

Phylogenetic estimation

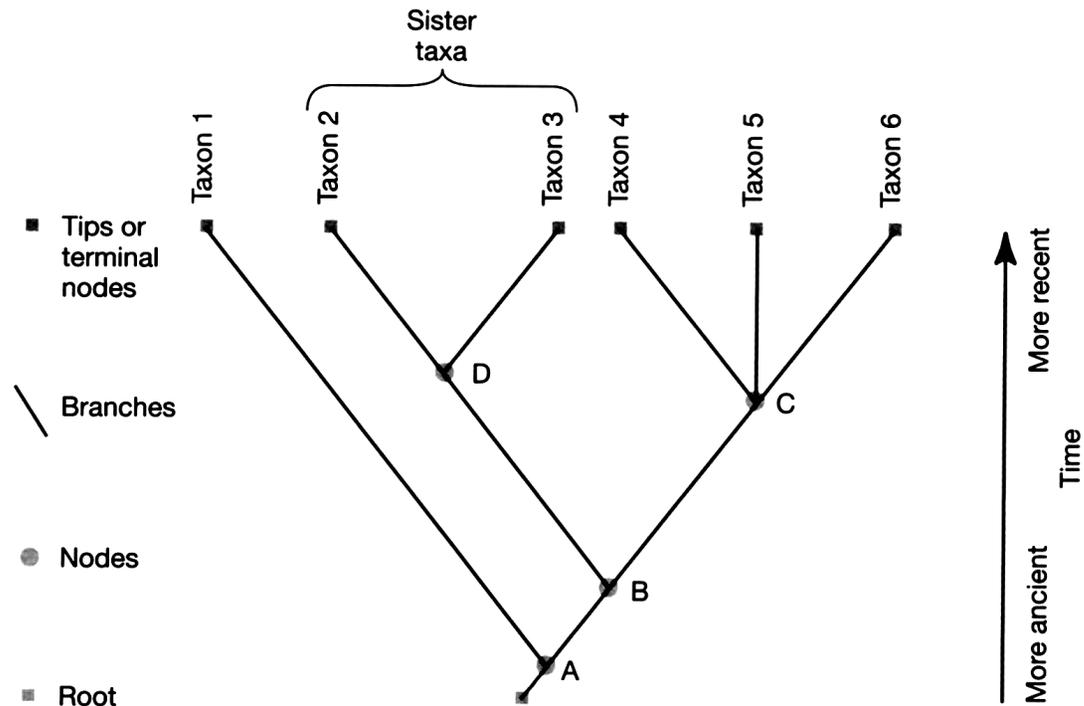
- Reconstructing evolutionary history
 - Phylogeny building
 - Parsimony
 - Other methods
- Using phylogeny in evolutionary analysis
 - Rates of change
 - Classification
 - Hypothesis testing

Phylogeny and Evolution

- The evolutionary relationships among groups of organisms
 - Reflects single unique history of life
 - Pictured as a phylogeny or ‘cladogram’
 - ‘clade’ is related group of organisms

Phylogenetic tree

- Nodes
- Branches
- Taxa
- Clade



How to make a tree

- Principle of parsimony
 - Less complicated explanations more likely to be correct
 - In evolutionary biology, phylogenies that require fewer evolutionary transitions more likely to be correct

Cladistic methods

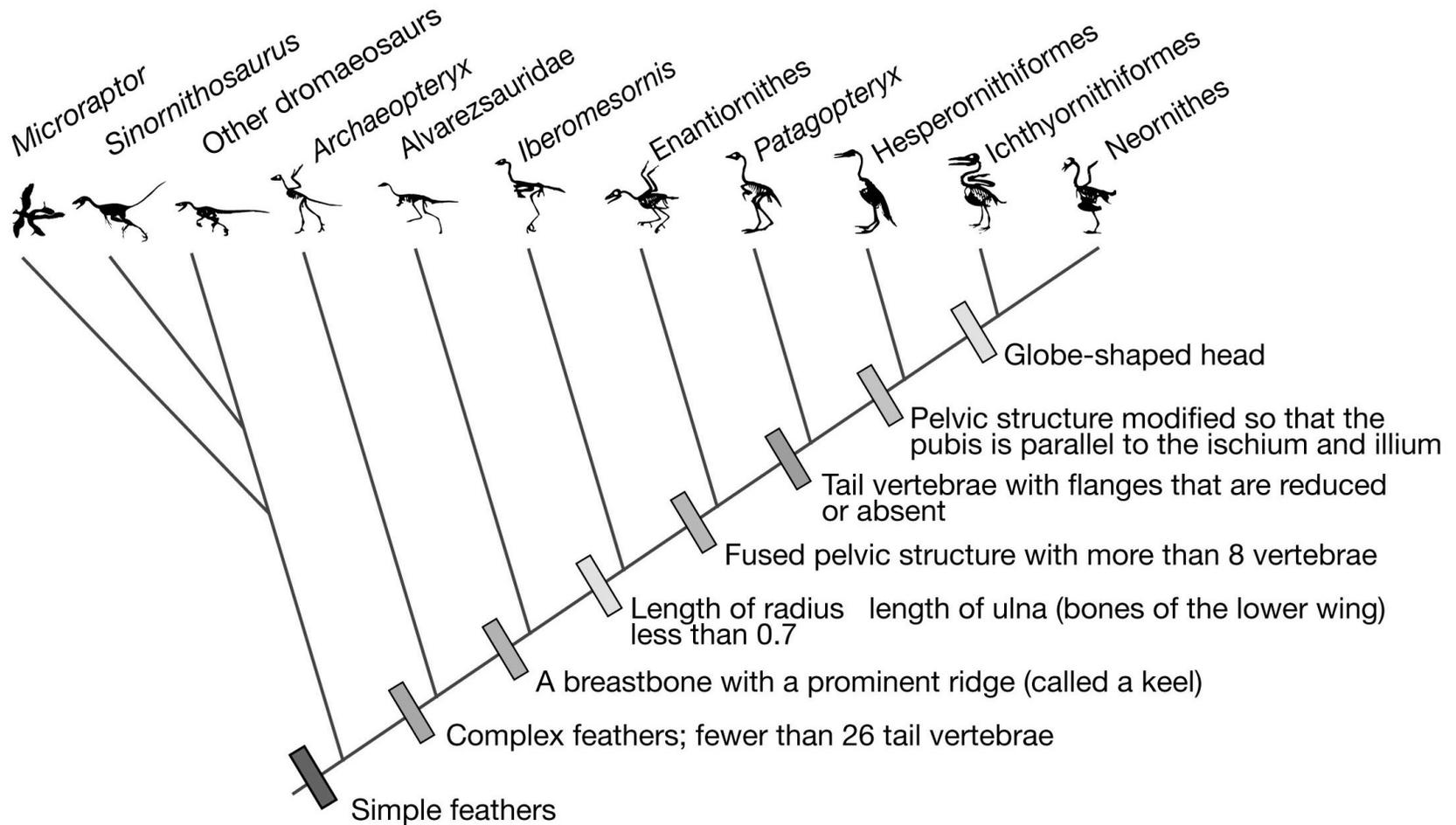
- Synapomorphy = shared derived traits
 - E.g. mammals and hair
 - Reflect true evolutionary history
- Homoplasy = ‘noise’ character similarity does not reflect evolutionary relationships
 - trait reversals
 - Convergent evolution

Applying cladistic methods

- Identify synapomorphic traits
 - Homology: structural, developmental, genetic
- Code taxa for traits
- Use parsimony to infer phylogenetic relationships
- Validating and assessing tree

Synapomorphy in bird evolution

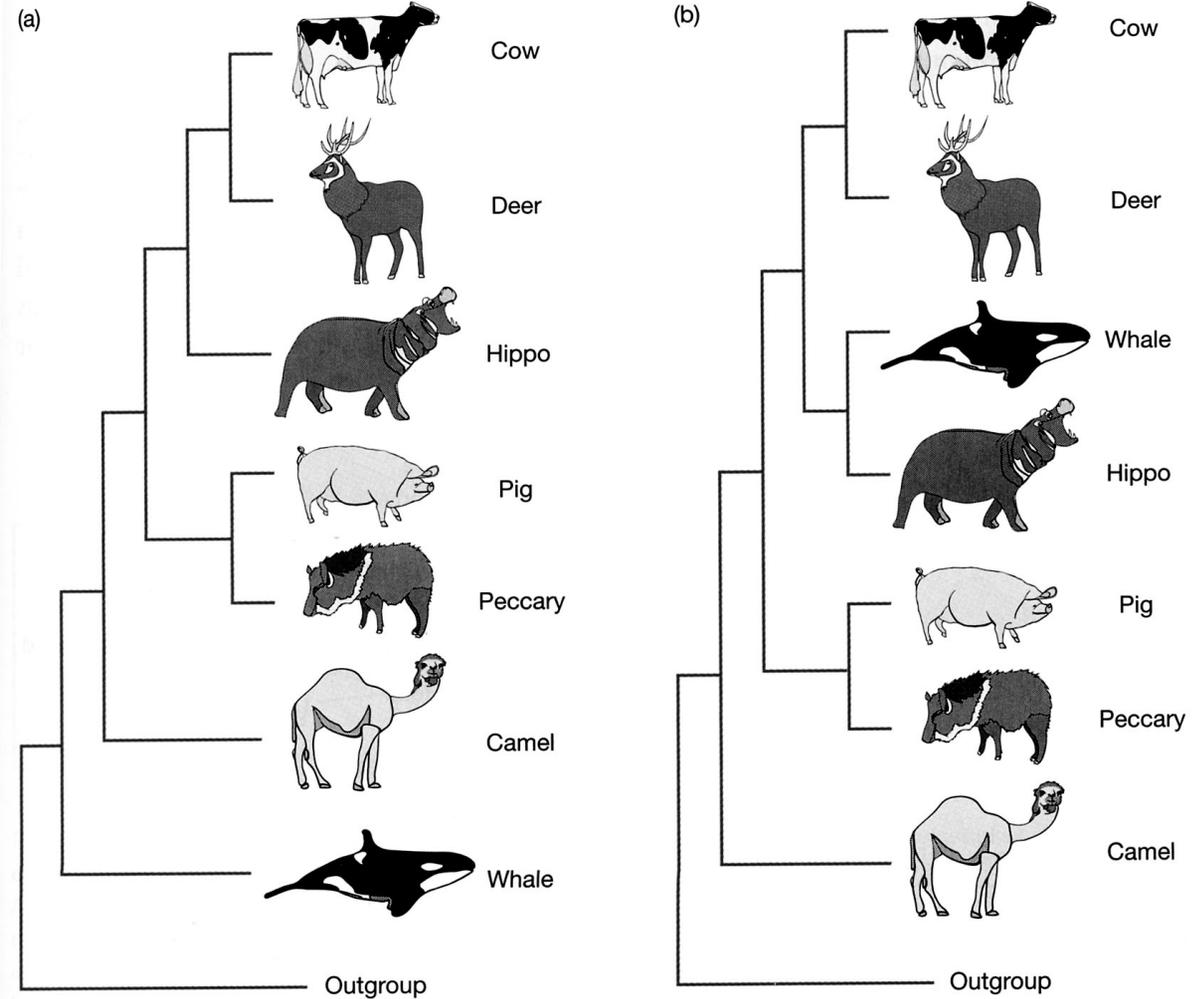
(b)



Example: the evolutionary relationships of whales



A phylogeny is a hypothesis



What data might test these hypotheses?

- Morphology, including fossils
 - 55 mya fossil ankle bones, resembled fossil mammals called mesonychians
 - Morphologically resemble extant Artiodactyls
- DNA sequences
 - Suggest relationship to Hippopotami

Advantages and limitations: morphology

- Only data available for fossils (+)
- Can reduce homoplasy through study of development (+)
 - But convergent evolution may still cause a false sense of relatedness (-)
- Very slow (-)

Advantages and limitations: DNA

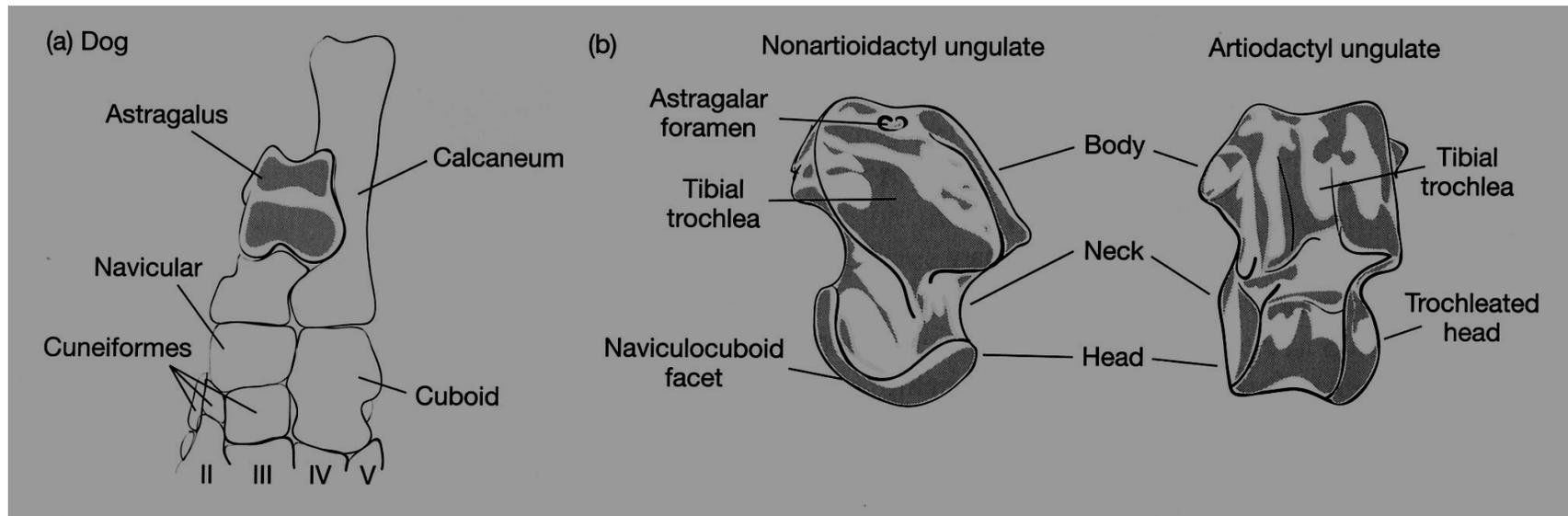
- Fairly fast and easy (+)
- Homoplasy not independently tested (-)
- Few character states (A, C, T, G)
 - Reversals more likely (-)
 - ‘saturation’ = no new changes possible (-)
- Problems and usefulness depends on how fast DNA evolves and age of taxa analyzed
 - Fast evolving good for species, populations, even ‘DNA fingerprinting’
 - Slowly evolving good for more distantly related taxa

Often best approach combines

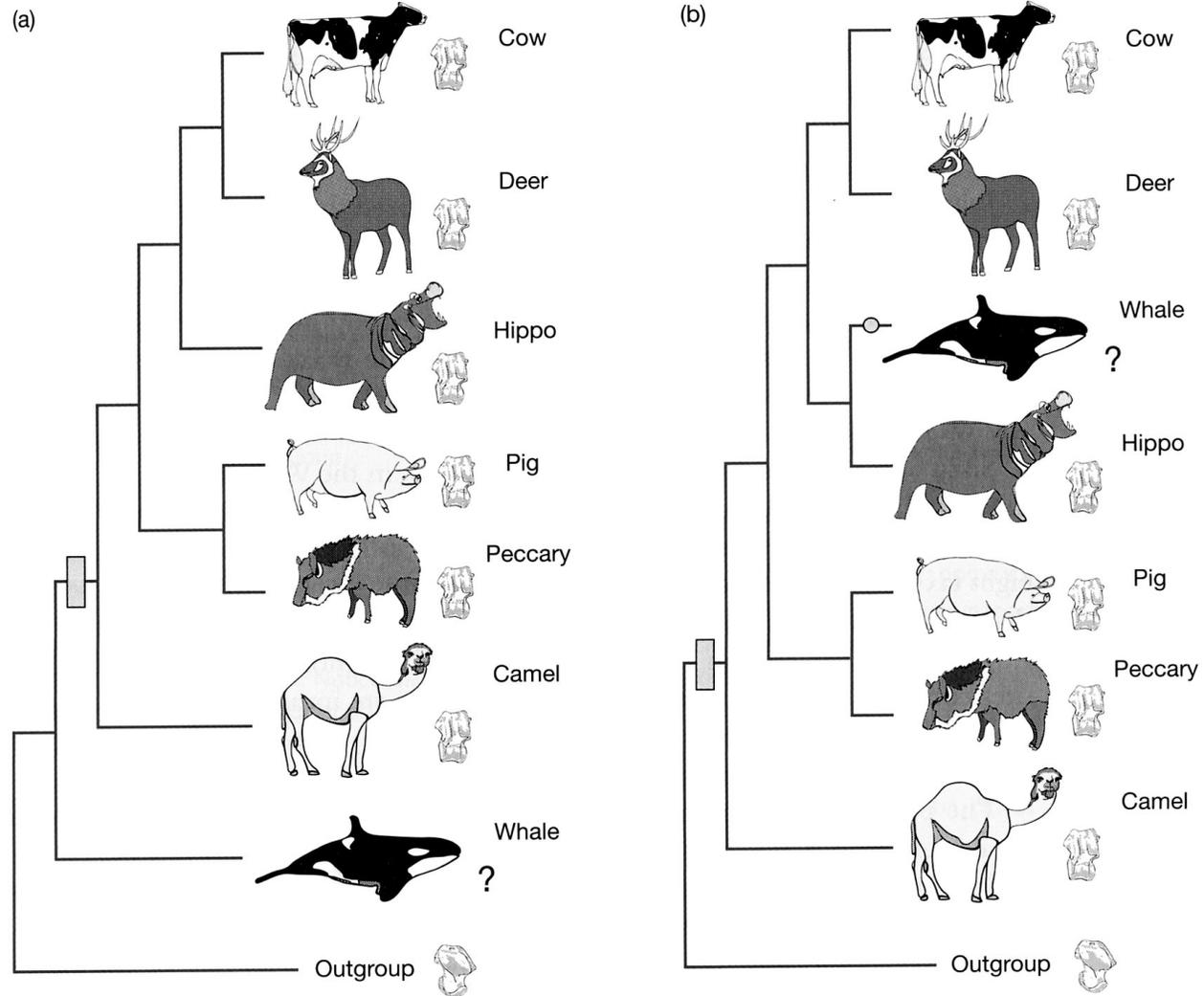
- morphology
- Uses different sections of DNA
 - Mitochondrial
 - Nuclear
 - Coding v non-coding

Astragalus ankle-bone evidence

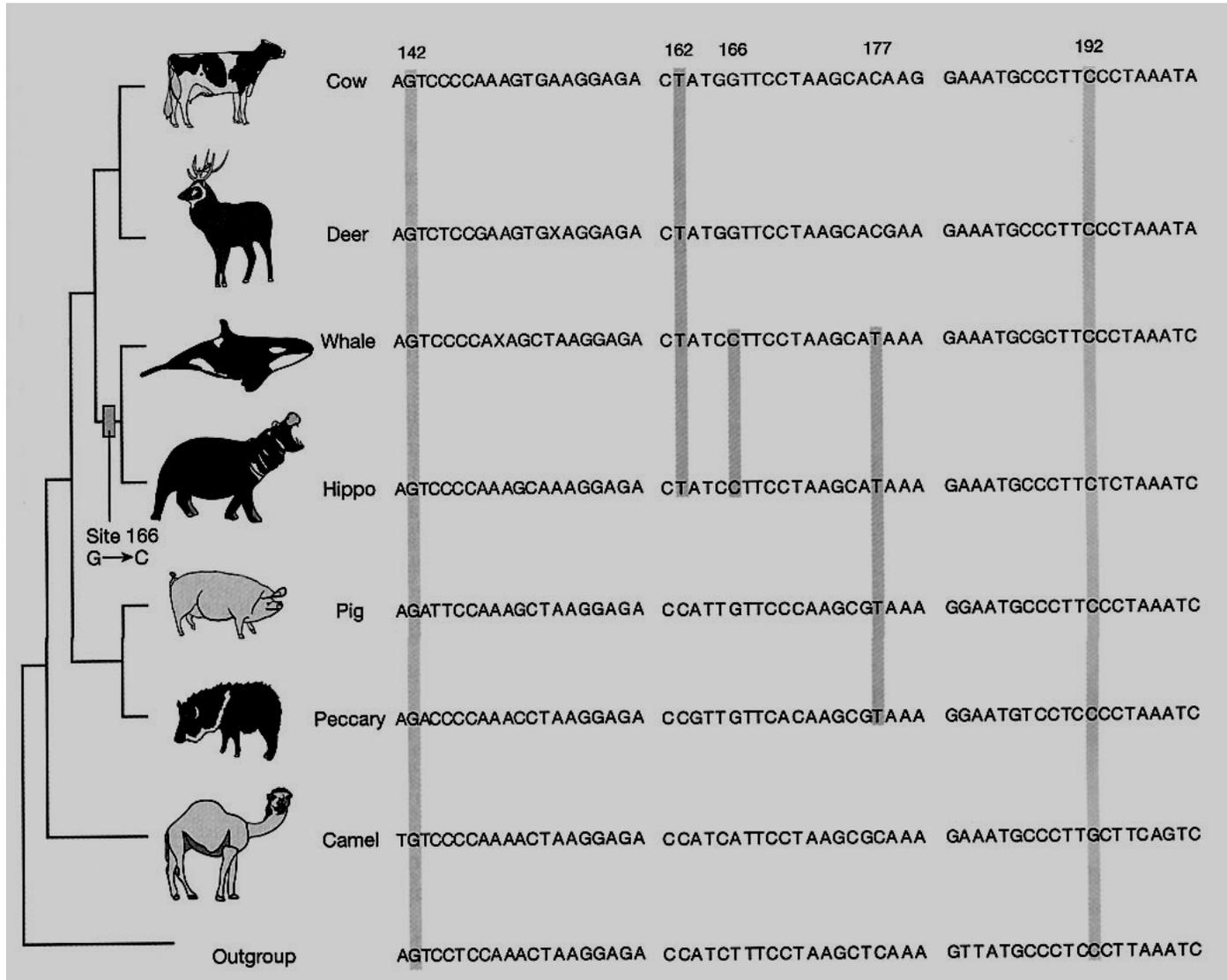
- Single morphological character
- All Artiodactyls have pulley shaped and smooth astragalus on both ends



Whales, parsimony, and astragalus



Parsimony with molecules



Comparing trees and their support

- Many different trees are possible
 - For four taxa, 3 possible trees
 - For five taxa, 15 possible trees
 - Six taxa -> 105 possible
 - Seven -> 945
 - Eight -> 10,395
- Often not possible to evaluate every possible tree

Tree evaluation

- Could be several equally most parsimonious trees
- Branches in agreement are well supported
 - Strict consensus tree
 - Majority rule consensus tree
- Resample data, called ‘bootstrapping’
 - Estimates support for branches

Comparing different methods

- Parsimony and bootstrapping support whales + hippos scenario
- Other methods do too
 - Distance matrix methods
 - Maximum likelihood

Overall support

- Confidence in a phylogeny increases if:
 - Diverse data sets agree
 - Different analysis methods agree
 - Statistical support strong
- A phylogeny is always a working hypothesis, subject to further testing

What good is a phylogeny?

- Analyzing rates of change
 - Molecular clock
- Classification
- Testing hypotheses

Molecular clock

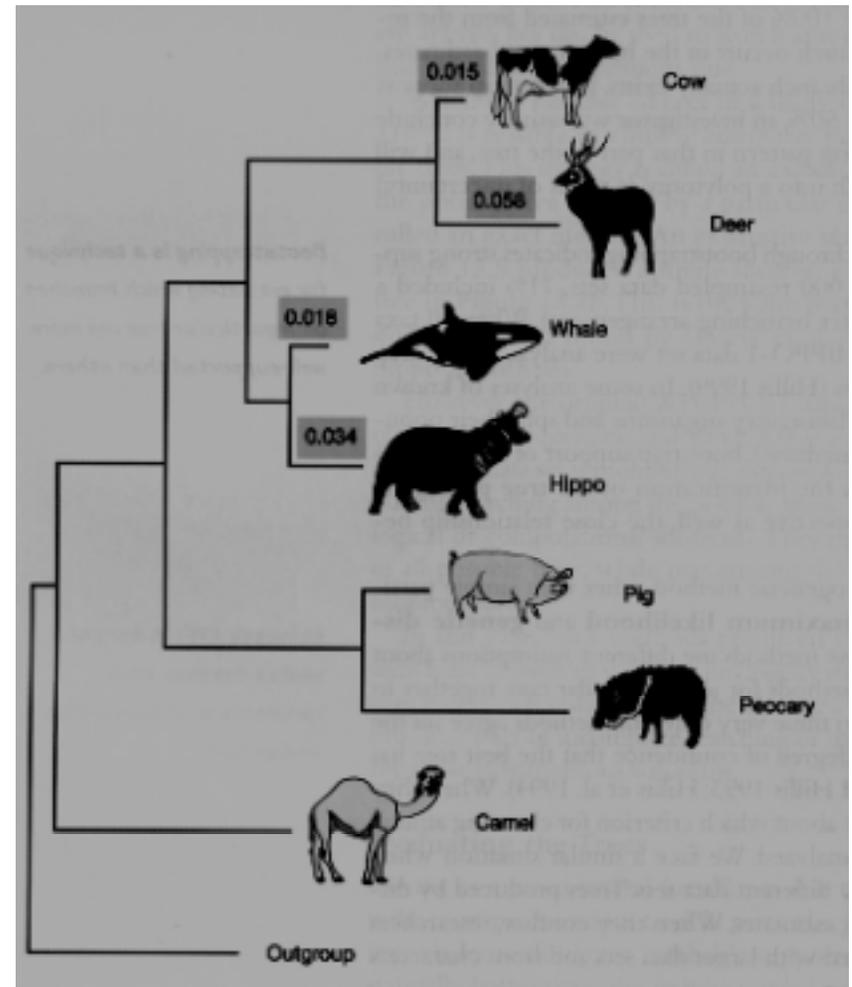
- Basic idea
 - If mutation rates are about constant
 - And if generation time is about constant
 - Then nucleotide changes should accumulate in proportion to time
- Then you could estimate date of divergence of taxa from the nucleotide data

DNA clock calibration

- Calibrate to known divergence time
 - E.g. geological ages based on radiocarbon or other dating techniques
- Calibrate molecular clock for
 - Type of organism working with (generation time)
 - Type of DNA working with
- E.g., vertebrate mitochondrial DNA clock estimates average about 2% divergence per million years
 - Or 1% change per lineage

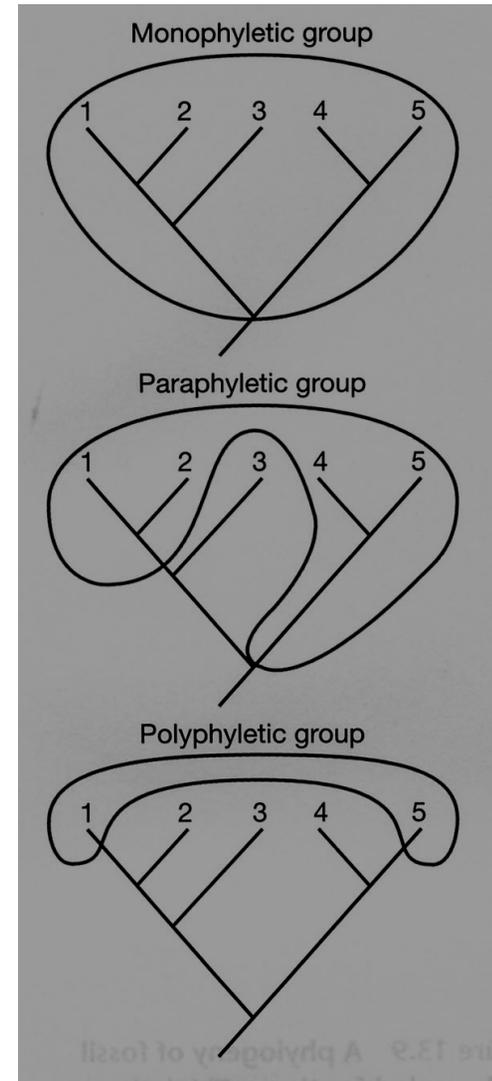
Phylogenetic classification

- We discussed problems with species concepts.
- But worse, what is a ‘genus’ a ‘family’ or other higher taxonomic category?
- If Artiodactyla is an Order, then why aren't whales considered Artiodactyls?



Phylogenetic systematics

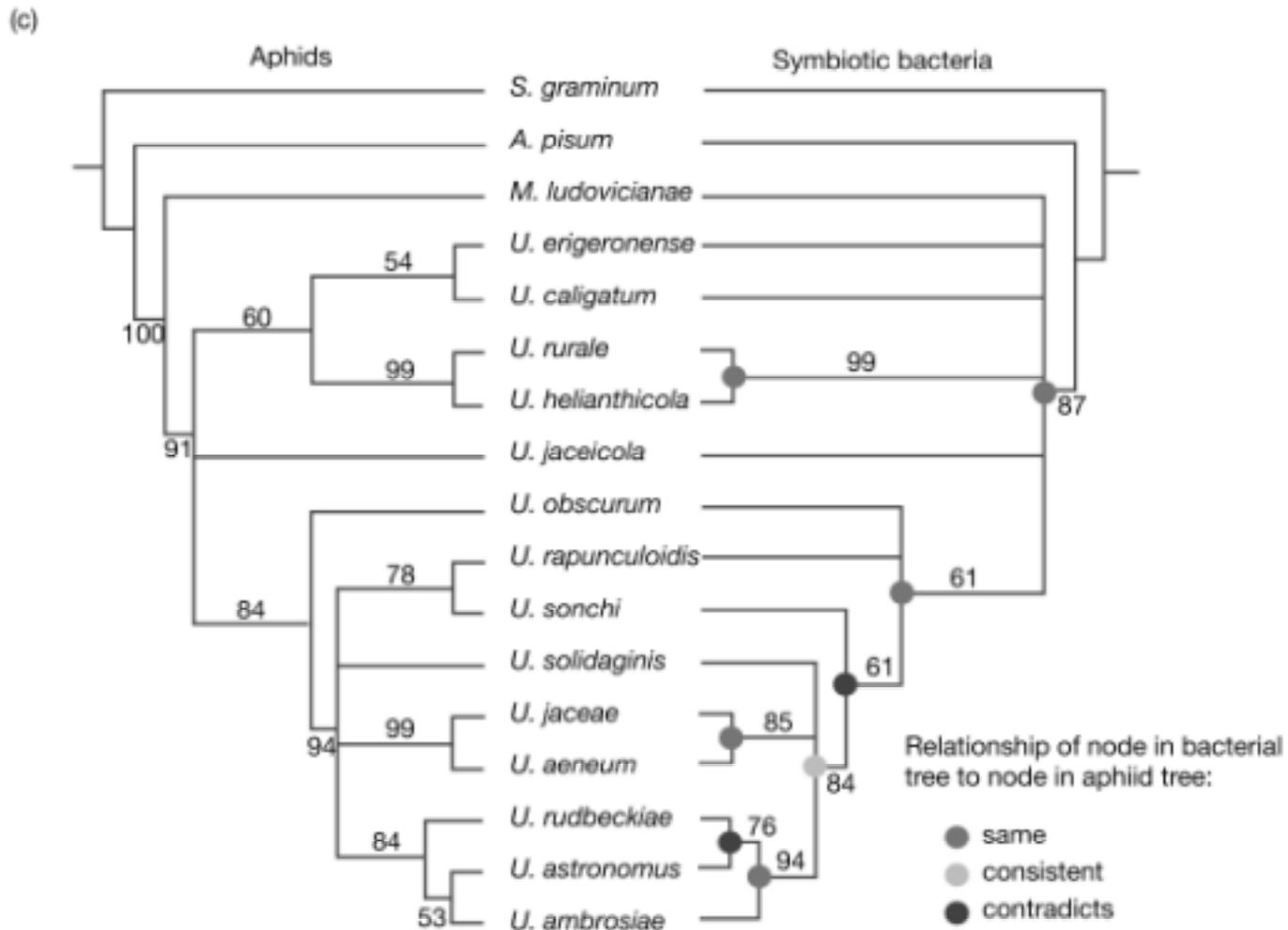
- Only monophyletic groups should be named
- Monophyletic groups contain common ancestor and all of its descendents
- Paraphyletic has common ancestor, but not all descendents
- Polyphyletic does not have recent common ancestor



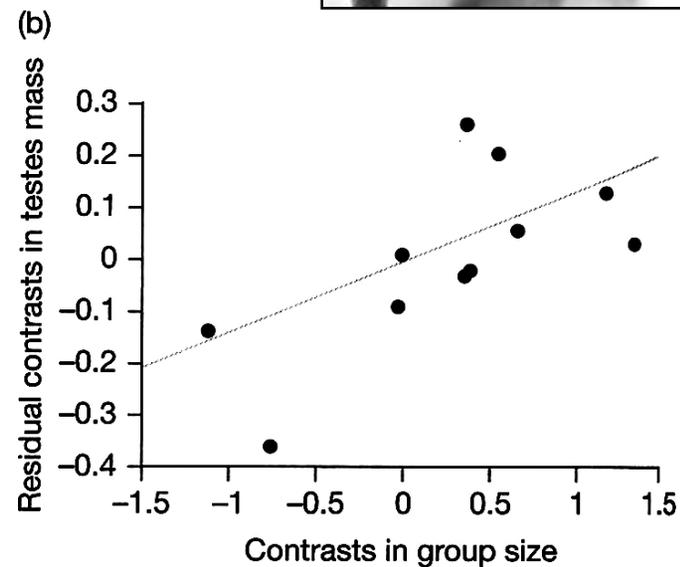
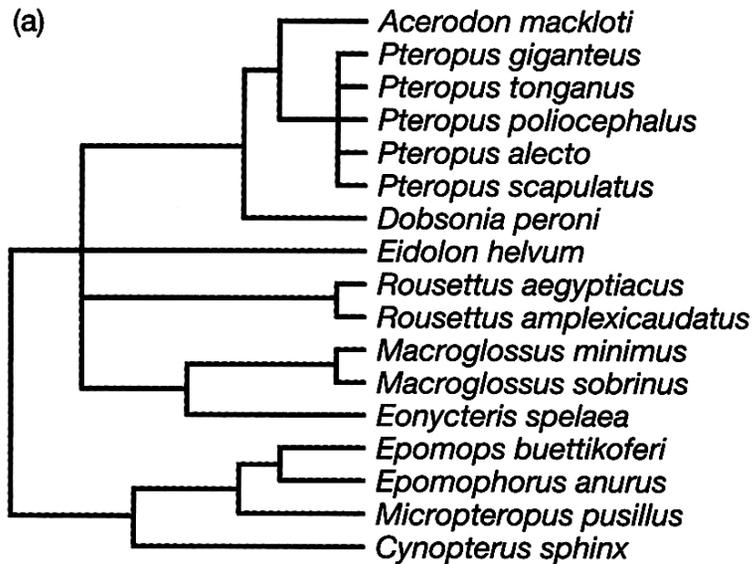
Studying coevolution

- Coevolution = interactions between species that result in reciprocal adaptation
 - We might expect that repeated interaction over time would lead to specialization
 - Specialization might lead to co-speciation
 - When one partner speciates, the other gets dragged along

Aphids and endosymbiont bacteria co-speciation



Testing adaptive hypotheses



Informing public health policy

- Major reforms in physician-patient contact initiated after demonstration that a dentist transmitted HIV to patients

