

EEB 2245 & EEB 2245W
Preliminary STUDY GUIDE for EXAM 2
 SPRING 2019

Evolution of Biodiversity and Extinction

- 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 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)
- Is there evidence that plants experienced mass extinctions? If not, why not?
- 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); what major groups characterize each?
- # marine animal families now vs. in the past?
- 3 types of conditions that may foster increases in diversity within an individual taxon: Ecological displacement and Ecological Replacement: What are they? How do they differ? Recognize/provide an example of each; key innovations/adaptive radiation: what is this? Recognize/provide an example.
- Anthropocene: What is it? When is/was it? What is its cause? Criteria for a new interval to be added to the Geological Time Scale? Options of such criteria for the Anthropocene?

Characters, Homology and Homoplasy

- Distinction between direct and indirect evidence for elucidating patterns of evolutionary change.
- Distinction between macro- and microevolution?
- Types of characters (e.g. morphology, molecular, etc.); what is a character-state? Be able to distinguish between characters and character-states 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:
 - Convergence: What is it? Describe an example of convergence; recognize convergence on a phylogenetic tree or from a verbal description in which necessary taxonomic context is provided.
 - Parallelism: What is it? Describe an example of parallelism; recognize parallelism on a phylogenetic tree or from a verbal description in which necessary taxonomic context is provided.
 - How would you distinguish parallelism from convergence? Reversal: What is it? Recognize a reversal on a phylogenetic tree or from a verbal description in which necessary taxonomic context is provided. Be able to recognize 3 different types of homoplasy with different character types (i.e., morphological, chemical, molecular, etc.) and on a phylogenetic tree.

Reconstructing Evolutionary History from Indirect Evidence

- BE CERTAIN TO COMPLETE THE PROBLEM SET DISTRIBUTED IN CLASS AND 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, use of outgroups
- 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, apomorphy, synapomorphy
- Distinction between ingroup and outgroup- how do they differ? Criteria for selection of each; importance of 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) in statements of homology
 - Role outgroup plays in systematics (allows polarization of character states- i.e., determination of ancestral/plesiomorphic state 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).
 - Understand that there are other methods for generating phylogenetic trees (i.e., Likelihood, Bayesian methods); you don't need to know these methods, but you should know they exist.
 - Be able to identify all possible sets of (dichotomous) 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.; from morphological and molecular data matrices; be able to use outgroup data to polarize both binary and multistate characters; limitations of outgroup for polarization of multistate characters.
 - Be able to summarize character data in a data matrix; be able to interpret character data from a data matrix for both morphological and molecular data for both binary and multistate characters; be able to map characters on a tree from a data matrix with either type of characters.
 - Be able to determine which tree topology is most parsimonious and generate the most parsimonious tree topology based on a 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, etc.) and disadvantages (multiple hits, etc.); understand that all 3 types of homoplasy exist with molecular character data; recognize examples of each.

Biogeography and Continental Drift

- 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)
- What is biogeography? What are its 2 major components? (description of distributions vs. explanations for distributions)
- Formal descriptions of distributions of organisms: common recurring distributional patterns and the 8 Biogeographic realms: Palearctic, Nearctic, Neotropical, Ethiopian, Oriental, Australian, Oceania & Antarctic) What are they? Where are they? 3 main types of barriers (climate, mountains, etc.); barriers bounding each biogeographic realm; Wallace's line-What is it? Where is it? Understand that barriers differ in imperviousness depending on type of organisms (e.g. Panama isthmus); barriers also change over time, example?
- What is vagility? Variation in imperviousness of barriers depending on type and vagility of organisms.
- Terminology for types of distributions (i.e., endemic, cosmopolitan, etc.); what do they mean? Illustrate and/or recognize examples of each.
- Physical features of the earth worth considering in developing explanations for distributions: continental shelf—what is it? Where is it? Distinguish between continental vs. oceanic islands; recognize islands of each type from a map illustrating continental shelf; provide an example of each type of island; differences in effects of changes in sea level on each type of island and implications for dispersal and thus distributions of organisms; continental drift—what is it? Know basic sequence and time of continental configurations of Pangaea, Laurasia, Gondwana, modern positions; why theory of continental drift was initially poorly received by scientific community; discovery that changed this situation? Alfred Wegener's biological evidence for continental drift (i.e., situation with repeated patterns in the *Glossopteris* flora and *Lystrosaurus*).
- Explanations for distributions: (we will update the study guide with this material immediately after lecture on Tuesday)

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.