

EEB 2245 & EEB 2245W
Final STUDY GUIDE for EXAM 2
 SPRING 2014

Evolution of Biodiversity and Extinction

- recognize that diversification includes increase in number of species (i.e., diversity) and increase in major body forms (i.e., disparity)
- total number of taxa at any time is difference between diversification and extinction rates
- relationship between # fossils found and sediment volume (& explanation for this relationship)
- Pull of the recent: what is it? Example?
- Evidence of qualitative changes in diversity over time? Examples?
- Evidence of quantitative changes in diversity over time? Category of taxonomic classification most appropriate for addressing this question & why this category is most appropriate (i.e., families vs. species or phyla, etc.)
- Description of, and differences between, Background and Mass extinctions (global vs local causes; are causes for both events the same? etc.); proposed cause of the Mass extinction at the end of the Cretaceous and evidence that supports that explanation; explanations for other 4 mass extinctions; same or different causes? (asteroid impact?; other cause of each)
- What is a diversity profile? Be able to interpret diversity profiles for different taxa
- Sepkoski's 3 marine animal faunas (focused on families), what are they (Cambrian, Paleozoic, Modern)
- Ecological displacement and Ecological Replacement: what are they? How do they differ? Recognize/provide an example of each?

Characters, Homology and Homoplasy

- Fossil record provides point source for taxa, but does not show how taxa are related to one another (how do we "connect the dots"), i.e., determine phylogenetic relationships?
- distinction between macro- and microevolution?; level at which systematic methods apply
- what is a character (e.g. morphology, molecular, etc.)? What is a character-state? Be able to distinguish between them and recognize/provide examples of each
- mosaic evolution: what is it? How does it relate to the concept of entire species being "primitive" or "derived"? example?
- in reconstructing evolutionary relationships, seek homologies, rather than homoplasies (i.e., rather than features that are merely analogous in two taxa)
- understand and be able to define the concept of homology; basic criteria used to determine homology (e.g., position, structure, etc.); must always identify the taxonomic context
- problems with organisms that look similar, but are not closely related (i.e. homoplasy)
- be able to explain the difference between homoplasy and homology
- why strive to use homologies over homoplasies for the generation of phylogenetic trees?
- definition of homoplasy; describe/distinguish among the 3 different types of homoplasy: parallelism- what is it? Describe an example of parallelism; be able to recognize an example of parallelism; recognize parallelism on a phylogenetic tree. Convergence- what is it? Describe an example of convergence; recognize convergence on a phylogenetic tree; be able to recognize an example of convergence. How would you distinguish parallelism from convergence? Reversal- what is it? Describe an example of a reversal; recognize a reversal on a phylogenetic tree; be able to recognize an example of a reversal; Homobatrachotoxin- describe its taxonomic distribution; it is an example of which type of homoplasy? Homoplasy across character types (i.e., morphological, chemical, molecular, etc.)

Reconstructing Evolutionary History from Indirect Evidence

- BE CERTAIN TO COMPLETE THE EXERCISES POSTED ON THE COURSE WEBSITE.
- What is systematics? What is a phylogenetic tree?
- How do we infer branching patterns among taxa? Initial methods were subjective (e.g., Haeckel, Romer)
- Hennig's contributions: developed a formalized, objective, character-based method
- understand and be able to define, and/or recognize in a data matrix and/or on a phylogenetic tree as appropriate the following terms: terminal taxon, node, branch, dichotomy, polytomy, sister taxon (taxa), most recent common ancestor, distant common ancestor, root, clade/monophyletic group, paraphyletic group, character, character-state, plesiomorphy, symplesiomorphy, apomorphy, synapomorphy
- ingroup vs outgroup- how do they differ? Criteria for selection of each; monophyly of ingroup

- relative to outgroup
- understand the distinction between an ancestral homology and a derived homology; importance of including taxonomic context (i.e., group under consideration)
- role outgroup plays in systematics (allows polarization of character states- i.e., determination of ancestral/plesiomorphic versus derived/apomorphic states of characters; state in outgroup is plesiomorphic); be able to polarize characters using an outgroup
- What is parsimony? What role does the principle of parsimony play in systematics? Steps in conducting a phylogenetic analysis using parsimony as the optimality criterion; be able to map characters on tree topologies from a data matrix optimally (i.e., so as to minimize the total number of changes for each character on a particular tree topology).
- Other methods for generating phylogenetic trees (i.e., Likelihood, Bayesian methods)
- Be able to identify the possible sets of relationships (tree topologies) for a SMALL set of taxa, identify plesiomorphic vs. apomorphic states of characters using an outgroup, map characters onto the possible tree topologies, determine the most parsimonious topology, etc.; for morphological and molecular data set/matrix
- summarizing character data in a data matrix (be able to do so); be able to interpret a data matrix of in the context of a phylogenetic tree (e.g., determine which topology is most parsimonious); for morphological and molecular data
- Be able to generate the most parsimonious tree topology from a *simple* data matrix for a SMALL set of taxa
- Why are computer programs required to determine the most parsimonious tree topology/set of relationships when dealing with greater than 4 or so taxa?
- Molecular data: advantages (large number of characters, broadly comparable) and disadvantages (multiple hits, alignment, etc.); understand that all 3 types of homoplasy exist with molecular character data. Sources of sequence data: nuclear, organelle (mitochondria, chloroplasts, etc.); sources of differences between nuclear and organelle gene trees (endosymbiotic origin of organelles, maternal inheritance of mitochondria)

Biogeography and Continental Drift

- What is biogeography? What are its 2 major components? (description of distributions vs. explanations for distributions)
- Importance of knowing the actual distribution of a taxon before attempting to explain it
- Importance of understanding phylogenetic relationships of taxon before attempting to explain its distribution (group under consideration should be monophyletic)
- Common recurring distributional patterns and the Biogeographic realms: Palearctic, Nearctic, Neotropical, Ethiopian, Oriental, Australian, Oceania & Antarctic) What are they? Where are they? 3 major categories of barriers; barriers bounding each biogeographic realm; Wallace's line- What is it? Where is it?
- Vagility and fact that varies among types of organisms
- Terminology for types of distributions- endemism, cosmopolitan, disjunct: what do they mean, provide and/or recognize examples
- Differences between vicariance vs dispersal explanations for geographic distributions of organisms
- Barriers change over time, example?
- Continental Drift- what is it? know basic sequence and time of continental configurations of Pangaea, Laurasia, Gondwana, modern positions; plate tectonics as a mechanism (why not Rodinia?)
- Examples of vicariant events explained by continental drift (e.g., *Glossopteris* flora, *Lystrosaurus*)
- Historical biogeography: importance of establishing age of a taxon and its phylogenetic relationships prior to developing explanations for its distribution.
- Example of major Dispersal event (Great American Interchange)

NOTE: you are not responsible for the information presented by our Prominent Evolutionary Biologists who visited the class...but a bonus question is not beyond possibility.