

Genetics and Evolution IB 201 06- Lecture 3

I. General Information about Trees

I. Historical Sketch

Early (before Darwin) tree diagrams usually represented the great chain of being, from the smallest cells progressing up the chain to man, considered the top of the chain—the pinnacle of evolution.

After Darwin, trees were likely to reflect the “descent from common ancestor” concept (e.g., Darwins’ tree; Haeckel’s tree).

A century later, the rules for quantitative, rigorous reconstruction of trees developed (W. Hennig’s rules; J. Farris’ maximum parsimony algorithm; J. Felsenstein’s maximum likelihood method).

This led to the view that *Classifications* should be based on the strict interpretation of phylogeny

- **Nested hierarchies of *monophyletic* groups**

II. Rules for Recognizing Groups in Classifications

1. Recognize only monophyletic groups in classifications
 - **Monophyly**—

2. Corollary: Reject paraphyletic and polyphyletic groups
 - **Paraphyly**--

 - **Polyphyly**--

Examples: Cartoon (monophyly, paraphyly, polyphyly)

Examples: Real

III. Reading Trees

- **Rotating branches**

- **Swapping branches**
 - **exponential increase in possible number of trees as taxa are added**

- **Parentheses to represent trees**

- **Dichotomous branching**

- **Polytomies (e.g., trichotomous branching)**
 1. **Soft polytomy**

 2. **Hard polytomy**

 3. **Star phylogeny**

- **Rooted vs. Unrooted trees (exercises in class)**

- **Diagonal cladograms vs. horizontal cladograms vs. phylograms**

Refs: General—Page, RD and EC Holmes. 1998. *Molecular Evolution, A Phylogenetic Approach*. Blackwell Science, Oxford.

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