Bio 1M: Phylogeny and the history of life

1 Phylogeny — S25.1; Bioskill 11 (2ndEd S27.1; Bioskills 3)

- *Bioskills are in the back of your 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

- 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

- 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 — (see Bioskill)

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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Flight as evidence

- Oaks and fish don't fly, but birds do

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- Mosquitoes and birds fly, but fish don't

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What characters are derived?

- Derived compared to what?

  - The common ancestor (characteristics of the common ancestor are called **basal** or **ancestral** characters).
    * What if our flight example was ostriches, hawks, and sparrows?
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  - 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. 25.3 (2ndEd 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?

Activity: 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

- 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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Genetic vs. morphological

- Why was the genetic analysis more effective than the morphological?

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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
  - Our guesses often change over time

2 The history of life — S1.5 (2ndEd 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 1.7 (2ndEd 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 web of life

- The tree is only part of the story!

    - If genes (or even whole bacteria) can be transferred, life is not really a tree

- Reuniting can create new species

    - Hybridization or allopolyploidy

- Wolf-coyote example — `http://advances.sciencemag.org/content/2/7/e1501714`

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. 520–522 (2ndEd pp. 526–528)

- A **fossil** is a physical trace of an organism from the past — Table 25.4 (2ndEd 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

- Orchid phylogeny — `http://www.nature.com/news/2007/070829/full/news070827-4.html`

2.3   Putting the timeline together — Fig. 25.6–7

- 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. 525–527 (2ndEd 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 25.8 (2ndEd Fig 27.14)
    - Anolis lizards — Fig 25.9 (2ndEd 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 tetrapod body plan
        * reptiles, mammals . . .
    - Flowering plants
        * This opened many new opportunities for *everyone* (insects, mammals, birds), not just the innovators
        *

Hox genes — Fig 25.14 (2ndEd 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

    - A rare but important type of mutation
    - Natural selection must have played a role in the development of this much complexity

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 — S25.4 (2ndEd 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
        * sexual mixing occurs at different scales

- 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