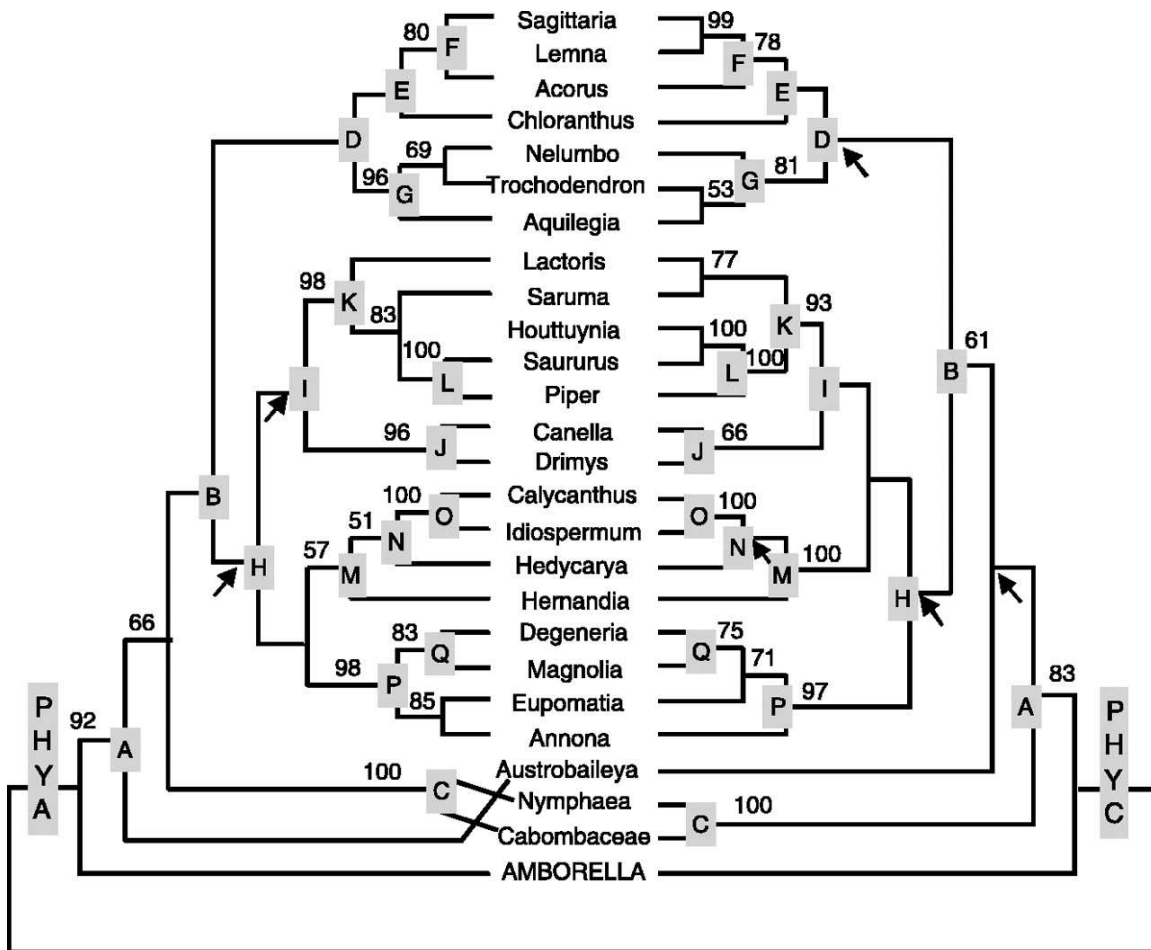


Tree thinking quiz II
D. A. Baum, S. D. Smith, and S. D. Donovan

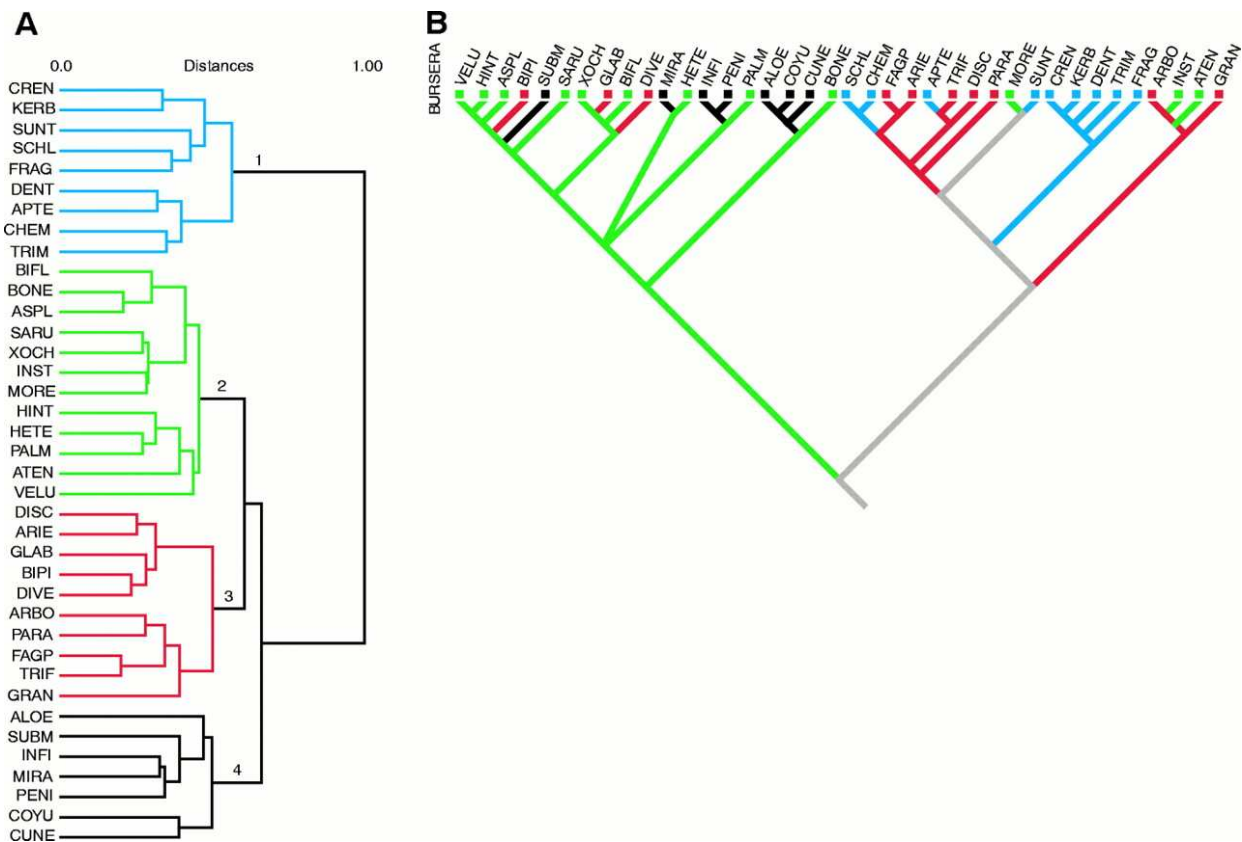
Each question in this quiz is built around a *Science* paper that depicted a phylogenetic tree. It should not be necessary to consult the original article to answer the questions.



S. Mathews, M. J. Donoghue. The root of angiosperm phylogeny inferred from duplicate phytochrome genes. *Science* **286**, 947 (1999).

1) The figure above shows the phylogeny estimated for a sample of flowering plants (angiosperms) from *PHYTOCHROME A* and *PHYTOCHROME C*, a pair of genes that duplicated prior to the origin of the angiosperms. Which of the following sets of taxa constitute a clade (=monophyletic group) on one gene tree but not on the other?

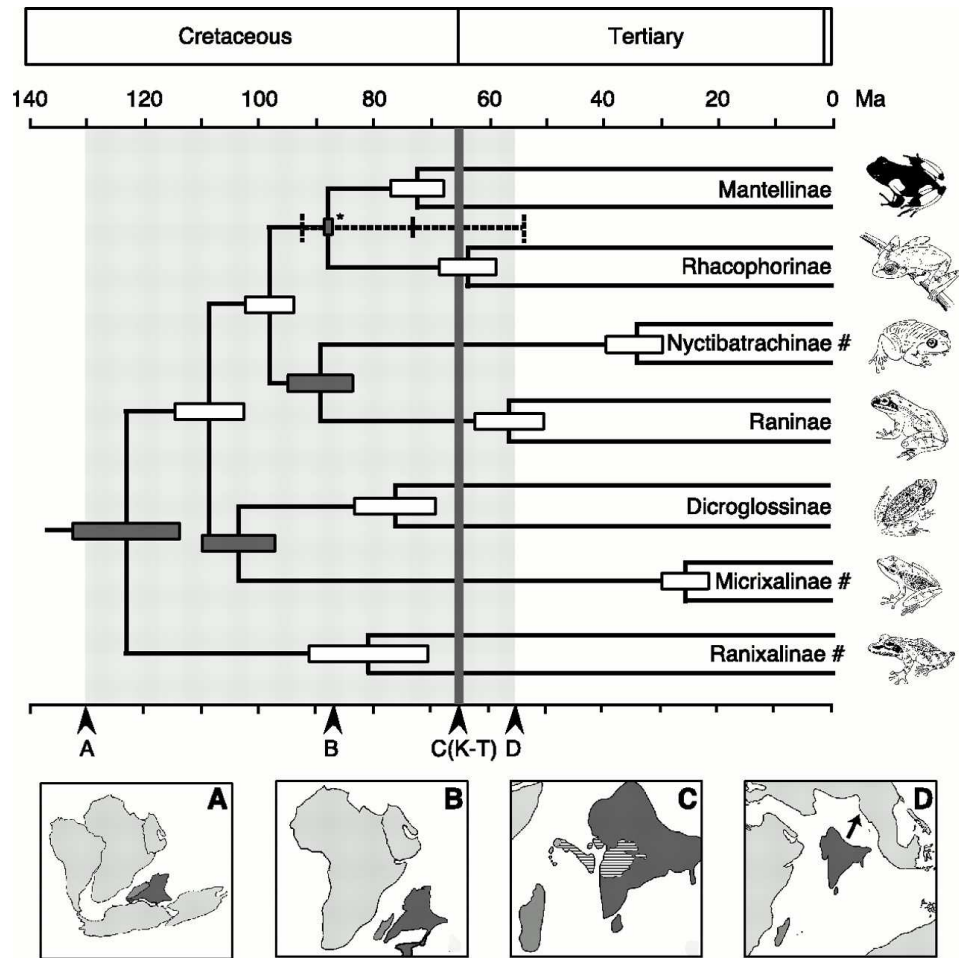
- Degeneria-Magnolia-Eupomatia*
- All angiosperms except *Amborella*
- Austrobaileya-Nymphaea-Cabombaceae*
- Nelumbo-Trochodendron-Aquilegia*



J. X. Becerra. Insects on plants: macroevolutionary chemical trends in host use. *Science* **276**, 253 (1997).

2) The dendrogram on the left clusters plant species by chemical similarity; each of the four main chemical groups is indicated with a different color. This tree does not depict descent relationships, just degree of chemical similarity. On the right, the evolution of these chemical types is reconstructed on a phylogeny of the plants (this does depict inferred evolutionary relationships). The colors correspond to the chemical groups on the left, and the gray branches indicate uncertainty in character reconstruction. What does a comparison of these two figures tell us about the evolution of plant secondary chemistry?

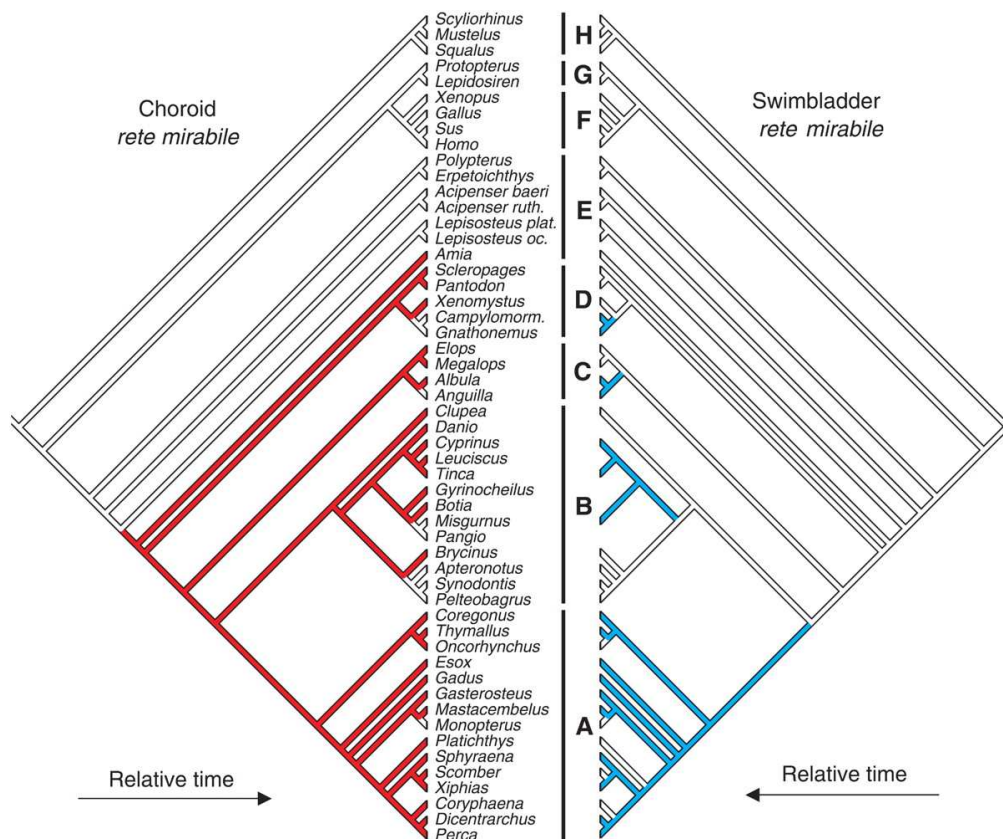
- The four groups of chemically similar species each constitutes a distinct evolutionary lineage
- The group colored "black" has the most advanced chemical defenses
- The red (3) and blue (1) chemical groups are most distantly related
- The chemical groups have each been gained and/or lost multiple times in evolution



F. Bossuyt, M. C. Milinkovitch. Amphibians as indicators of early tertiary "out-of-India" dispersal of vertebrates. *Science* **292**, 93 (2001).

3) This tree depicts inferred relationships among some major frog groups with branches drawn proportional to absolute time. Error bars on internal nodes depict confidence intervals on the dates of estimated nodes. Assuming this tree and the associated ages are correct which of the following statements is true?

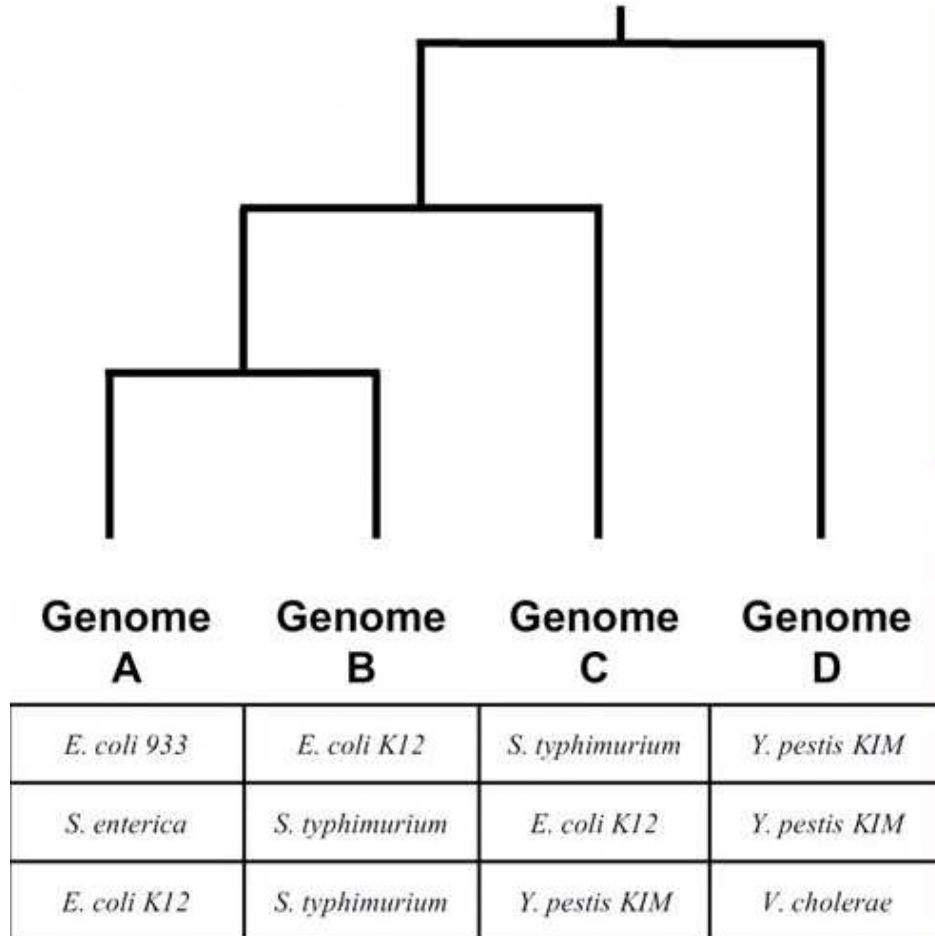
- No individual living before 70 million years ago is an ancestor of Raninae
- Raninae and Dicroglossinae shared a common ancestor about 75 million years ago
- The divergence of Raninae and Nyctibatrachinae occurred more recently than the 85 million year old separation of India from Madagascar
- The last common ancestor of Micrixalinae and Dicroglossinae lived before India and Madagascar separated (85 million years ago)



M. Berenbrink, P. Koldkjaer, O. Kepp, A. R. Cossins, Evolution of oxygen secretion in fishes and the emergence of a complex physiological system. *Science* **307**, 1752 (2005).

4) *Retia mirabilia* (sing. *rete mirabile*) are vascular bundles that allow fish to secrete O_2 . In the above figure, red branches indicate lineages with choroid *retia*, blue branches indicate those with swimbladder *retia*, and white branches indicate absence of *retia*. Assuming the phylogeny and character evolution have been accurately inferred, we can see that:

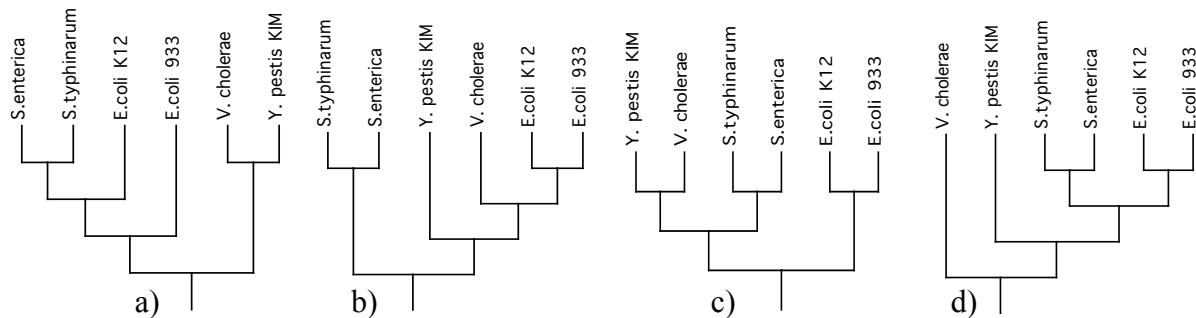
- Swimbladder *retia* predate choroid *retia*
- Gains of swimbladder *retia* primarily took place in lineages that already had choroid *retia*.
- Loss of choroid *retia* causes gain of swimbladder *retia*
- Choroid *retia* have been gained more often than swimbladder *retia*

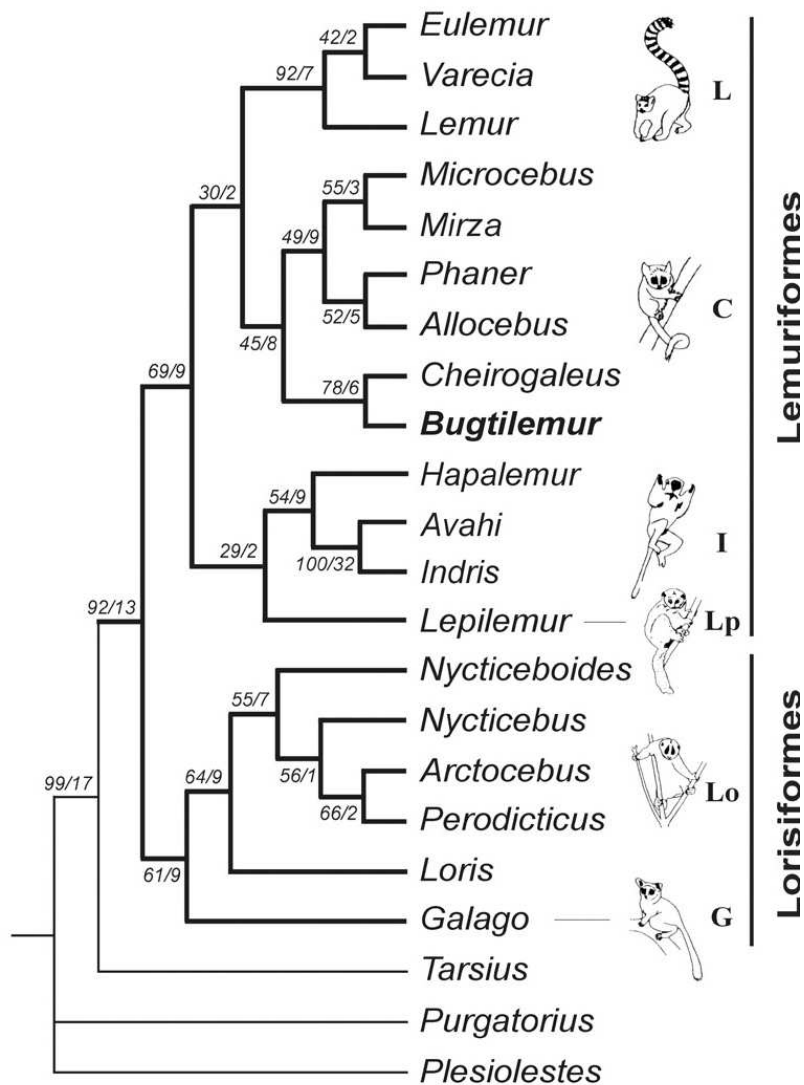


V. Daubin, N. A. Moran, H. Ochman. Phylogenetics and the cohesion of bacterial genomes. *Science* **301**, 829 (2003).

[The above is only a portion of the figure].

5) Each row in the table above lists a set of four bacterial taxa whose relationship follows the topology shown. Thus each row can be read as a four-taxon tree. Which of the four trees below is compatible with the information in the three rows of the table?



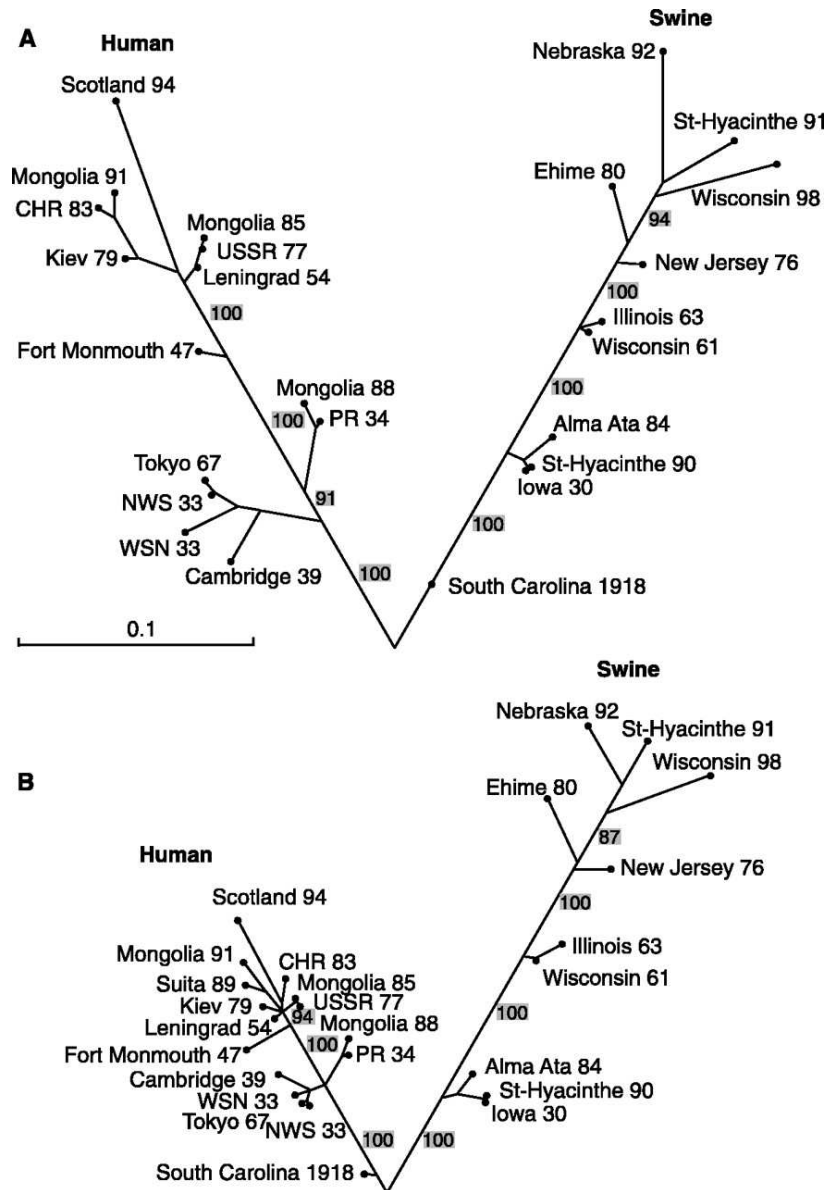


L. Marivaux *et al.* A fossil lemur from the Oligocene of Pakistan. *Science* **294**, 587 (2001).

[The above is only a portion of the figure]

6) Lemuriformes are currently restricted to Madagascar, whereas Lorisiformes are found in Africa and Asia but not Madagascar, and *Tarsius* is Asian. The tree above was generated in order to assess the relationship of a fossil, *Bugtilemur*, found in 30 million year old deposits in Pakistan. Each branch of the tree has been annotated with two numbers, the first of which is the bootstrap percentage, a measure of support. In order to hold that *Bugtilemur* is more closely related to Lorisiformes than to Lemuriformes what is the minimum number of branches, with what bootstrap support, that would need to be incorrect?

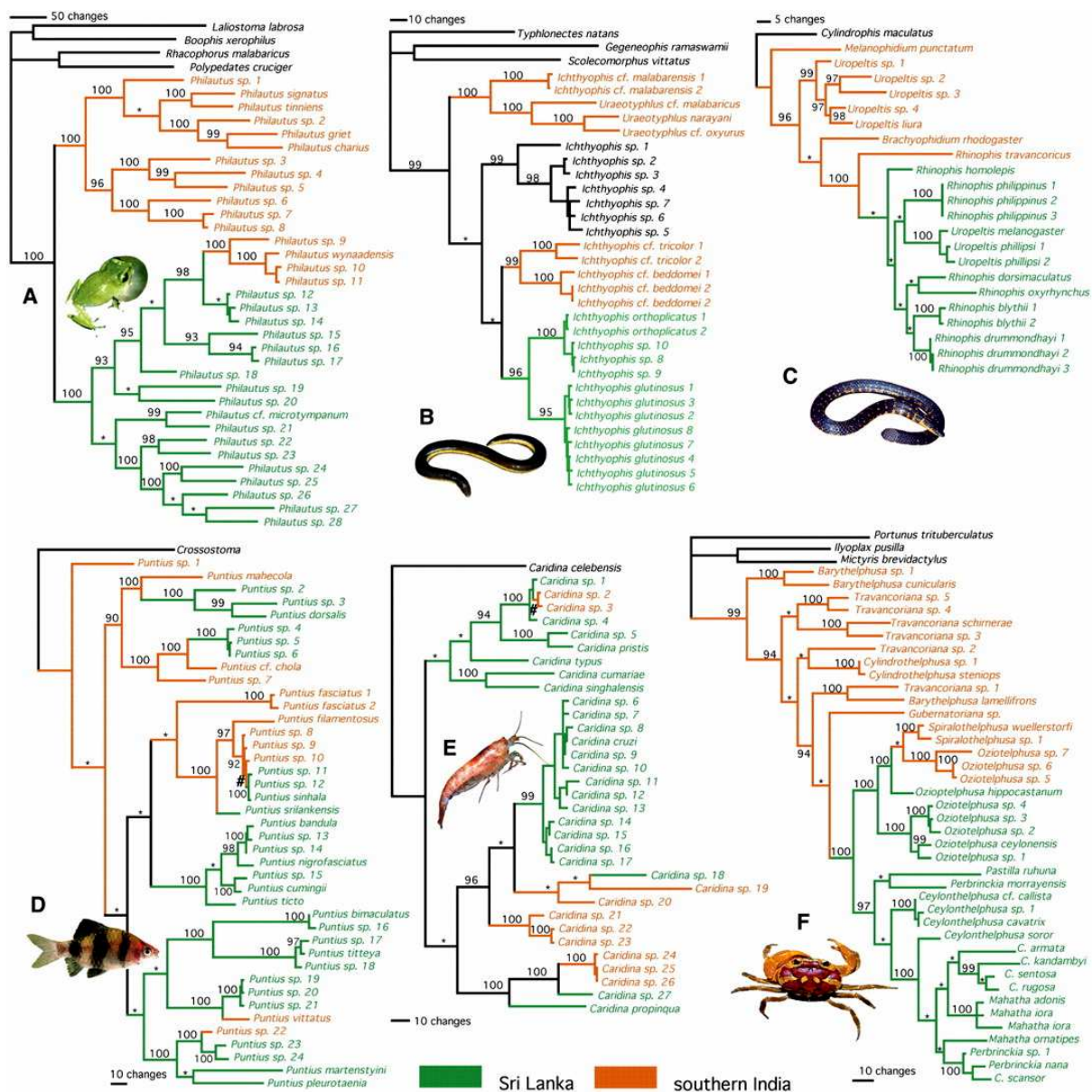
- 1: 92%
- 2: 78%, 69%
- 4: 78%, 45%, 30%, 69%
- 4: 78%, 45%, 30%, 29%



M. J. Gibbs, J. S. Armstrong, A. J. Gibbs. Recombination in the hemagglutinin gene of the 1918 "Spanish flu". *Science* **293**, 1842 (2001).

7) The trees show the phylogeny estimated for the same mammalian H1 influenzas based on portions of the haemagglutinin genes. Tree A was estimated from bases 310-870 whereas tree B was estimated from bases 1070-1650. Under the assumption that these trees are correctly rooted, how does this result support the inference that the South Carolina 1918 strain (the only exemplar from the 1918 flu pandemic) arose from recombination between a human and a swine virus?

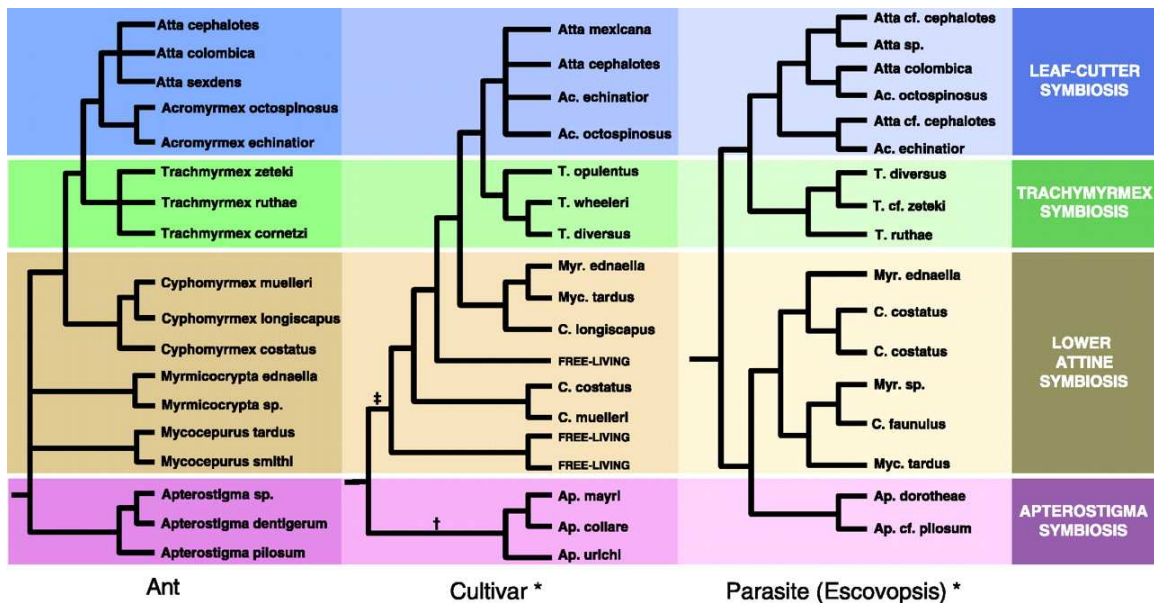
- The fact that the South Carolina 1918 strain is near the root of both trees suggests that it is of mixed identity
- The fact that the South Carolina 1918 strain is more closely related to the swine strains in tree A but to the human strains in tree B
- The fact that the South Carolina 1918 strain is a direct ancestor of all the swine strains in tree A but was isolated from a human
- The fact that the South Carolina 1918 strain is more closely related to the Iowa 30 swine strain than to the Scotland 94 human strain in both trees



F. Bossuyt *et al.* Local endemism within the Western Ghats-Sri Lanka biodiversity hotspot. *Science* **306**, 479 (2004).

8) These trees for six different groups of organisms for (A) tree frogs, (B) caecilians, (C) uropeltid snakes, (D) freshwater fishes, (E) freshwater shrimps, and (F) freshwater crabs are all colored based on whether the species come from mainland India or Sri Lanka. Assuming these trees and the reconstruction of ancestral geographic distributions are accurate, which of the trees includes a single well-supported migration from Sri Lanka back to southern India?

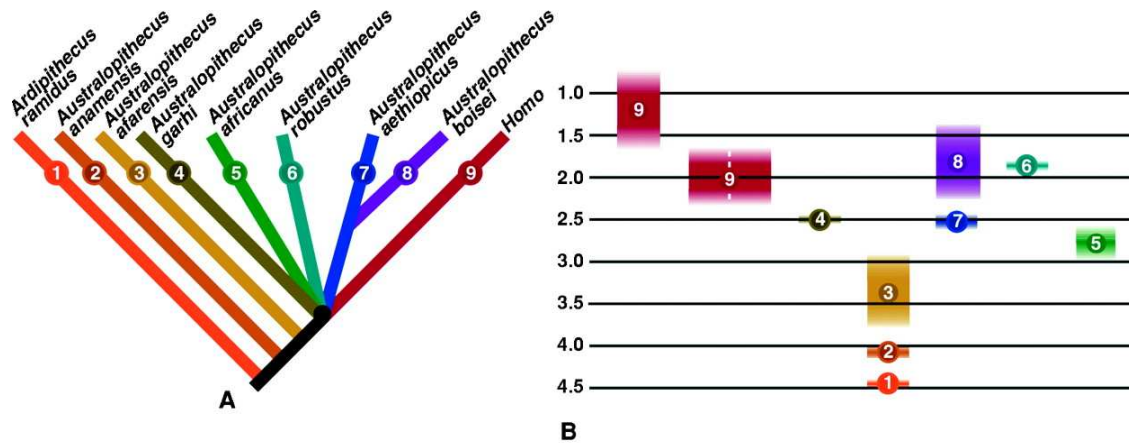
- A, F
- B, C
- C
- A, B



C. R. Currie *et al.* Ancient tripartite coevolution in the attine ant-microbe symbiosis. *Science* **299**, 325. (2003).

9) The three trees depict the relationships between leaf cutter ants (left), fungi cultivated by those ants (middle) and fungi parasitizing ant gardens (right). By comparing the phylogenies, we can distinguish whether fungi are usually passed on vertically (through generations of an ant lineage) or horizontally (e.g., among unrelated ants). Allowing that differences between trees could reflect error in phylogenetic inference, what does the similarity between the three phylogenies suggest?

- Cultivars are passed horizontally and parasites vertically
- Cultivars are passed vertically and parasites horizontally
- Cultivars and parasites are passed vertically
- Cultivars and parasites are passed horizontally



B. Asfaw *et al.* *Australopithecus garhi*: a new species of early hominid from Ethiopia. *Science* **284**, 629 (1999).
 [The above is only a portion of the figure]

10) The above tree summarizes the inferred relationships among a number of hominid fossils as related to humans (*Homo*). The point where multiple lineages arise from a single node (a polytomy) is here intended to indicate uncertainty rather than evidence of a simultaneous divergence of an ancestral lineage into five descendant lineages. The fossil ages of each taxon are color-coded on the right. Note that fossils of species 7 predate those of its sister taxon, species 8. If the tree is accurate representation of the evolutionary history of these species, what is the minimum age we could infer for lineage 8?

- a) 2.25
- b) 2.5
- c) 3.0
- d) It cannot be determined from these data