

Bio 1M: Chapter 27: Phylogeny and the history of life

1 Phylogeny — S27.1; Bioskills 3 (back of book)

- Phylogeny is the evolutionary history of a group of organisms
- Based on the idea that organisms are related by evolution
- Understanding these relationships is critical to our understanding of both evolution, and how biological processes work

Phylogenetic trees — Fig B3.1–2

- A **phylogenetic tree** is a model of how a group of organisms descended from a common ancestor
- The model consists of **nodes**, where groups split, **branches** where evolution occurs, and **tips** representing observed **taxa** which are the endpoints of the process we are trying to model.
- A point where more than two branches diverge is called a *polytomy*.
 - Polytomies mean we don't know which event happened first.

Monophyletic group

- A **monophyletic group** is a group *defined by* a single common ancestor
 - All descendants of the ancestor must be in the group
- Monophyletic groups can also be called **clades** or **taxa**.
- As biologists, we should try to think in terms of clades
 - Are flying vertebrates a clade?
 - What are some prominent groups that are not clades?

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Sister taxa

- Sister taxa can be a useful way of thinking about trees
 - two taxa that share a common node
 - You need to take the whole taxon, when appropriate
- E.g., sisters of: *Homo sapiens*; *Homo erectus*; humans?
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Reading phylogenetic trees

- The tree indicates the pattern of branching of **lineages** (evolving lines)
- Tips are *assumed* by the model to be monophyletic
- A tree is a model of how evolution occurred
 - Trees that correspond to the same model are considered equivalent — Figure B3.3

Order of species

- Except for the branching pattern, we don't interpret anything about the order of a tree
 - No species are higher or lower than others, according to the tree
 - We've all been evolving for the same amount of time
- How do we judge how closely related two organisms are, according to a tree?
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1.1 Constructing phylogenetic trees

- First, measure **characteristics** (or **characters**) of the taxa of interest – i.e., anything that seems useful to measure
 - Can be **morphological** (i.e., physical) or genetic
- Then infer (make an educated guess about) the phylogenetic relationships.
 - **Phenetic** approaches use measures of distance between organisms
 - **Cladistic** approaches are based on modeling how evolution occurs on the tree

Morphological vs. genetic characteristics

- Should we use morphological or genetic characteristics to infer phylogenies?
 - We usually have more information from genetic characteristics, and this information is easier to measure precisely
- When should we use morphological characteristics?
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Phenetic vs. cladistic analysis

- Cladistic analysis makes use of the phylogenetic model of organisms evolving from each other to infer phylogenies
- Phenetic analysis ignores the phylogenetic model of organisms evolving from each other while inferring phylogenies
- Which is better?
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- When should we use the other one?
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Synapomorphies

- Classical cladistic analysis is based on **synapomorphies** – shared, **derived** characters
 - as evidence that two taxa are related
- Why do we focus on derived characters?
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 - Example: flight in oaks, birds, fish
 - Example: flight in mosquitoes, birds, fish

What characters are derived?

- Derived compared to what?
 - The common ancestor (characteristics of the common ancestor are called **basal** characters).
 - A **derived** character is a character not shared by the common ancestor of the group that we are currently thinking about
 - One way to think about cladistic vs. phenetic analysis is that phenetic analysis treats derived and basal characters equally

Inferring the common ancestor

- We want to know what the common ancestor was like, so we can tell which characters are derived (as opposed to basal)
- This can be done sometimes by common sense
- Inferring the common ancestor statistically is difficult, for technical reasons
 - We can make use of an **outgroup** to study a group. An outgroup is an organism closely related to, but outside, the group being studied.
 - We assume that the the **root**, or beginning, of the tree is where the outgroup branches from the group

Confusing the phylogeny

- Two species may have the same trait because the trait evolved twice independently – **convergent evolution**
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- An organism may lack a character that its ancestors had – **secondary loss**
 - This can be even more confusing
- Similarities that are not homologies (ie., not due to common ancestry) are called **homoplasies** — Fig. 27.2

Parsimony

- Classical cladistic analysis is based on searching for the tree that can explain the observed data most **parsimoniously** – with the fewest number of changes necessary.
- How do we address the problem of convergent evolution and homoplasy?
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1.2 Example: the evolution of whales

- Whales seem, on the surface, to be pretty different from other mammals, including the closest group, the artiodactyls
- Early phenetic analyses showed whales in their own group (sisters to artiodactyls)
 - Whales lack the distinctive artiodactyl ankle structure (surprise!)
- What about cladistic analysis?

Tree-construction analysis

- Hippos have derived characters A, B, C, D, Z
- Cows have derived character A, Z
- Whales have derived characters B, C, D, E, F, G, H, I, Z
- Calculate distances, and make a phenetic tree
- List synapomorphies, and make a cladistic tree

Tree discussion

- What is the effect of universal characteristics (like Z, above)?
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- What is the effect of unique characteristics (like E, F, G, H, I)
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- Why might whales have more derived characters than the other species?
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Confirmation — Fig 24.11

- Intermediate forms between hippo-like animals and whales
- Discovered *after* they were predicted from DNA evidence!

Lessons

- Phenetic analysis can be misleading
- Any analysis can be misleading, if data are limited
 - This is almost always a concern
- Inferences about the common ancestor can be crucial
 - What if we thought the artiodactyl ancestor was aquatic?
 - * E, F, G, H and I could all be basal characters
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Phylogenetic trees are approximations!

- Phylogenetic trees are tremendously useful and powerful tools for organizing, understanding and analyzing biological data
- But they have limitations:
 - The true history of life cannot really be summarized by a tree
 - * Sex, other forms of combination or gene transfer
 - Trees constructed by humans are not necessarily even the best approximations to the true history of life (and our guesses may change over time)

2 The history of life — S1.4

2.1 The shape of the tree

- Big recent innovations have told us a lot about the history of life
 - Detailed genetic information
 - Sophisticated analysis techniques
 - Electronic computers

Three domains — Fig 1.6

- Bacteria
 - no nuclei; mostly small
 - most of the micro-organisms you see
- Archaea
 - no nuclei; mostly small
 - rarer, or live in more extreme environments
- Eukarya
 - large, nucleated cells

Eukaryotes

- Seem to be sisters with archaea, according to most of our key genes
- Characterized by **nuclei** and **mitochondria**
- Mitochondria came later, and are captured bacteria!
- Where did the nucleus come from?
 - Nobody knows
- The tree is only part of the story!
 - If genes (or even whole bacteria) can be transferred, life is not really a tree

Five kingdoms

- Not really a good way to describe the evolution of life
- So why has this idea persisted for so long?
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2.2 The fossil record — (pp. 526–528)

- A **fossil** is a physical trace of an organism from the past — Fig 27.7
 - Intact fossils retain their form and substance
 - Compression fossils are squashed into a thin film
 - Cast fossils occur when the decomposing piece is replaced by minerals different from the surrounding ones
 - Permineralized fossils occur if minerals infiltrate cells as they are decomposing

Biases in the fossil record

- Scientists have learned a lot from studying fossils, but care is needed. Very few things fossilize, and some things are much more likely to fossilize than others, for example:
 - Things that live in swampy areas, or underground (**Habitat bias**)
 - Hard things, or hard parts of things (**Taxonomic bias**)
 - Things that lived more recently have had less time to be destroyed, or to be buried too deep for recovery (**Temporal bias**)
 - Things that are more abundant have more chances to be preserved (**Abundance bias**)

Accounting for biases

- Because the fossil record is biased, scientists must be very careful about making inferences from what they see
 - Just because you don't see it, doesn't mean that it wasn't there
 - Just because you see a lot, doesn't mean that there were a lot (relatively speaking)
- Trying to figure out what happened based on what kind of fossils we happen to find is tricky

2.3 Putting the timeline together

- Dates of specimens can be inferred using radioactive isotopes (harder than it sounds)
- Geologic inferences can be made about the relative age of different things (for example, if one was deposited on top of another).
- Molecular clocks are based on inferences about how fast things are evolving
- These techniques are complicated, and making the timeline is a difficult and exciting puzzle

3 Processes of diversification

- Diversity sometimes arises gradually, and sometimes dramatically (**radiation** events)
- Species (and families, and bigger groups) sometimes disappear gradually, and sometimes dramatically (**mass extinction** events)

3.1 Adaptive radiations — pp. 530–534

- An **adaptive radiation** occurs when a single lineage produces many descendant species, in a short period of time, that make their living in a variety of different ways
- Triggered by opportunity, either in the environment, or because of the evolution of the organisms themselves

Triggers for adaptive radiation

- Ecological opportunity
 - An organism arrives in an area with no similar organisms
 - A group of competing species is driven extinct (or nearly extinct) by some other cause
- Morphological innovation: an organism comes up with a good, new idea
 - Legs in tetrapods
 - New body plans in the Cambrian explosion
 - Multi-cellularity
- Co-evolution: the evolution of one group creates new niches for another group, and vice versa
 - The insects and the flowering plants

Colonization

- In many different cases, a new kind of organism has colonized an area, and diversified rapidly
- This is an opportunity for studying how evolution can go:
 - What is the same, and what is different, between similar cases?
 - Finches — (earlier chapters)
 - Silverswords in Hawaii — Fig 27.14
 - Anolis lizards — Fig 27.15

Competition

- Mammals did very well after the dinosaurs went extinct
- We have seen major tree extinctions due to introduced diseases in the last century

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Morphological innovation

- A new adaptive mutation can open up further possibilities for adaptation
 - **Hox gene** mutations allowed early animals to develop complex body plans
 - The arthropod body plan
 - * insects, arachnids, crustaceans ...
 - The arthropod body plan
 - * reptiles, mammals ...
 - Flowering plants
 - * This opened many new opportunities for *everyone* (insects, mammals, birds), not just the innovators
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Hox genes — Fig 27.21

- **Hox genes** are involved in determining the identity of different body parts
- Taxa with simpler body structures tend to have fewer hox genes
 - Phylogenetic comparisons provide important evidence that hox genes were involved in evolution of complex body plans
- Evidence that new hox genes were largely created by **gene duplication** events

Gene duplication

- One or more genes may be accidentally duplicated so that the genome has two copies of each gene
- This may make the organism less efficient, and thus be selected against
- It may also allow for innovation. Why?

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3.2 Mass extinctions — (pp. 575-578)

- Five major mass extinctions so far
- The last one (and maybe others) was caused by a cosmic impact
 - It could happen again
- Are we in the middle of a mass extinction now?
 - Extinction rate very high over the last 400 years
 - Time will tell, but we should be worried

Conclusion

- The best way to reconstruct evolution is with a *model* of how it occurred
 - Molecular information, and computer modeling has changed our view of the tree of life
 - life is not really a tree – genetic information can be transferred
- Scientists use many clues to figure out the history of life on earth
 - Fossils, geology, phylogeny
- Life has diversified both gradually, and with dramatic episodes
 - Adaptive radiations, mass extinctions