

Plant and Microbial Biology 220. Critical Thinking in Microbiology
Tu-Th 12:30-2:00 pm
John Taylor - 2006

Evolution

Week 10 – Phylogenetics, the big tree of life.

Week 11 – Microbial species concepts.

Week 12 – Microbial genetic exchange.

Week 10 – Phylogenetics, the Big Tree of Life

Introduction

What are trees good for?

- Tools for comparative biology.
- Study the relationships of all of life.
- Infer the order and timing of past events.
- Gauge the relationship of your favorite organism to a model organism.
- Are we working on the same organism?
- Evolution of phenotype compared to evolution of genotype.
- Has convergence occurred?
- Compare your organism to others at the same point in time.
- Co-evolution
- Radiation?
- Genomic analyses.
- What is a species?
- Horizontal gene transfer.

The tree of life and how to make one.

Comparative biology. Sign of maturity in a field, enough data for comparison.
Promise of prediction.

Three big advances in the past few decades.

Quantitative comparative biology. Numerical taxonomy, phenetics.

Sneath, PHA, Sokal, RR, 1973. Numerical taxonomy: the principles and practice of numerical classification. San Francisco, W.H. Freeman. UCB Bios QH83.S581

Sokal, RR and Rohlf, FJ. 1995. Biometry: the principles and practice of statistics in biological research. 3rd ed. NY, W. H. Freeman. UCB Bios QH323.5.S63 1995

Spread of Hennig's ideas on cladistics.

Hennig, W. 1950. Grundzuge einer Theorie der phylogenetischen Systematik. Berlin, Deutscher zentralverlag. UCB Bios QL351.H4

Hennig, W. 1966. Phylogenetic systematics. Translated by D. D. Davis and Rainer Zangerl. Urbana, U. Illinois Press. UCB Bios QL351.H413, also a 1979 edition with same call number.

Access to nucleic acid variability.

Phenotypic characters and genotypic characters.

Key assumption, homology of characters.

Homology, paralogy

Secondary assumption, independence of characters.

TAXA, organisms or genes.

Types of phylogenetic methods

Methods currently in practice:

General

Avise, J. C. 1994. Molecular markers, natural history and evolution. Chapman and Hall, New York.

Felsenstein, Joseph. 2004. Inferring phylogenies. Sunderland, Mass.: Sinauer Associates. Bioscience QH83.F45 2004. Moffitt QH83.F45 2004

Page, R. D. M. (ed.). 2003. Tangled trees : phylogeny, cospeciation, and coevolution. Chicago, Ill. : The University of Chicago Press. Bioscience QH367.5.T36 2003

Page, R. D. M. and E. C. Holmes. 1998. Molecular evolution : a phylogenetic approach. Oxford ; Malden, MA : Blackwell Science. Bioscience QH390.P34 1998

How to

Hillis, D. M., C. Moritz, and B. K. Mable. 1996. Molecular Systematics. Sinauer Associates, Sunderland, Mass.

Li, W.-H. 1997. Molecular Evolution. Sinauer Associates. UCB Bios QH325.L655 1997

Hoch, PC, Stephenson, AG. 1995. Experimental and molecular approaches to plant biosystematics. St. Louis, Missouri Bot. Garden UCB Bios QK95.E96 1995

Salemi, M. and Vandamme, A.-M.. 2003. The phylogenetic handbook : a practical approach to DNA and protein phylogeny. Cambridge U Press.

Maddison, W. P., and D. R. Maddison. 2000. MacClade: analysis of phylogeny and character evolution, version 4. Sinauer Associates, Sunderland, Mass.

Hall, Barry G. 2004. Phylogenetic trees made easy: a how-to manual, 2nd ed. Sinauer, Sunderland, Mass. : Sinauer Associates. Bioscience QH367.5.H27 2004

Bayesian

Huelsenbeck, J. P., F. Ronquist, R. Nielsen, and J. P. Bollback. 2001. Evolution - Bayesian inference of phylogeny and its impact on evolutionary biology. *Science* V294:2310-2314.

Huelsenbeck, J.P., Larget, B., Miller, R.E., Ronquist, F. 2002. Potential Applications and Pitfalls of Bayesian Inference of Phylogeny. *Syst. Biol.* 51:673-688.

Lewis, P.O. 2001. Phylogenetic systematics turns over a new leaf. *TREE* 16:30-37.

Holder, M. and P. O. Lewis. 2003. "Phylogeny estimation: Traditional and Bayesian approaches." *Nature Reviews Genetics* 4(4): 275-284

Phylogenetic Approach

Problem, Define it.

Select likely data

Collect data from a subset of your taxa. Blast, Entrez-Taxonomy, NCBI, Google entrez.

ABI sequencer.

Determine homology

ClustalW, ClustalX alignment (google clustal)

Your brain

Analyze data phylogenetically

UC Museum of Paleontology

<http://www.ucmp.berkeley.edu/subway/phylo/phylosoft.html>

Joe Felsenstein at the University of Washington

<http://evolution.genetics.washington.edu/phylip/software.html>

Distance methods

UPGMA, Fitch Margoliash, Neighbor-Joining

Multiple hit corrections

Jukes/Cantor, Kimura, etc.

Character based methods

Parsimony

Maximum Likelihood, Model Test

(<http://darwin.uvigo.es/software/modeltest.html>), Posada D and Crandall KA

1998. Modeltest: testing the model of DNA substitution. *Bioinformatics* 14 (9): 817-818

Bayesian methods, likelihood with probabilities

Assess significance

Bremmer/Decay index

Bootstrap resampling

Bayesian posterior probability

If the result is not significant, go back to selecting new data.

If the result is significant, obtain data for all taxa and go back to analysis.

If the result is significant, but is not in agreement (congruent) with hypotheses based on other data, test for significance of incongruence.

Tests of congruence

Kishino-Hasegawa Test

Shimodaira-Hasagawa Test

Incongruity Length Difference/Partition homogeneity test

If the two hypotheses are significantly incongruent, reexamine both data sets.

One can be wrong, the other can be wrong, both can be wrong, but both cannot be right.

Pitfalls of Phylogenetics

Not enough taxa (two taxon trees).

Wakefield, A. E., S. E. Peters, S. Banerji, P. D. Bridge, G. S. Hall, D. L.

Hawksworth, L. A. Guuiver, A. G. Allen, and J. M. Hopkin. 1992.

Pneumocystis carinii shows DNA homology with the ustomycetous red yeast fungi. *Molecular Microbiology* 6:1903-1911

Taylor, J. W., and B. H. Bowman. 1993. *Pneumocystis carinii* and the ustomycetous red yeast fungi. *Molecular Microbiology* 8:425-426.

The homoplasy proof “super character”

Morden, C. W., and S. S. Golden. 1989. *psbA* genes indicate common ancestry of prochlorophytes and chloroplasts. *Nature* 337:382-385.

Morden, C. W., and S. S. Golden. 1991. Sequence analysis and phylogenetic reconstruction of the genes encoding the large and small subunits of ribulose-1,5-bisphosphate carboxylase/oxygenase from the chlorophyll b-containing prokaryote *Prochlorothrix hollandica*. *J. Mol. Evol.* 32:379-395.

Shimada, A., S. Kanai, and T. Maruyama. 1995. Partial sequence of ribulose-1,5-bisphosphate carboxylase-oxygenase and the phylogeny of *Prochloron* and *Prochlorococcus* (Prochlorales). *Journal of Molecular Evolution* 40:671-677.

Rooting

Lewis, M. T., and J. F. Feldman. 1996. Evolution of the frequency (frq) clock locus in ascomycete fungi. *Mol. Biol. Evol.* 13:1233-1241.

Background for today’s material

Baldauf, S. L. (2003). Phylogeny for the faint of heart: a tutorial. *Trends in Genetics* **19**, 345-351

- Berbee, M., and J. W. Taylor. 1999. Fungal Phylogeny. Pp. 12-77 *in* R. P. Oliver and N. N. Schweizer, eds. *Molecular Fungal Biology*. Cambridge University Press, Cambridge.
- Lewis, P.O. 2001. Phylogenetic systematics turns over a new leaf. *TREE* 16:30-37 (Bayesian methods).
- Walsh, D. A. and W. F. Doolittle. 2005. The real 'domains' of life. *Current Biology* 15:R237-R240.

Reading for Thursday:

- Brown, J. R. and W. F. Doolittle (1997). "Archaea and the prokaryote-to-eukaryote transition." *Microbiology and Molecular Biology Reviews* **61**(4): 456-502.
- Jeffroy, O., Brinkmann, H., Delsuc, F. & Philippe, H. (2006). Phylogenomics: the beginning of incongruence? *Trends in Genetics* **22**, 225-231
- Rokas, A., B. L. Williams, N. King and S. B. Carroll (2003). "Genome-scale approaches to resolving incongruence in molecular phylogenies." *Nature* **425**(6960): 798-804.