUS NESTED PATTERN



TREES ARE HYPOTHESES, NOT PERMANENT FACTS

CLADOGRAM

Shows branching relationships based on shared characters; branch length need not represent time.

PHYLOGENETIC TREE

May include estimates of time or amount of change when the scale is explicitly shown.

NEW EVIDENCE CAN REVISE THE TREE

Fossils, anatomy, DNA, and proteins may favor a different topology. Revision is a strength because the model is tested against evidence.

FINAL MAP

Character data -> shared derived traits -> nested clades -> inferred tree -> testing and revision.