Macroevolution

Introduction to Macroevolution

In this session on macroevolution, we delve into the reconstruction of deep evolutionary history. While microevolution deals with changes within populations over shorter time scales, macroevolution focuses on the broader patterns and processes shaping life over millennia.

- Microevolution: Changes at the population level.
- **Macroevolution**: Deep history and evolutionary relationships.

This discussion highlights the tools, concepts, and challenges of understanding the evolutionary tree of life.

Evolutionary Trees: Hypotheses of Relationship

Understanding Evolutionary Trees

Evolutionary trees (also called cladograms or phylogenetic trees) represent hypotheses about relationships among taxa. The key components of these trees include:

- **Nodes**: Represent common ancestors.
- **Branches**: Indicate evolutionary pathways.
- Terminal taxa: The species or groups at the ends of branches.

For example, in the simplest three-taxon tree:

- Birds (Aves) and crocodiles (Crocodylia) are each other's closest relatives.
- Lizards (Squamata) are the outgroup, more distantly related to both.

Misleading Appearances

Relationships in evolutionary trees are based on common ancestry, not superficial similarities. For instance:

• Crocodiles may visually resemble lizards, but they are more closely related to birds.

Evidence for Building Evolutionary Trees

Evolutionary biologists rely on shared, derived traits (**synapomorphies**) to construct trees. Types of evidence include:

Morphological Characters

- Bone structure (e.g., four-chambered hearts).
- Muscle anatomy.

Molecular Characters

• DNA, RNA, and protein sequences.

Developmental Characters

• Embryonic development stages (e.g., metamorphosis).

Behavioral Characters

• Nest-building behavior in archosaurs (birds, crocodiles, and dinosaurs).

Biochemical Characters

• Venom types in snakes: neurotoxins (Elapids) vs. muscle toxins (Vipers).

These traits provide a framework to hypothesize relationships and construct parsimonious trees that minimize the number of evolutionary changes.

Why Evolutionary Biologists Are Annoying

Evolutionary biologists often make provocative statements like, "Humans are fish," or "Birds are dinosaurs." These statements reflect:

- **Monophyletic groups**: Include all descendants of a common ancestor (e.g., humans and all great apes).
- **Paraphyletic groups**: Exclude some descendants (e.g., excluding humans from "great apes" is evolutionarily inaccurate).

By adhering to monophyletic naming conventions, evolutionary biologists maintain historical accuracy in classification.

Two Ways to Be Similar: Homology vs. Convergence

Homology: Similarity Through Shared History

- **Example**: The forelimbs of tetrapods (e.g., humans, bats, whales) have homologous structures, modified for different functions (e.g., flying, swimming, grasping).
- Key Point: Shared ancestry explains these similarities.

Convergence: Independent Evolution of Similar Traits

- Example 1: Wings in bats and birds evolved independently.
- **Example 2**: Streamlined body shapes in tuna and lamnid sharks reflect adaptation to similar environments, not shared ancestry.
- Key Point: Similar selective pressures can lead to similar solutions.

Constructing Evolutionary Trees

Evolutionary trees are built using data sets of morphological, molecular, and other characters. Key principles include:

- **Parsimony**: The simplest tree (fewest evolutionary changes) is most likely correct.
- **Descent with Modification**: Groups are related by a common ancestor, and traits change over time.
- **Bifurcation**: Lineages split into two (not three or more) at each node.

Examples of Evolutionary Similarities and Differences

Homology in Action

- Scales, Feathers, and Fur: Feathers and fur evolved from ancestral scales.
- Jaws: Vertebrate jaws evolved from gill arches in early ancestors.

Convergent Evolution

- **Saber-tooth Morphology**: Similar skull adaptations in unrelated species like Smilodon (placental mammal) and Thylacosmilus (marsupial).
- **Leglessness in Lizards**: Multiple independent losses of legs in different lineages, including snakes and legless lizards.

Summary of Key Assumptions in Deep History Reconstruction

- 1. Groups of organisms are related by common descent.
- 2. Characteristics change over time in lineages.
- 3. Species split in a bifurcating pattern.

Together, these principles embody the concept of **descent with modification** and guide our understanding of macroevolution.

Next Steps

In the next session, we will explore the "hostile forces of nature," including:

- Gliding mechanisms.
- The evolutionary adaptations of hoatzins, leafcutter ants, and more.

Stay tuned for an engaging exploration of evolutionary challenges and solutions!