Integrative Biology 200   "PRINCIPLES OF PHYLOGENETICS"   Spring 2016
University of California, Berkeley   B.D. Mishler

April 8, 2016**. Phylogenetics and conservation biology**

A. The value of biodiversity:
- <u>Ethical:</u> each lineage is a thread in an heirloom fabric that we have the responsibility to pass on to future generations.
- <u>Intellectual:</u> we have a basic need to understand the world, how it came to be, and where we fit in it.
- <u>Ecological:</u> a diversity of interactors is needed for proper function of ecosystems, and a diversity of a replicators is needed as the raw material for natural selection (future evolutionary potential).
- <u>Economic:</u> natural lineages are a potential source for a myriad of products of direct economic benefit (medicines, food, esthetics, shelter, etc.).

B. Criteria than can be used for prioritizing conservation:
- Threat of extirpation/extinction
- Ecological importance -- keystone species; ecosystem services; resilience to climate change
- Rarity

C. Metrics for conservation:
- Taxon-based measures
- Phylogeny-based measures

D. Targets for conservation:
- Individual taxa or lineages
- Landscape and Habitat-based ("communites")

E. Key concepts behind conservation planning (Sarkar et al. 2006)
- Complementarity – 'quantitative contribution to the biodiversity features of a site that are not adequately represented in the existing set'
- Irreplaceability – the contribution of a given site in a potential set of targets to achieve a particular goal
- Vulnerability – probability of persistence of a population or other features of an area

F. Phylogenetics and conservation
    There has been tremendous recent progress in understanding the relationships of organisms at all levels, due to two different advances, whose cumulative impact has been great. One advance is theoretical and methodological -- a revolution in how any sort of data can be used to reconstruct phylogenies and interpret evolution and ecology. The other is empirical -- the sudden availability of copious new phylogenetic data from the DNA level and spatial data from digitizing of museum collections. Unfortunately, these advances have not yet made their way fully into applied biology and the critical task of conserving biodiversity.
    We systematists understand now that biodiversity is the whole tree of life, not just the named species. There are lineages smaller and larger than the traditional species level. Furthermore, species are not comparable between lineages in any manner. Thus counting species or measuring their ranges and abundances is a poor measure of biodiversity; we must develop measures of the actual diversity of lineages taking into account their evolutionary

properties and phylogenetic position. New quantitative measures for phylogenetic biodiversity, which take into account the number of branch points (and possibly branch lengths) separating two lineages have been developed, which can be applied to rarity assessment and conservation planning. This relatively new phylogenetic worldview can clarify greatly what "rarity" means: *rarity fundamentally means not having many living close relatives*. We can now quantitatively define what we mean by "*many*" and "*close*."

      As we have discussed already, all "species" are not equal in a phylogenetic sense (or any other sense for that matter). As has been pointed out by a number of pioneering cladistic conservation biologists, conservation priorities can best be set by a consideration of the phylogenetic relationships among species. This is because all attributes of organisms (genetic similarities, ecological roles, morphological specializations) tend strongly to be associated with phylogeny. From the standpoint of preserving the maximum phylogenetic diversity (and its associated attributes), saving a "long-branch" species (i.e., one such as the Coast Redwood or Santa Lucia Fir with much change along the terminal branch, either due to extinction or rapid evolution) should carry a higher priority than saving a "short-branch" species (i.e., a dandelion differing in only a few minor features from near relatives). Furthermore, saving a community of 100 species of diverse phylogenetic relationships should carry a higher priority than saving a community of 200 species belonging to only a few large clades (see the figure below for an illustration of these points). Thus, phylogenetic considerations should play a much more important role in conservation biology than they have to date.

      In an ideal world all species could be preserved -- in this world of limited resources (time, money, and public goodwill) indices based on phylogeny are being developed to help us preserve the maximal genetic, morphological, chemical, and ecological diversity. The general public will be much more supportive of species preservation efforts that are carefully focused and justified in this way, rather than of uncritical, across-the-board efforts. Phylogeny reconstruction is thus not just an academic exercise, but rather the fundamental basis of a truly practical taxonomy.

Right. A hypothetical cladogram illustrating the potential role of phylogeny in setting conservation priorities. Shown is a phylogeny of 43 "species"; the branch lengths are proportional in the vertical direction to the number of evolutionary character changes along that branch.

      Exercise: if you were offered three alternative conservation scenarios that would save the seven species in either group A or B or C, how would you rank them? How would you explain your ranking to a biodiversity manager who is not familiar with phylogenetic concepts?
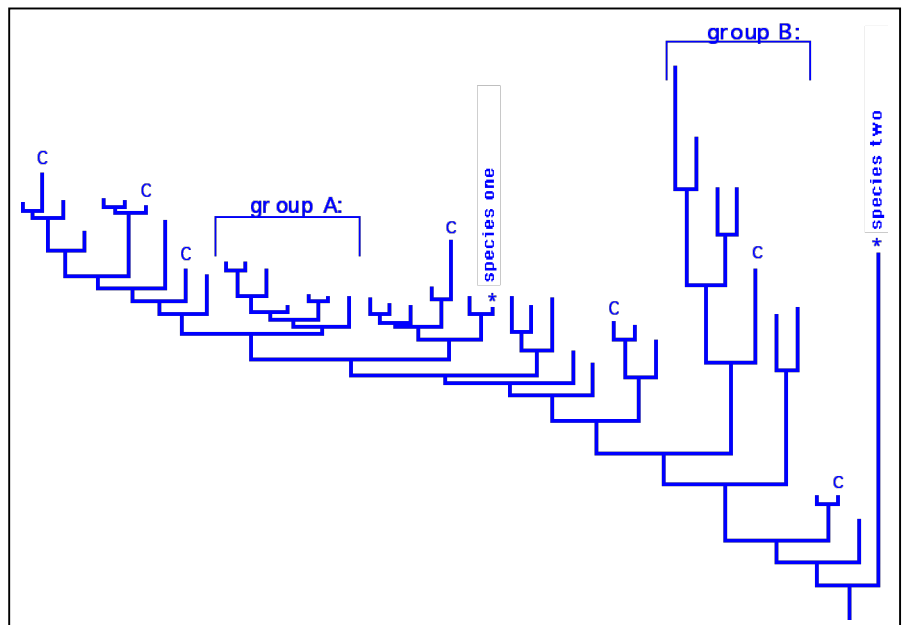
G. Phylogenetic Diversity and Phylogenetic Endemism.

      So, biodiversity is not just species – instead it is the full set of nested clades representing phylogenetic relationships among organisms at all levels. Species are, at best, only one level of clades among thousands, smaller and larger. Likewise, endemism is not just about species, even though virtually all endemism studies focus solely on the species level. Clades at all levels can be endemic and all levels are relevant to discovery and evaluation of centers of endemism.

Endemism, rather than being species-centric, should be more broadly defined to mean the geographic rarity of that portion of a phylogenetic tree found in a given area. This phylogenetically-based definition encompasses clades that are at the traditional species level, but also takes into account clades larger than or smaller than named species, and so provides a much more complete picture of rarity.

Phylogenetic measures of biodiversity were pioneered by Faith, who developed the concept of phylogenetic diversity (PD), which has been increasingly explored in recent years. Faith et al. and Rosauer et al. pioneered phylogenetic concepts of endemism (PE). Faith et al.'s approach was to identify what parts of a phylogenetic tree are absolutely restricted to a given region, an approach that could be called "absolute PE." Rosauer et al.'s approach considered the relative breadth of geographic distribution of parts of a phylogenetic tree that are found in a given region, an approach that could be called "weighted PE."

H. Quantitative methods

Phylogenetic diversity and endemism *(see also slides shown today and online)*

PD = sum of branch lengths of subtree connecting selected taxa with root.

PE = sum of branch lengths of range-weighted subtree (i.e., where each branch length has been divided by the branch range) connecting selected taxa with root.

Relative Phylogenetic Diversity (RPD) = PD calculated using the original tree ÷
PD calculated using a comparison tree with all branch lengths equal

Relative Phylogenetic Endemism (RPE) = PE calculated using the original tree ÷
PE calculated using a comparison tree with all branch lengths equal

CANAPE: Categorical Analysis of Neo- And Paleo-Endemism (Mishler et al., 2014)
      Uses RPE to find and classify centers of endemism through a two-step process:
      First, to determine if a place is a center of significantly high PE, a grid cell needs to be
        significantly high (one-tailed test) in either the numerator, the denominator, or both.
      Second, if (and only if) a grid cell passes one of those tests, we divide the centers of
        endemism into three meaningful, non-overlapping categories.

The program *Biodiverse* (to be explored further in an upcoming lab) can calculate many metrics, including the above as well as terminal taxon richness (TR) and weighted endemism for terminal taxa (WE). The statistical significance of these metrics is assessed in *Biodiverse* using a randomization wherein species occurrences in grid cells are randomly reassigned to grid cells without replacement, keeping constant both the total number of grid cells for each species and the species richness of each grid cell.

A few R tools:
    picante library:
        pd - Faith's phylogenetic diversity
        psc/psd/pse/psr/psv - phylogenetic species diversity metrics of Helmus et al. 2007
        specaccum.psr - rarefaction curve for phylogenetic species richness (psr)
    vegan library:
        diversity - general diversity and rarefaction metrics
        betadiver - general beta diversity metrics
        taxondive - taxonomic diversity indices using a distance matrix (you can substitute a phylo
        distance or trait distance matrix)

G. Introduction to literature

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