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1 Evolutionary Thinking

Introduction (Lecture)

- ▷ Essential questions of evolutionary biology:
 - Why do organisms look so different?
 - Why develop elaborate sexual traits?
 - Why do organisms senesce?
- ▷ Evolution is mainly an historical science and thus must rely on other methods of reconstructing the past or making inferences about evolutionary forces.
- ▷ **Proximate**: a question about a mechanistic cause; provides an immediate explanation about **how** a mechanistic cause functions.
- ▷ **Ultimate**: **why**, or the reason, a trait or organism is the way it is; an evolutionary explanation.
- ▷ Example of proximate vs ultimate in Galapagos finches:
 - Proximate: developmental growth factor is increased/decreased in some birds.
 - Ultimate: different habits are selected on breaks that maximize food gathering ability.
- ▷ Evolutionary biology's approach to answering questions:
 - **Empirical data**: **observation** studies, experiments; the *comparative method*.
 - **Theory**: **predictions** that use models and mathematical reasoning which can be **tested** with empirical data.
- ▷ Overview of the components of evolution by natural selection:
 - Genetic variation exists, via mutations.
 - Mutations are heritable.
 - There is an advantage to survival and/or reproduction from the mutation.
 - Individuals with the advantage in survival/reproduction are selected for.

10 Studying Adaptation

Hypothesis Testing: Oxpeckers Reconsidered

- ▷ **Adaption:** a trait, or a suite of traits, that increases the fitness of its possessor.
- ▷ No hypothesis for the adaptive value of a trait should be accepted simply because of its plausibility.
- ▷ Oxpeckers and impalas traditionally were thought to have a mutually beneficial existence; oxpeckers ate ticks and impalas provided a safe environment.
- ▷ Experiments on cattle were done to test whether this observation was true:
 - Results show red-billed oxpeckers have no effect tick loads of cattle.
 - Red-billed oxpeckers maintained open wounds, even enlarging existing wounds to feed on the cattle's blood.
 - Red-billed oxpeckers removed hosts' earwax; whether this is good or bad is unclear.
 - Even these results must remain in question, as cattle are not the native host for the birds.
- ▷ Other important points to remember:
 - Differences among populations or species are not always adaptive.
 - Not every trait is adaptive.
 - Not every adaptation is perfect, often the adaptation just happened to work well enough or by chance better than other adaptations.

Experimental Design

- ▷ Defining and testing effective control groups is critical.
- ▷ Treatments of controls and experimental measures must be handled as close to exactly alike as possible.
- ▷ Randomization is a key technique for equalizing miscellaneous effects and a tool to avoid bias.
- ▷ Reproduction is essential in order to help remove potential outlier effects.
 - Allows for greater understanding of precision, accuracy, and variation by providing more data for statistical tests.

4 Evolutionary Trees

How to Read an Evolutionary Tree

- ▷ **Phylogeny:** aka evolutionary tree or phylogenetic tree, is a diagram showing the history of divergence and evolutionary change. Essentially, it's the **genealogical relationships** of organisms based on descent with modification.
 - **Taxa:** the units you are analyzing, e.g. certain species or DNA sequences.
 - **Character:** a feature or trait present among the taxa of interest, e.g. teeth of mammals or nucleotides of DNA sequences.
 - *Character state(s):* an **alternative condition** of a character, which are able to evolve one to another, e.g. pointed/flat teeth of mammals.
 - **Ancestral character:** a trait that was **possessed by the common ancestor**.
 - **Derived character:** a trait the was **not possessed by the common ancestor** and instead **evolved** in at least one of the descendants.
 - **Synapomorphy:** derived character state shared by **two or more** taxa and used to define a clade of taxa.
 - **Autapomorphy:** derived character state in only **one** taxon.
 - **Outgroup:** a taxon or taxa that are used to root the phylogeny or determine ancestral character states.
 - **Ingroup:** the set of taxa that are the focus of the phylogeny.
 - **Nodes:** points at which the tree splits; represents mutations, speciation events, or **character changes**.
 - **Anagenesis:** descent with modification, but **no speciation**.
 - **Cladogenesis:** **speciation**, origin of clades.
 - **Clade:** also known as a **monophyletic group**, an ancestor and **all** of its descendants.
 - **Paraphyletic group:** a group of organisms consisting of an ancestor and **some** of its descendants.
 - **Sister:** a taxa or clade that are most closely related to each other; they **share the most recent** common ancestor.
- ▷ **Homology:** similarity due to common descent; **continuity** of a trait, character, or character state through time.

- *Homologous trait*: found in a taxa that inherited the trait from a common ancestor.
- ▷ **Homoplasy**: or analogous, similarity in the characters or traits in different taxa due to convergent evolution, parallelism, or reversal, but **not due to common descent**.
 - **Convergent evolution**: similar traits due to selective forces and **not shared ancestry**.
 - **Parallelism**: convergent evolution in **recently diverged** taxa.
 - **Reversal**: derived traits or character states that revert to the ancestral form.

Inferring Phylogenetic Trees

- ▷ **Parsimony**: the hypothesis of relationshipsthat requires the **smallest number of character changes** is most likely to be correct.
 - Based on **derived** traits(synapomorphies).
 - Reconstruction using parsimony:
 1. Code characters.
 2. Make up a taxon x character matrix.
 3. Search for synapomorphies, and theshortest tree.
 - Outgroups can help polarize the characters.
 - **Treelength**: a measure of evolutionary change using parsimony.
 - Shortest tree length produces most parsimonious tree.
 - Length determined by number of synapomorphies.
 - Homoplasious characters increase tree length.
- ▷ **Distance Methods**: converts a sequence alignment to genetic distances between pairs of sequences.
 - Branch length is proportional to genetic differences.
- ▷ **Baysian**
- ▷ **Bootstraping**

3 Natural Selection

Lecture Notes

▷

Discussion Questions: Dog Domestication

▷ Background and Goals

- What hypotheses about dog domestication are examined in this paper?
 - The origin of domestic dogs was the main focus; genetic data suggests East Asia, but other data suggests Europe and Siberia.
- What predictions do these hypotheses make? What would the expected phylogenetic trees look like under each of these hypotheses (i.e. what are the expected topologies)?
 - Dogs and wolves would fall under a monophyletic group from a particular area indicating origin.

▷ Methods

- What taxa were sampled for this study?
 - Hypothesis was tested using DNA extracted to trace mitochondrial genomes from 18 prehistoric canids and 20 modern wolves from Eurasian and American origin.
- What gene sequences were used for this study?
 - Wolves, dogs, including divergent breeds, recently published chinese indigenous dogs, and coyotes. (148 mitochondrial genomes)
- What phylogenetic methods were used to reconstruct the phylogenetic tree in Figure 1?
 - Maximum likelihood, coalescence, and bayesian.

▷ Results and Discussion

- In Figure 1, which wolf sequence is most closely related to the extant dog clade A, and what geographic region is it from?
 - Argentina (pre-Columbian within clade A)
- In Figure 1, which clade of modern dog sequences has the oldest origin? Approximately how old is this clade?
 - Dog clade C, Germany, 14,700 years ago.

- Based upon Figure 1, how many times does it appear that modern extant dogs could possibly have been domesticated?
 - Figure 1 suggests 4, but the the authors state, "the inferred recent divergence of clade B from wolves now found in Sweden and Ukraine implies that is might represent a mitochondrial genome introgressed from wolves rather than one established by domestication."
- What was the topology of the phylogenetic tree that was recovered, and therefore, which hypothesis was supported?
 - The findings support the conclusion that legacy of dogs derives from wolves of European origin.
 - Analysis of coalescence times support divergence time of >15,000 years ago.
 - Past mitochondrial and Y chromosome analysis suggested non-European, but had less supported data than these findings.

▷ Conclusions

- What are the major conclusions of the paper?
 - Three of four modern dog clades are more closely related to sequences from ancient European rather than extant wolves with divergence times >15,000 years ago.
- Was the taxonomic sampling sufficient to rule out alternative hypotheses?
 - Ancient panel did not contain specimens from Middle East or China. No, no ancient dog remains older than 13,000 years are known from those regions.
 - The mtDNA sequence tree is well supported, but represents a single genetic locus. Independent loci could offer more power to resolve phylogenetic relations.

6 Mendelian Genetics



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