

April 25, 2018. **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, different genes, 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” 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).

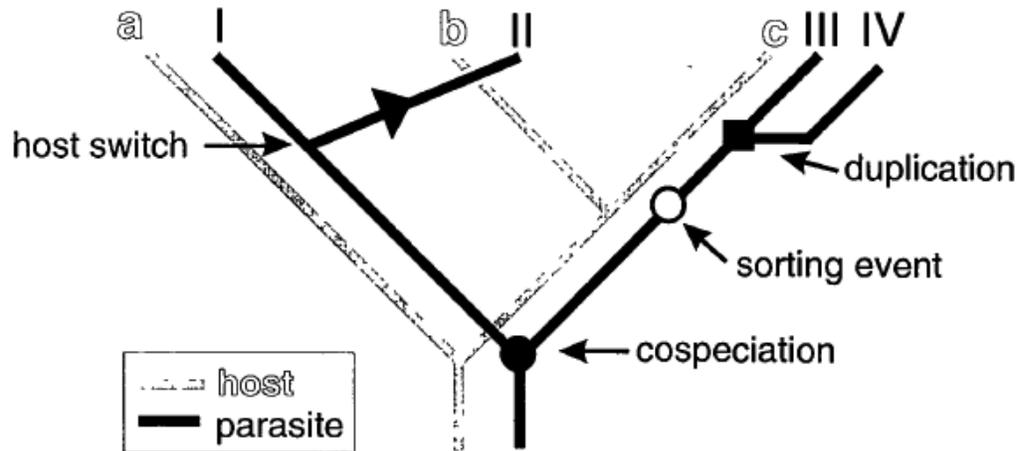


FIGURE 2. A host and parasite phylogeny showing a cospeciation event (●), a duplication (■), a host switch (▶), and a sorting event (○).

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 or calibrated ages on the phylogeny, 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.

Citations:

** papers and websites for cophylogeny software

- Althoff, David M., Kari A. Seagraves, and Marc TJ Johnson. "Testing for coevolutionary diversification: linking pattern with process." *Trends in ecology & evolution* 29.2 (2014): 82-89.
- Brooks, D.R., & D. McLennan. 1991. *Phylogeny, Ecology, and Behavior*. University of Chicago Press.
- **Charleston, MA and DL Robertson. 2002. Preferential host switching by primate lentiviruses can account for phylogenetic similarity with the primate phylogeny. *Syst Biol*, 51(3):528-535. TreeMap3 web site: <http://sydney.edu.au/engineering/it/~mcharles/software/treemap/treemap3.html>
- **Conow, C., Fielder, D., Ovadia, Y., & Libeskind-Hadas, R. (2010). Jane: a new tool for the cophylogeny reconstruction problem. *Algorithms for Molecular Biology*, 5(1), 16. Now Jane4: <https://www.cs.hmc.edu/~hadas/jane/>
- Cruaud A, Rønsted N, Chantarasuwan B, Chou LS, Clement WL, Couloux A, Cousins B, Genson G, Harrison RD, Hanson PE, Hossaert-Mckey M. An extreme case of plant–insect codiversification: figs and fig-pollinating wasps. *Systematic Biology*. 2012 Oct 4;61(6):1029-47.
- de Vienne, D.M., Giraud, T. & Shykoff, J.A. (2007) When can host shifts produce congruent host and parasite phylogenies? A simulation approach. *Journal of evolutionary biology*, **20**, 1428-1438.
- de Vienne, D. M., Refrégier, G., López-Villavicencio, M., Tellier, A., Hood, M. E., & Giraud, T. (2013). Cospeciation vs host-shift speciation: methods for testing, evidence from natural associations and relation to coevolution. *New Phytologist*, 198(2), 347-385.
- Hafner, M. S., and S. A. Nadler. 1988. Phylogenetic Trees Support the Coevolution of Parasites and Their Hosts. *Nature* 332:258-259.
- Huelsenbeck, J. P., B. Rannala, and B. Larget. 2000. A Bayesian framework for the analysis of cospeciation. *Evolution* 54:352-364.
- Jousselin, E., van Noort, S., Berry, V., Rasplus, J.Y., Rønsted, N., Erasmus, J.C. & Greeff, J.M. (2008) One fig to bind them all: host conservatism in a fig wasp community unraveled by cospeciation analyses among pollinating and nonpollinating fig wasps. *Evolution; international journal of organic evolution*, **62**, 1777-1797.
- **Merkle D, Middendorf M. 2005. Reconstruction of the cophylogenetic history of related phylogenetic trees with divergence timing information. *Theor Biosci*. 123:277–299.
- Page, R. D. M. 1996. Temporal congruence revisited: Comparison of mitochondrial DNA sequence divergence in cospeciating pocket gophers and their chewing lice. *Systematic Biology* 45:151-167.
- Page, R. D. M., and M. A. Charleston. 1998. Trees within trees: phylogeny and historical associations. *Trends in Ecology & Evolution* 13:356-359.
- Page, R.D.M., editor. 2003. *Tangled trees: phylogeny, cospeciation, and coevolution*. Univ. of Chicago Press, Chicago.
- Percy, D. M., R. D. M. Page, and Q. C. B. Cronk. 2004. Plant-insect interactions: Double-dating associated insect and plant lineages reveals asynchronous radiations. *Systematic Biology* 53:120- 127.
- Refrégier, G., Le Gac, M., Jabbour, F., Widmer, A., Shykoff, J. A., Yockteng, R., ... & Giraud, T. (2008). Cophylogeny of the anther smut fungi and their caryophyllaceous hosts: prevalence of host shifts and importance of delimiting parasite species for inferring cospeciation. *BMC Evolutionary Biology*, 8(1), 100
- Stone, G.N., Hernandez-Lopez, A., Nicholls, J.A., di Pierro, E., Pujade-Villar, J., Melika, G. & Cook, J.M. (2009) Extreme host plant conservatism during at least 20 million years of host plant pursuit by oak gallwasps. *Evolution; international journal of organic evolution*, **63**, 854-869.
- Veá IM, Grimaldi DA. Putting scales into evolutionary time: the divergence of major scale insect lineages (Hemiptera) predates the radiation of modern angiosperm hosts. *Scientific reports*. 2016 Mar 22;6:23487.
- Weiblen, G. D., and G. L. Bush. 2002. Speciation in fig pollinators and parasites. *Molecular Ecology* 11:1573-1578.

