

April 28, 2014. **Comparing cladograms; coevolution; symbiosis**

-- There are many reasons why one would want to compare cladograms, falling into three basic categories:

-- *Within an analysis of one clade, with the same OTUs*; e.g., equally or nearly equally parsimonious (or likely) trees, trees resulting from different character partitions, models of evolution, or methods of analysis, and comparisons with trees from the literature.

-- *Within an analysis of one clade, with different OTUs*; trying to come up with a general tree for all OTUs, e.g. super trees, compartmentalization.

-- *Comparing analyses of different clades*, e.g., gene family evolution, migration between populations, vicariance biogeography, host/ parasite relationships, symbiosis, community evolution, or any long-term ecological association

"Coevolution" and "Symbiosis defined. What is it exactly? It can be over-broadly defined to include *any* interaction between different lineages; that makes it basically synonymous with plain ol' "evolution." So most people take it to mean a *long-term* interaction between lineages -- but how long-term? Janzen (1980) defined it in terms of trait evolution: "evolutionary change in a trait of the individuals of one population in response to a trait of the individuals of a second population, followed by an evolutionary response by the second population to the change in the first." (this definition essentially follows the original meaning from Ehrlich and Raven 1968)

-- Coevolution can occur in the context of many different ecological interactions. The interactions can be mutually beneficial, or beneficial to one lineage and either neutral or detrimental to the other:

Name of Interaction	Effect of Interaction	
	Species A	Species B
Competition	-	-
Predation/Herbivory/Parasitism	+	-
Mutualism	+	+
Commensalism/Facilitation	0	+

The term symbiosis refers to a *close and prolonged ecological relationship* between the individuals of two (or more) different species, and can involve mutualism, parasitism or other interactions.

If coevolution is defined to be a relationship that is long enough to continue through one or more divergences of the lineages involved, then it can be studied directly using phylogenetic comparative methods. Prolonged coevolution can lead to *cospeciation*, which will appear as phylogenetic congruence between two or more systems of lineages.

Cospeciation represents another generalization of the phylogeny/ homology relationship (which could be considered the "coevolution" of organism lineages and their characters), like other examples we have discussed such as vicariance biogeography (which is organism/ earth coevolution) or gene family evolution (which is gene/ genome coevolution).

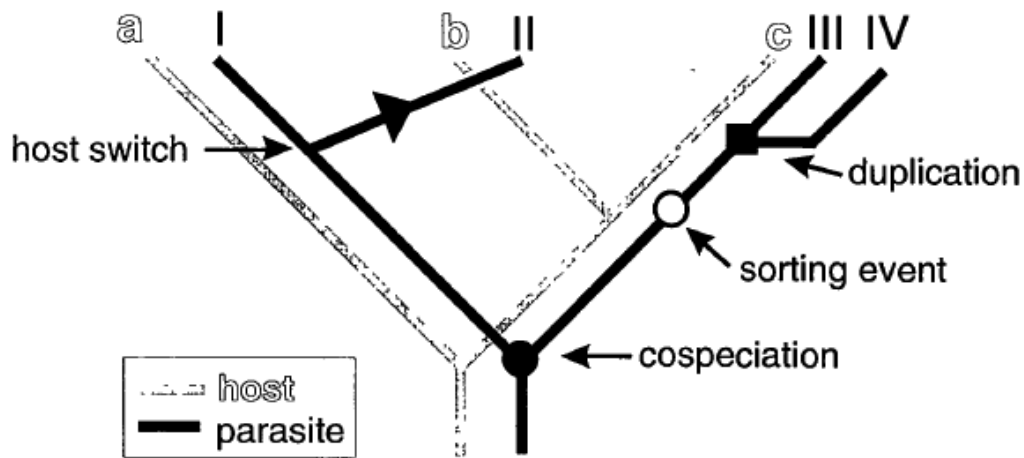


FIGURE 2. A host and parasite phylogeny showing a cospeciation event (●), a duplication (■), a host switch (►), and a sorting event (○).

Sorting events: parasite extinction, failure to speciate, 'miss the boat' when host speciates; missed collection.

Page 1996, Syst. Biology

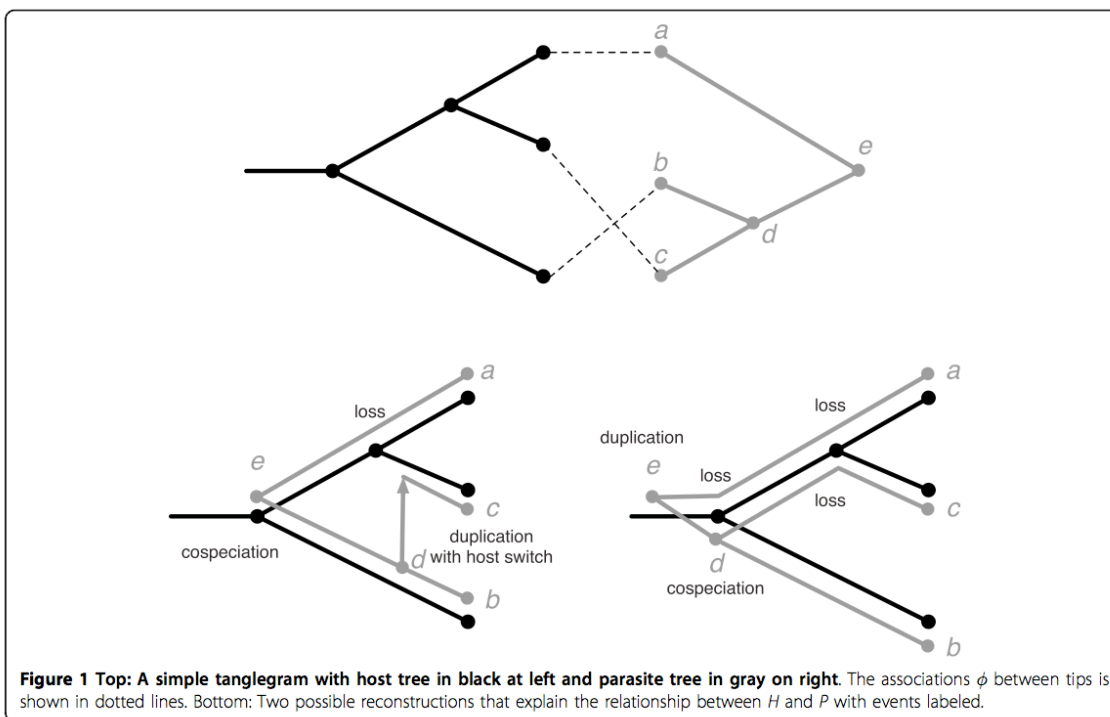
Methodology:

-- These kinds of questions always involve comparing different cladograms, yet how to do this can be hypothesis-dependent. In addition to comparing topologies per se, some questions would require comparing branch lengths on the topologies, or at least comparing the presence or absence of specific characters. See specific examples on the following sheets.

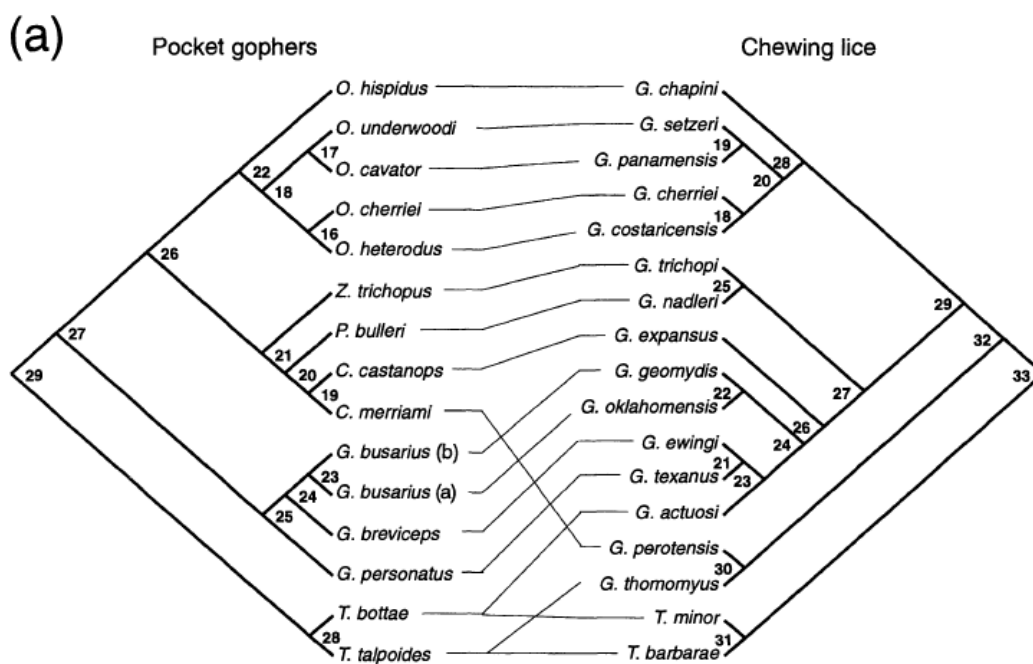
-- Like other areas of comparative methods we have discussed, the general approach is to first define the patterns you are looking for, carefully define the causal hypothesis to be tested, then specify a null hypothesis (what you would expect if the hypothesized cause is NOT working), and finally design a test that would let you reject the null hypothesis if it is indeed false.

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from Conow et al. 2010



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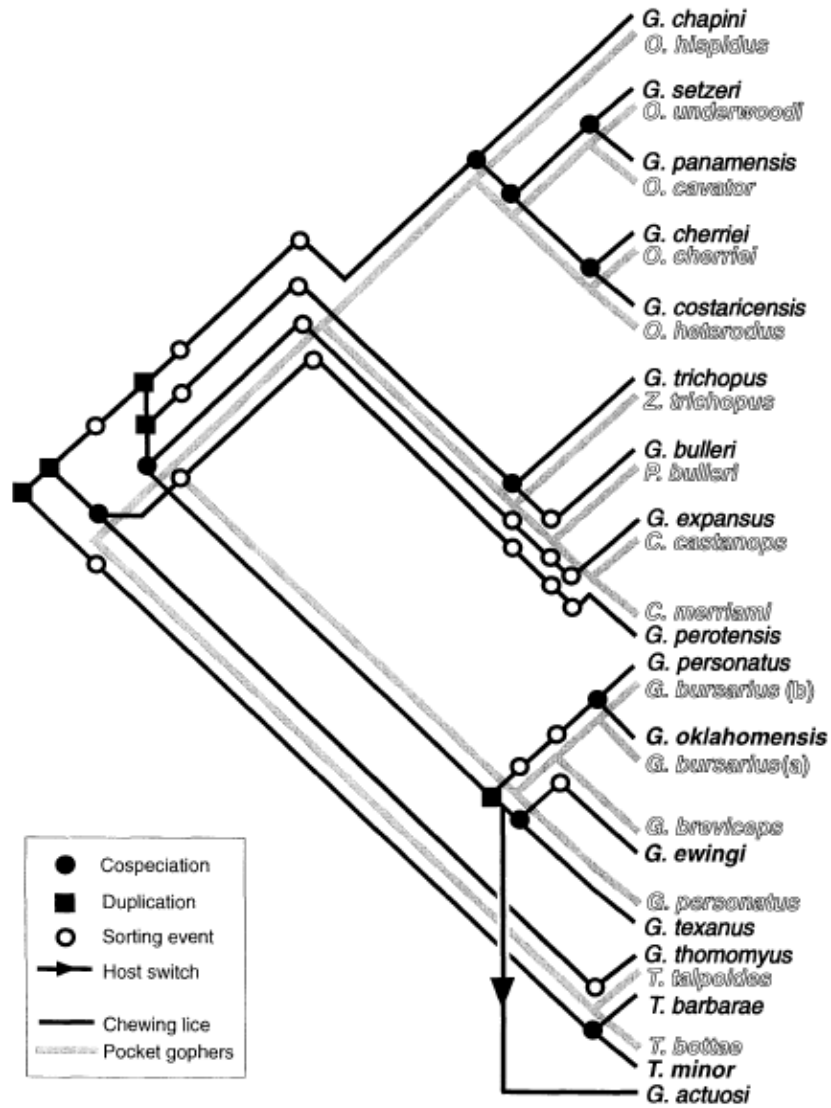


FIGURE 3. A possible reconstruction of the history of the gopher-lice association that postulates 10 co-speciation events, five duplications (in situ speciation of the lice on the same host), 20 sorting events (instances where louse lineages have been lost or remain undetected), and a single host switch (by *Geomydoecus actusosi*).

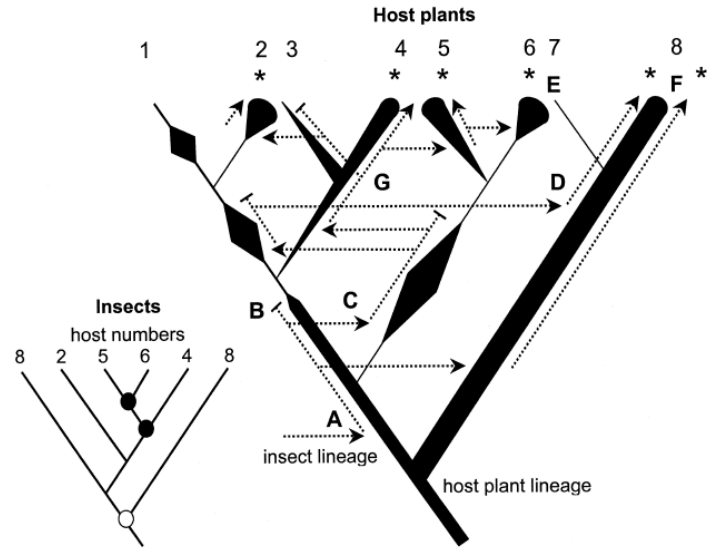
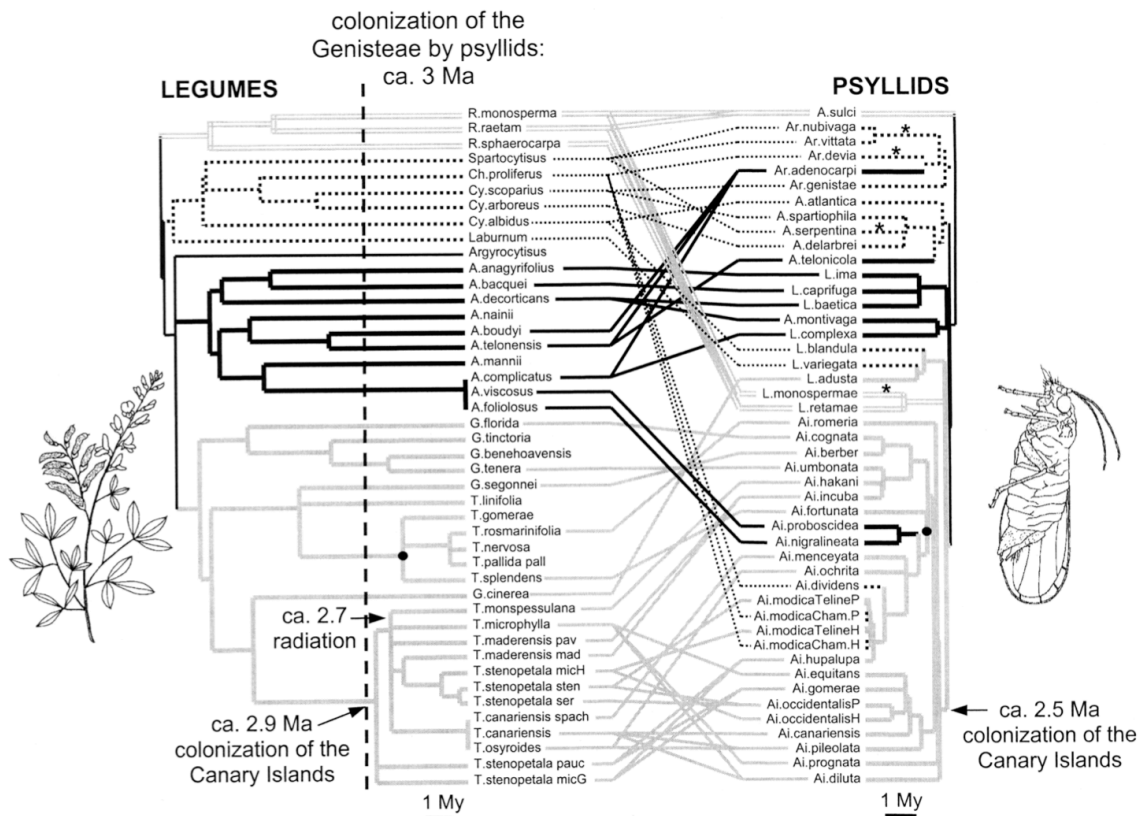


FIGURE 1. A hypothetical fluctuating host plant lineage (right), illustrating the factors that may influence how an insect lineage interacts with a fluctuating plant lineage and an interpretation of the resultant phylogenetic patterns (left). This model takes into account the susceptibility factors for host switching suggested by examination of the ecology of Canary Island psyllids and their legume hosts. Host abundance is indicated by line width. Examples of different events are labeled: A = colonization of preexisting host lineage by insect lineage; B = loss of insect due to extinction; C = increase in host abundance after bottleneck leads to vacant host, usually filled by near host switching from related plants; D = abundant host and geographical proximity may lead to wide host switching; E = rare plants are unlikely to be colonized; F = temporally stable host lineages may sustain multiple insect lineages; G = occasional cospeciation events. The asterisks indicate extant insect taxa, whose phylogeny is shown (left). Given the two phylogenies, certain events would be misinterpreted in a TreeMap analysis: the solid circles are cospeciation events, and the open circle is a duplication event (speciation of parasites in situ on the host).



Percy et al. 2004