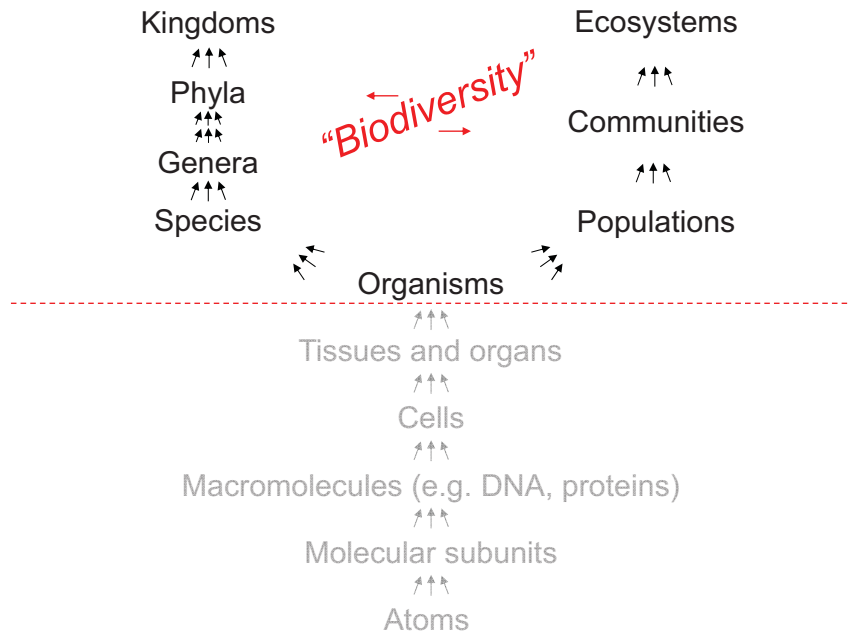
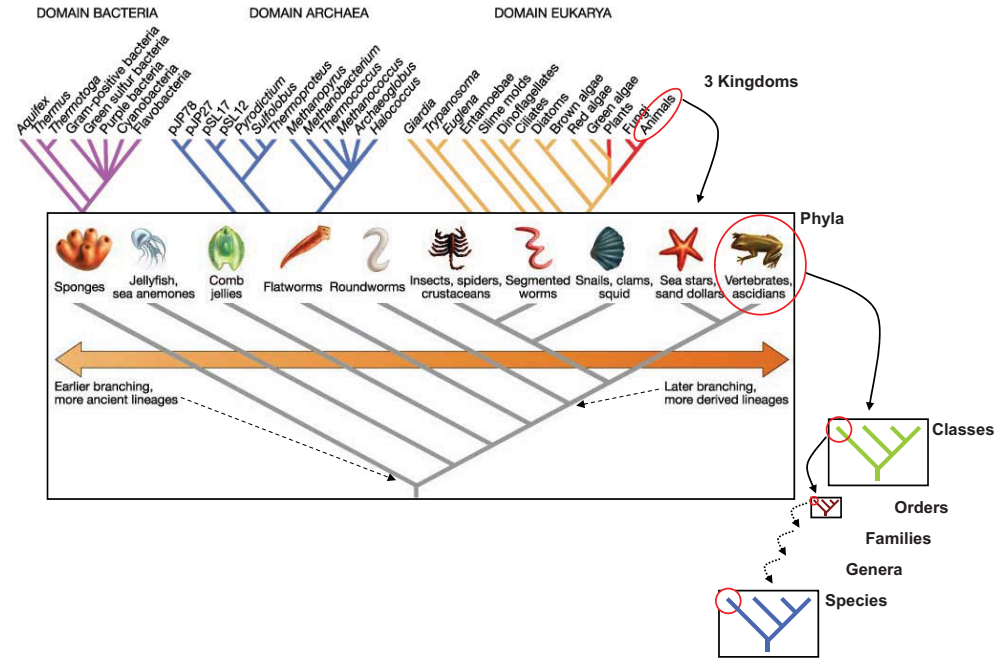


# Biology is hierarchical



# Biology is hierarchical



## Part III. Conserving biodiversity

I. How populations work

II. How communities & ecosystems work

III. The origins of biodiversity

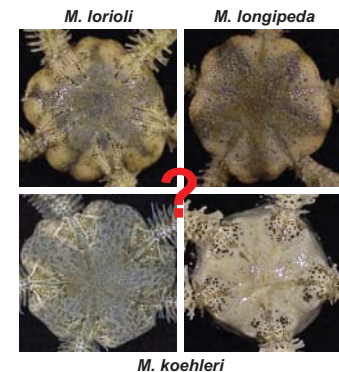
- **Species:** what are they, how are they distinguished, and how do they arise?
- **Phylogenetic trees:** how are they read, how are they produced, and how are they used?
- **Units 8-10:** Surveys of biodiversity and evolutionary innovations

### A. What are species?

Taxonomic units that are “evolutionarily independent”  
 → gene flow becomes low enough that lineages can diverge

### B. How can species be identified?

- **morphological distinctiveness** – useful for quick surveys of diversity



### “morphological species concept”

- ✓ practical?
- ✗ understanding of divergence?
- ✗ reliable?

## A. What are species?

Taxonomic units that are “**evolutionarily independent**”

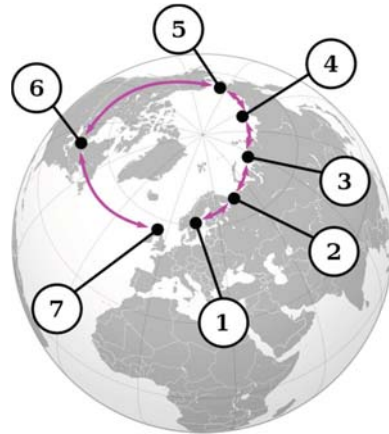
→ gene flow becomes low enough that lineages can diverge

## B. How can species be identified?

- **morphological distinctiveness** – useful for quick surveys of diversity
- **reproductive isolation** – no or inviable hybridization, confirms lack of gene flow



*Larus* gulls form a “ring species”



“**biological species concept**”

- ✗ practical?
- ✓ understanding of divergence?

## C. How do species arise?

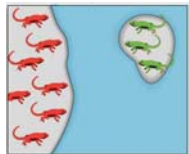
### 1. Genetic **separation** of populations...

→ **allopatric speciation** – involves **separation** by geography

### 2. Genetic **divergence**...

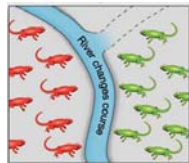
...can occur through:

founder effect



**colonization** of a new habitat

limited gene flow  
genetic drift  
change in selection  
sexual selection



**vicariance** – division of range  
rising of a land bridge (Panama)  
rising water level (Greenland, Madagascar)  
continental separation (ratites on 3 continents)  
etc.

### 3. Reproductive **isolation** (after recontact)...

- ...can occur through:
- **prezygotic reproductive isolation** > no cross-fertilization
  - **postzygotic reproductive isolation** > hybrids are less fit > “reinforcement”

3 steps: **genetic separation**  
**genetic divergence**  
**reproductive isolation**

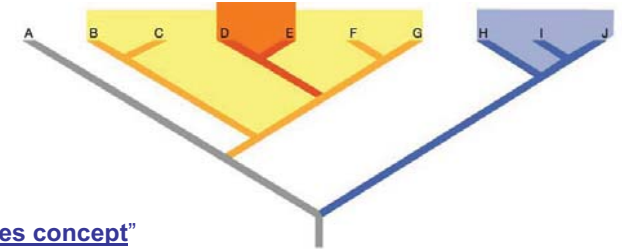
## A. What are species?

Taxonomic units that are “**evolutionarily independent**”

→ gene flow becomes low enough that lineages can diverge

## B. How can species be identified?

- **morphological distinctiveness** – useful for quick surveys of diversity
- **reproductive isolation** – no or inviable hybridization, confirms lack of gene flow
- **monophyly** – history holds information about evolutionary relationships



“**phylogenetic species concept**”

- ✓ practical?
- ✓ understanding of divergence *pattern*?

## C. How do species arise?

### 1. Genetic **separation** of populations...

→ **allopatric speciation** – involves **separation** by geography

→ **sympatric speciation** – involves **separation** by ecological habits

- e.g., differences in preferences (habitat, food, mates)

3 steps: **genetic separation**  
**genetic divergence**  
**reproductive isolation**

### Ex. Apple maggot fly (*Rhagoletis pomnella*)

- alternate feeding preferences promote assortative mating

some do it on apples...



some on hawthorns...



*Rhagoletis pomnella*

## C. How do species arise?

3 steps: genetic separation  
genetic divergence  
reproductive isolation

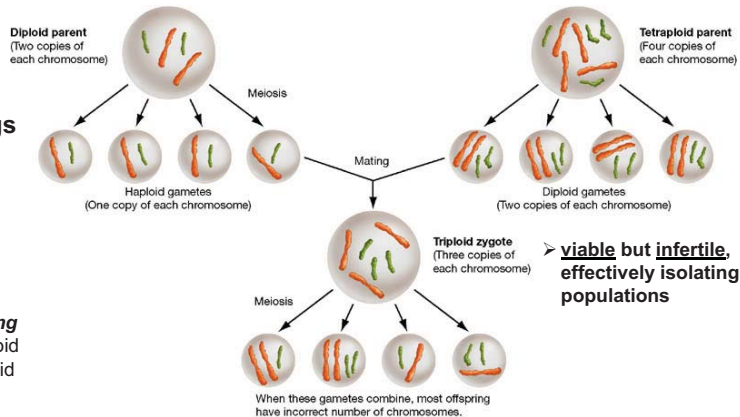
### 1. Genetic separation of populations...

- **allopatric speciation** – involves separation by *geography*
- **sympatric speciation** – involves separation by *ecological habits*  
- e.g., differences in preferences (habitat, food, mates)
- **stasipatric speciation** – involves isolation by *chromosomal incompatibility*  
- e.g., polyploidy, large chromosomal rearrangements

#### Ex. grey tree frogs



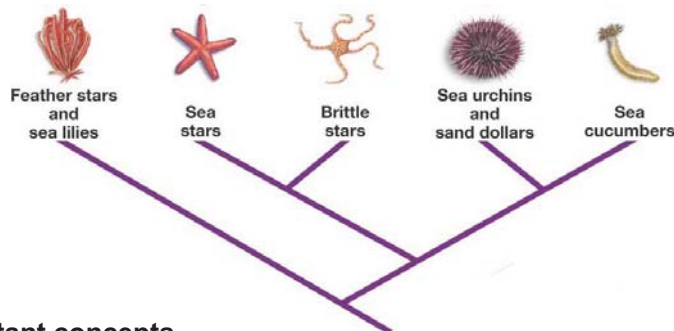
**chromosomal doubling**  
*Hyla chrysocelis* = diploid  
*H. versicolor* = tetraploid



## D. How to read a phylogenetic tree

**phylogeny** = hypothesis of evolutionary relationships  
(pictured as a tree of branching events)

Ex. Phylogeny of taxonomic classes in the phylum Echinodermata



### Important concepts

- What is a **common ancestor**?
- What is a **most recent common ancestor**?
- What is a **clade**?
- What is a **sister taxon**?
- What is meant by **more closely related**?
- Extant taxa are **relatives**, not **ancestors**.
- **Ancestors** were replaced by **descendants**.

## Part III. Conserving biodiversity

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## D. How to read a phylogenetic tree

➤ A **phylogenetic tree is a nested hierarchy of sister groups**

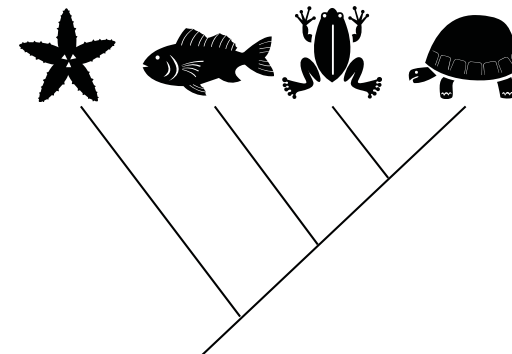
**SINGLE CHOICE.** According to this phylogeny...

1. the sister group to frogs is

- bony fish
- turtles
- echinoderms
- echinoderms + bony fish

2. the sister group to fish is:

- echinoderms
- amphibians
- amphibians + turtles
- echinoderms + amphibians + turtles

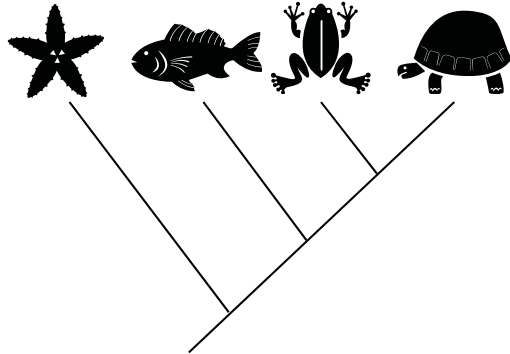


## D. How to read a phylogenetic tree

➤ *Reading a phylogenetic tree is like reading a map of history*

**MULTIPLE CHOICE.** According to this phylogeny, which of the following is true?

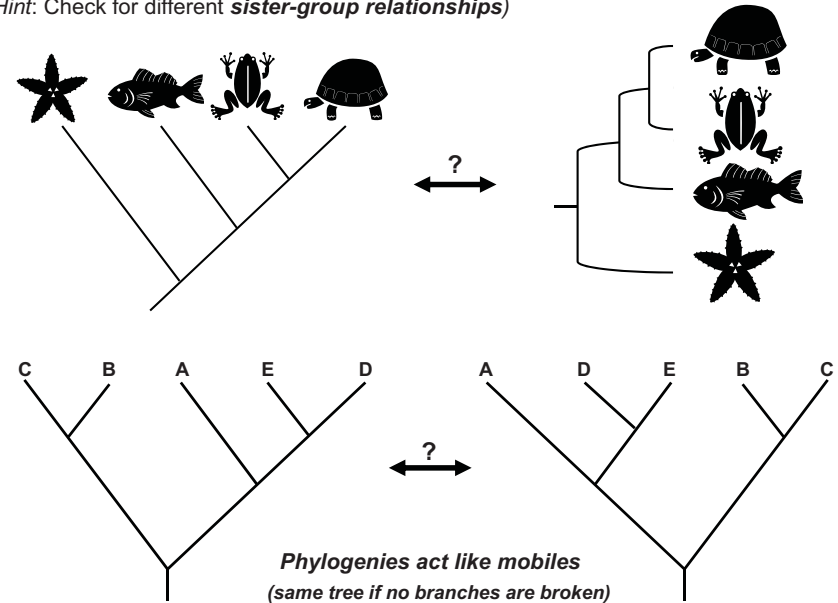
- The frog is more closely related to the **Turtle** than to the **Seastar**
- The fish is more closely related to the **Turtle** than to the **Seastar**
- The fish is equally related to the **Frog** and the **Seastar**
- The seastar is equally related to the **Fish** and the **Turtle**
- The turtle is more closely related to the **Fish** than to the **Seastar**



## D. How to read a phylogenetic tree

*Are these trees different?*

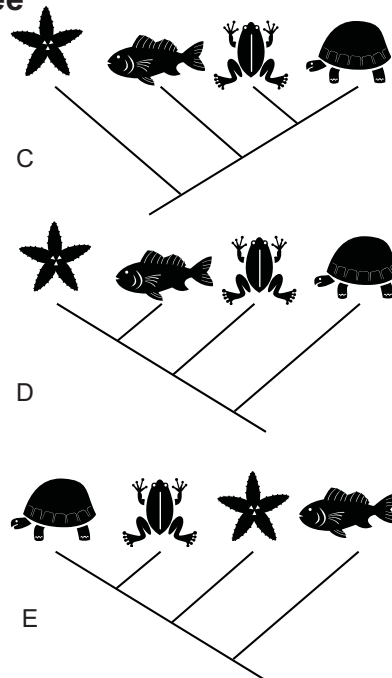
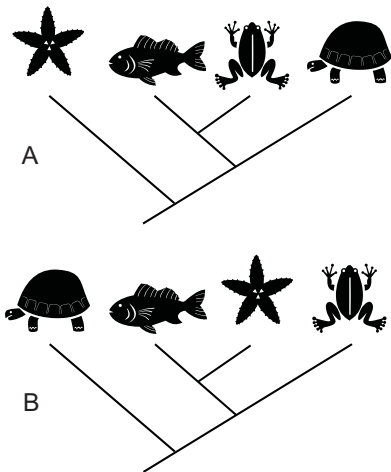
(Hint: Check for different *sister-group relationships*)



## D. How to read a phylogenetic tree

*How many different phylogenetic hypotheses are shown?*

Hint: Look for different *sister-group relationships*

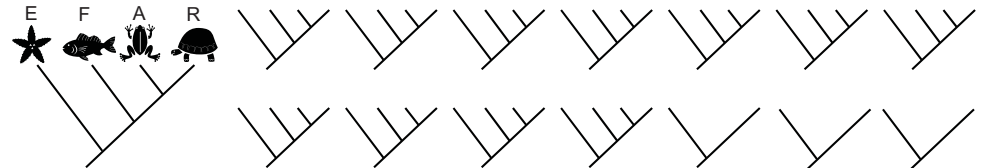


*How many are possible?*

## E. How to infer a phylogenetic tree

**Phylogenetic inference:** which phylogenetic hypothesis is best supported?

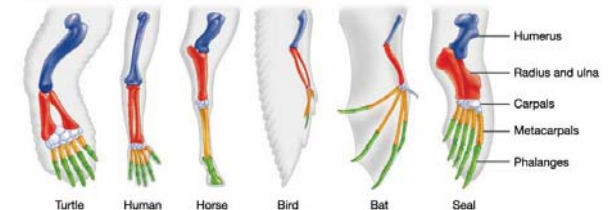
*Ex. Possible hypotheses for 4 taxa (15 total)*



**We expect that closely related taxa will share homologies**  
(= traits in common because they come from a common ancestor)

**Ex. the tetrapod forelimb**

- Different functions**  
(paddling, grasping, walking, flying)
- Different morphologies**  
(horse vs. seal vs. bat vs. bird?)
- But common bones reveal homology**

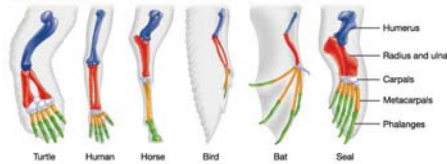




## E. How to infer a phylogenetic tree

**Phylogenetic inference:** which phylogenetic hypothesis is best supported?

Ex. the tetrapod forelimb



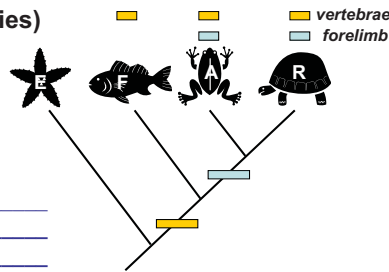
For phylogenetic inference, we must distinguish two levels of homology:

**derived** – a trait found only in the clade of interest (indicates membership in the clade)

**ancestral** – a trait that existed before the clade of interest arose

Only “shared **derived** traits” (= synapomorphies) show close evolutionary relationships

Q: Why?



Qs: For which clade are...

...vertebrae a shared, derived trait?

...vertebrae a shared, ancestral trait?

...forelimb a shared, ancestral trait?

## E. How to infer a phylogenetic tree

**Complication: traits may be shared for different reasons**

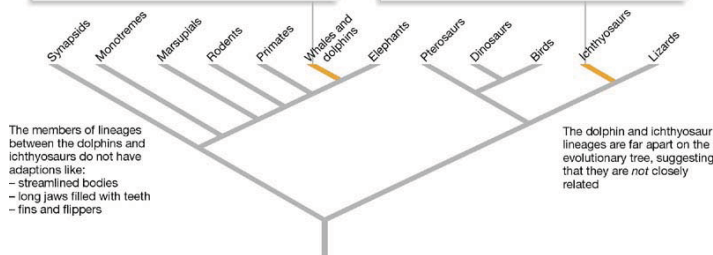
- common ancestry (**homology**)
- derived independently (**homoplasy**)

### Examples of homoplasy

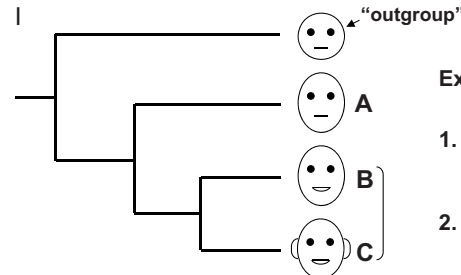
Ex. wings in bats & birds



Ex. swimming and feeding morphologies of dolphins and ichthyosaurs

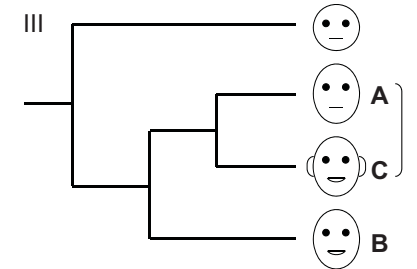
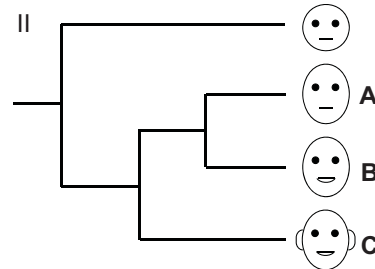


## E. How to infer a phylogenetic tree



Ex. 3 species (A,B,C) + outgroup  
3 traits (long head, smiling mouth, ears)

1. How many hypotheses are possible?  
*Hint: how many ways can you draw sister-group relationships?*
2. Which species are closest relatives?  
*Hint: what is the simplest way to account for distribution of traits?*
3. Which traits were “informative”?

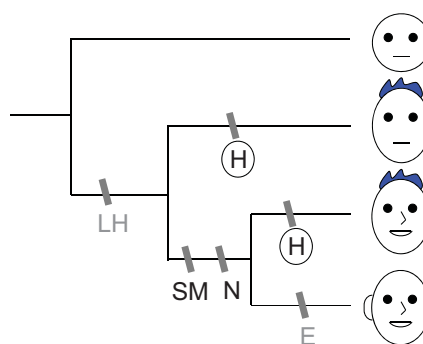


## E. How to infer a phylogenetic tree

one pattern could be caused by different evolutionary histories

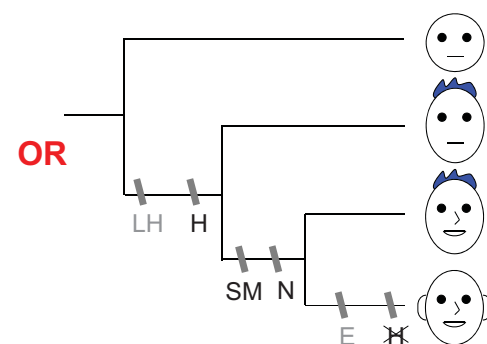
1. **homoplasy:** independent evolution of hair

(H) – homoplasious event



2. **homology:** plus one reversal to hairless

(X) – loss

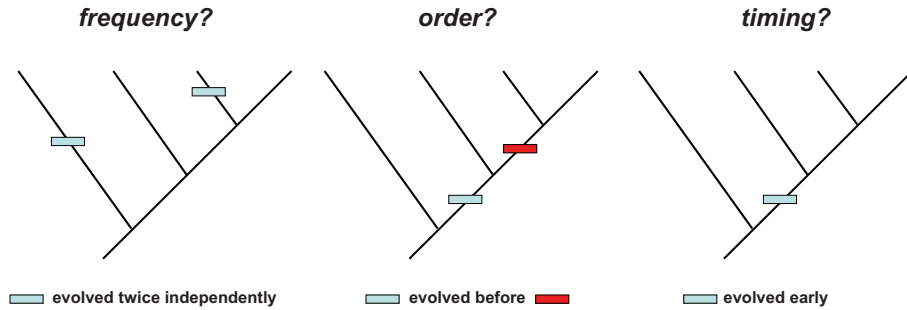


In either case, 2 evolutionary events needed to explain distribution of hair

## F. How phylogenetic trees are used

### 1) To study trait evolution

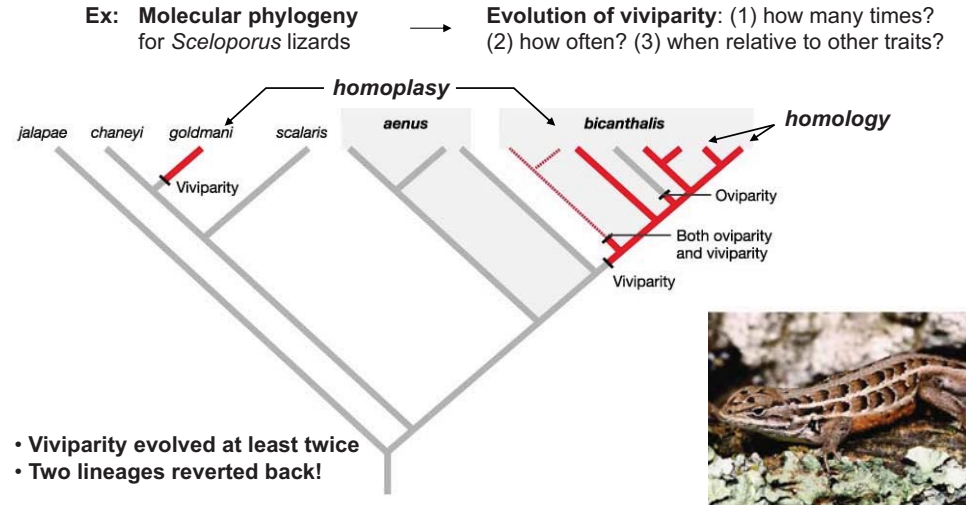
Find the best supported phylogenetic hypothesis → “Map” traits to infer evolutionary changes



## F. How phylogenetic trees are used

### 1) To study trait evolution

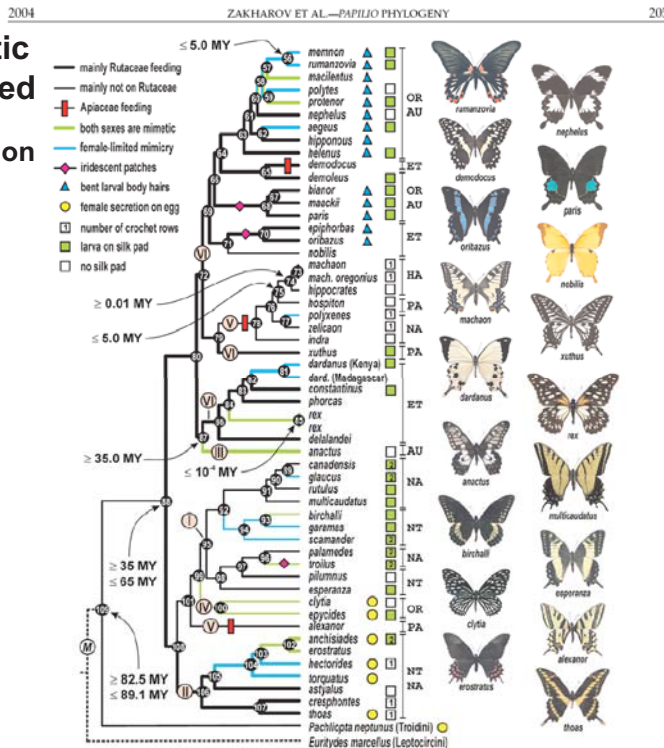
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## F. How phylogenetic trees are used

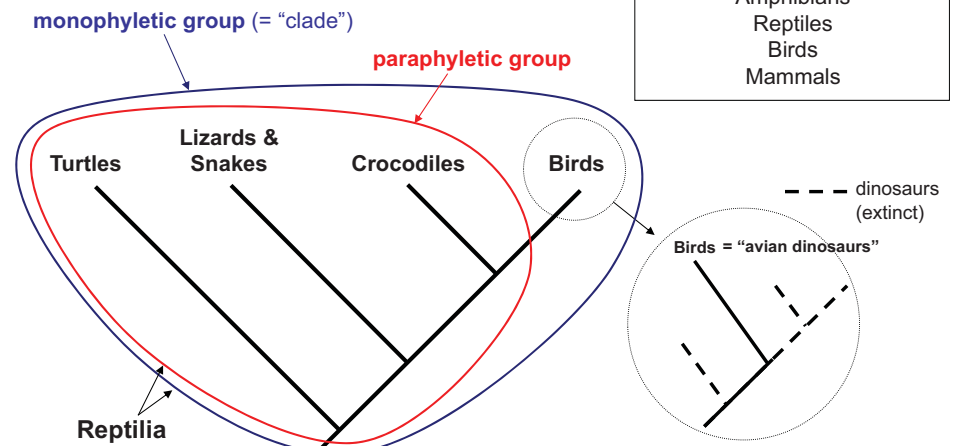
### 1) To study trait evolution

Ex. Mapping ecological traits onto a molecular phylogeny for *Papilio* butterflies



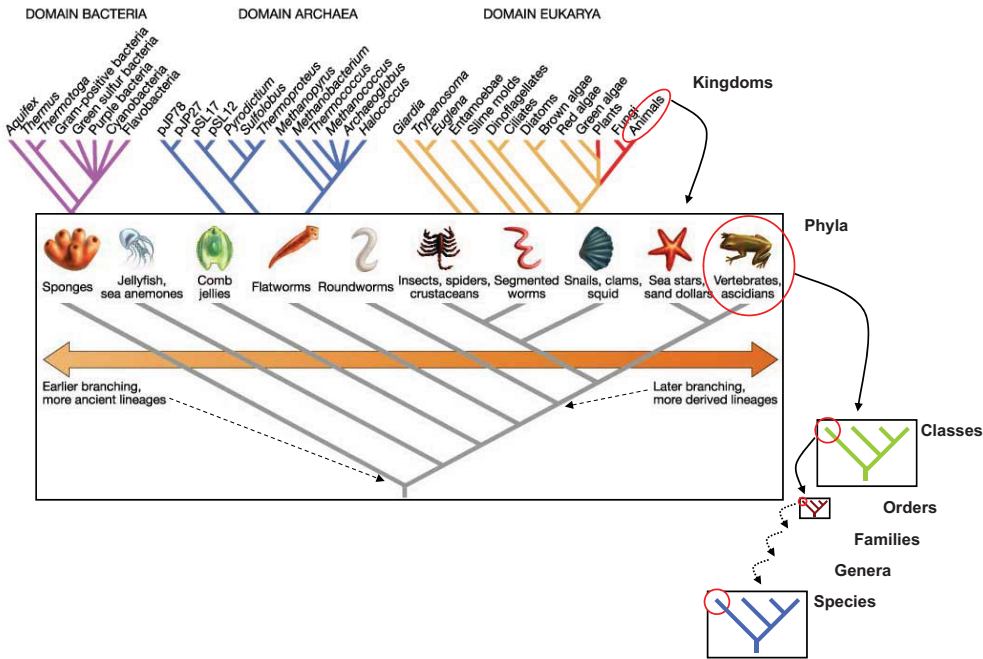
## F. How phylogenetic trees are used

### 2) To refine classification (taxonomy)



Q: Why is a paraphyletic grouping a problem?   
 Q: Should “birds” be considered reptiles?   
 Q: Are “birds” paraphyletic or monophyletic?   
 Q: Are birds distinguishable from dinosaurs?

## F. How phylogenetic trees are used: constructing the tree of life



## F. How phylogenetic trees are used

3) To reconstruct the history of *adaptive radiations*

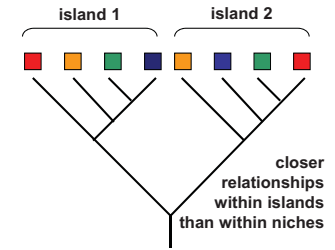
Ex. Anolis lizards in the lesser Antilles



Short-legged lizard



Long-legged lizard

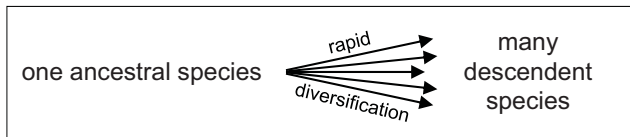


(b) Morphological diversity correlates with habitat diversity.



## F. How phylogenetic trees are used

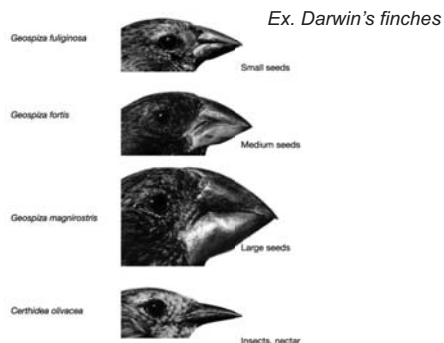
3) To reconstruct the history of adaptive radiations



### What triggers adaptive radiations?

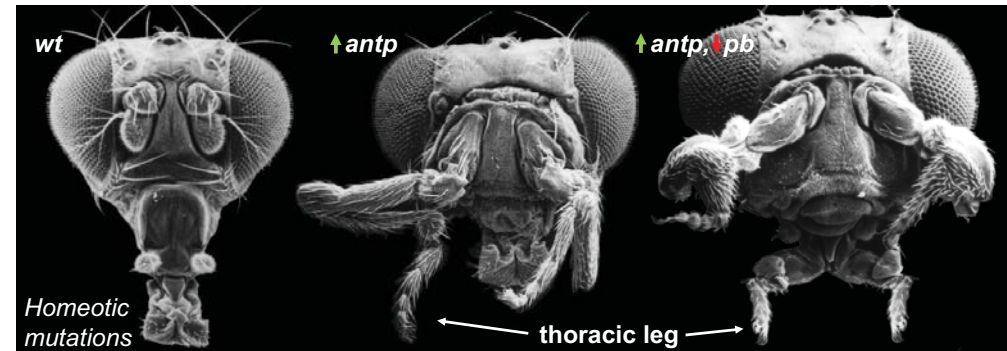
1. ecological opportunities (open niches)

2. morphological opportunities (innovative structures)



## G. How does innovation arise?

Microevolutionary processes (selection, mutation, drift, migration)  $\xrightarrow{?}$  Life's diversity

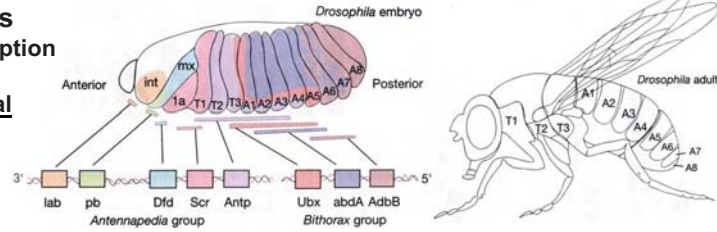




## G. How does innovation arise?

### Regulatory genes

- code for transcription factors
- specify positional information



## G. How does innovation arise?

### Regulatory genes

- code for transcription factors
- specify positional information
- small changes have large effects on the phenotype

