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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:** relationships that require the **smallest number of character changes** are most likely to be correct.
  - Based on shared and **derived** traits(synapomorphies).
  - Reconstruction using parsimony:
    1. Code characters.
    2. Make up a taxon×character matrix.
    3. Search for synapomorphies, and the shortest tree.
      - Outgroups can help polarize (ancestral vs derived) 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.
- ▷ **Maximum likelihood:** a method of estimating the parameters of a probability distribution by **maximizing a likelihood function**.
  - One of the more dominant means of statistical inference.
  - **Likelihood:** measure of goodness of fit of a statistical model to a sample of data for given values of the unknown parameters.
  - $P(D|H)$ ; probability(P), Data(D), Hypothesis(H)
  - **Bayesian:** uses the likelihood function to create a quantity called the *posterior probability* of trees using a model of evolution based on prior probabilities in order to produce the most likely tree.

- **Bootstrapping:** creating a value that indicates how many times out of 100 (normally) that the same branch was observed when repeating the phylogenetic reconstruction on re-sampled (pseudoreplicated) set of data.

## 6 Mechanisms of Evolutionary Change

### Hardy-Weinberg Equilibrium

- ▷ **Population:** a group of interbreeding individuals and their offspring.
- ▷ **Gene pool:** the set of all genes, or genetic information, in any population.
- ▷ **Genotypic frequency:** number of individuals with a given genotype divided by the total number of individuals in the population.
  - The proportion (i.e.,  $0 < f < 1$ ) of genotypes in a population.
- ▷ **Allele frequencies:** relative frequency of an allele at a particular locus in a population.
  - **Locus:** a fixed position on a chromosome where a particular gene or genetic marker is.
  - Monoploids: frequency of an allele is the result of the number of copies of the allele divided by sample size.
    - $p = i/N$
    - $p$ : frequency |  $i$ : copies of alleles |  $N$ : sample size
  - Diploids: frequency of alleles within three possible genotypes at a locus with two alleles.
    - $p = f(AA) + \frac{1}{2}f(AB)$  frequency of A-allele
    - $q = f(BB) + \frac{1}{2}f(AB)$  frequency of B-allele
  - Allele frequency can always be calculated from genotype frequency, whereas the reverse requires the *Hardy-Weinberg principle* of random mating apply.
- ▷ **Hardy-Weinberg principle:** allele and genotype frequencies in a population will remain constant in the absence of evolutionary influences.
  - Allele frequencies do not change from one generation to the next.
  - Genotypic frequencies after one generation of random mating:
 
$$p^2 + 2pq + q^2$$
  - Evolutionary influences: genetic drift, mate choice, assortative mating, natural selection, sexual selection, mutation, gene flow, meiotic drive, genetic hitchhiking, population bottleneck, founder effect, and inbreeding.
    - *Most of these influences will be discussed later.*



## Selection

- ▷ **Fitness:** success at which a organism produces fertile offspring.
- ▷ **Competition:** an interaction between organism in which the fitness of one is lowered by the presence of another.
- ▷ **Selection:** the act on a heritable phenotypic trait due to competition.
  - Can be members of the same of different species.
  - Not always directional and adaptive, instead selection pressure is applied and removes the less fit variants.
  - Can be classified in different ways, such as effect on a trait, on genetic diversity, by life cycle, by unit of selection, or by the resource in competition.
  - Most effective on large populations.

### By Effect on a Trait

- **Stablizing selection:** the simplies case in which selection acts to hold a trait at a stable optimum.
- **Directional selection:** favours extreme values of a trait.
- **Disruptive selection:** acts during transition periods when current mode is sub-optimal, but alters trait in more than one direction.
  - **Univariate:** when the trait is both quantitatively favoured in either direction and can lead to speciation.

### By Effect on Genetic Diversity

- **Purifying selection:** aka negative selection; acts to remove genetic variation from the population.
- **de novo mutation:** introduces new variation and opposes negative selection.
- **Balancing selection:** acts to maintain genetic variation, even in absence of *de novo* mutation by frequency-dependent selection.
  - **Frequency-dependent selection:** fitness that depends of the phenotypic or genotypic **composition** of a population.
    - **Positive:** fitness **increases** as frequency of the trait **increases**.
    - **Negative:** fitness **decreases** as the frequency of the trait **increases**.

- **Overdominance**, *aka heterozygote advantage*: when a combination of alleles confers a selective advantage over individuals with one allele.
- **Underdominance**, *aka heterozygote disadvantage*: when the heterozygote has lower fitness than either homozygote.

### By Life Cycle Stage

- **Viability selection**: *aka survival selection*: increases probability of survival.
  - Can act to improve probability of survival before and after reproduction.
- **Fecundity selection**: increases the rate of reproduction given survival.
  - May be split into sub-components including sexual selection, gametic selection, gamete viability, compatability selection, and zygote formation.

## Mutation

- ▷ **Mutation**: alteration in the nucleotide sequence of the genome of an organism.
  - May not produce discernible phenotypic changes.
  - The ultimate source of genetic variation.
  - Have several types of changes, from no effect, to small changes, or complete loss of function.

### Large-Scale Structural Mutations

- **Gene duplications**, *aka amplifications*: repetition of a chromosomal segment or attachment of extra piece of chromosome to another, leading to multiple copies of chromosomal regions.
- Deletions of large chromosomal regions.
- **Fusion genes**: mutations that join previously separated genes into one new distinct gene.
- **Chromosomal rearrangement**: large scale changes in structure of chromosomes, leading to speciation in isolated, inbred populations. Includes:
  - **Chromosomal translocations**: interchange of genetic parts from nonhomologous chromosomes.

- **Chromosomal inversions:** reversing the orientation of a chromosomal segment.
- Non-homologous chromosomal crossover.
- **Interstitial deletions:** inverse of fusion genes; removes a segment of DNA joining distant genes.
- **Loss of heterozygosity:** loss of one allele, by deletion or genetic recombination, in a organism that previously had two different alleles.

### Small-Scale Mutations

- **Point mutation:** a single nucleotide base change, that can result in a variety of effects.
- **Insertions:** add one or more extra nucleotides into the DNA.
  - Usually caused by transposable elements, or errors during replication or repeating elements.
  - Can cause *reading frame shift*, possibly effecting how many codons are read, and thus altering the gene product.
- **Deletions:** remove one or more nucleotides from the DNA.
  - Also can cause a reading frame shift like insertions.
  - Generally irreversible.
- **Substitutions:** exchange of a single nucleotide for another.
  - Often classified as transitions or transversions.
  - Generally a purine (A-G) for a purine, or a pyrimidine (C-T) for a pyrimidine.
  - Can be reversed by another point mutation.

### Impact on Protein Sequence

- Effect of mutation depends heavily on where it occurs, particularly in a coding or non-coding region.
- Regulator sequences, e.g. promoters, enhancers, silencers, can alter gene expression but are less likely to alter protein sequence.
- **Frameshift mutation:** caused by insertion or deletion of nucleotides that is not divisible by three, resulting in a different translation from the original.
- **Synonymous substitution:** a codon replacement with another that codes for same amino acid.
  - **Silent substitution:** no phenotypic difference after a synonymous substitution.
- **Nonsynonymous substitution:** a codon replacement that codes for a different amino acid.
  - **Missense mutation:** codon replacement that renders the resulting protein nonfunctional.
  - **Nonsense mutation:** codon replacement that results in a premature stop codon that produces a truncated and often nonfunctional protein.

### Migration

- ▷ **Gene flow:** movement of alleles, or genetic variation, between populations.
  - If the rate of gene flow is high enough, then two populations are considered to have equivalent allele frequencies and thus a single population.
  - Constrains speciation by combining gene pools of the groups.
  - May result in the addition of novel genetic variants in the gene pool.

### Factors of Gene Flow

- Gene flow is expected to be lower in species that:
  - have low mobility or dispersal.
  - occur in fragmented habitats.
  - have long distances between populations.
  - have small population sizes.
- **Allopatric speciation:** when gene flow is blocked by **physical** barriers that inhibit gene flow.
- **Sympatric speciation:** result of gene flow that is blocked due to **non-physical** barriers that inhibit gene flow.
  - Often reproduction barriers are the main factors.

### Genetic Drift

- ▷ **Genetic drift:** the change in the **allele frequencies** in a population due to **random sampling**.
  - Not influenced by environmental factors.
- ▷ May cause certain gene variants to become fixed or lost by chance.
- ▷ Generally drives populations towards genetic uniformity over time, **decreasing heterozygosity**.
- ▷ Only mutation or gene flow can introduce new alleles, which acts against genetic drift.
- ▷ **Founder effect:** result of sampling error which has an increased likelihood on populations with low numbers.
  - By chance certain alleles can be dominant when they otherwise wouldn't be in a new founding population.
  - Often acts to drastically increase rate of genetic drift.
- ▷ **Genetic bottleneck:** a sharp reduction in the size of population due to environmental events.
  - Can essentially cause a founder effect, though it's not a new population.

## Coalescent Theory

- **Coalescent theory:** how gene variants sampled from a population may have **originated** from a common ancestor.
  - Assumes no recombination, no natural selection, no gene flow in the simplest case.
- Aims to look backward in time by merging alleles into a single ancestral copy according to a random process in coalescence events.
- Many theoretical genealogies are made in order to compare to observed data in order to test assumptions about demographic history of a population.
  - Used to make inference about population genetic parameters, such as migration, population size, and recombination.
- **Coalescent time:** number of preceding generations where the coalescence took place, not calendar time.
  - Estimation of the time can be made multiplied by  $2N_e$  with the average time between generations.
  - Time to coalescence for a pair of alleles at a locus is **dependent** on population size.
  - Formula:  $P_c(t) = \left(1 - \frac{1}{2N_e}\right)^{t-1} \left(\frac{1}{2N_e}\right)$
- Can also be used to model the amount of variation in DNA sequences expected from genetic drift and mutation.

## Molecular Evolution

- ▷ **Molecular evolution:** the process of change in the sequence composition of cellular molecules across generations.
- ▷ **Polymorphism:** occurrence of two or more clearly different morphs, or alternative phenotypes, in the population of a species.
  - **Substitution:** when alleles become fixed or lost in a population and polymorphism is ended.
    - Substitution rate ( $k$ ):  $k = sN\mu$
    - $s$  = probability of fixation.
    - $N\mu$  = mutation rate of population.

## Recombination

- **Recombination:** the process that results in genetic exchange between chromosomes or chromosomal regions.
  - Can also cause mutations due to misalignment after recombination.
  - **Gene repair:** a type of recombination that is the product of DNA repair that corrects damage using a homologous template.
    - Often responsible for homogenizing sequences of duplicate genes over long periods of time, which reduces nucleotide divergence.
- **Genetic hitchhiking:** change in allele frequency not because of natural selection, but due to proximity to a gene undergoing selective sweep.
  - **Selective sweep:** a beneficial mutation that increases frequency and generally becomes fixed.

## Neutral Theory

- **Neutral theory of molecular evolution:** most evolutionary changes occur at the molecular level.
- Most variation is due to random genetic drift of mutant alleles that are selectively neutral.
- Compatible with phenotypic evolution, as phenotypes are driven by molecular changes.
- Most mutations are neutral with respect to fitness.
- A minority of mutations are advantageous.
- Substitution rate predicted to be neutral, equal to per-individual mutation rate, **independent** of population size.
- $K_A/K_S$  test used to determine direction selection based on evolutionary history.
  - $K_A$ : number of nonsynonymous substitutions (replacement).
  - $K_S$ : number of synonymous substitutions (silent).
  - $K_A > K_S$  signals for **positive selection**.
  - $K_A < K_S$  signals for **purifying selection**.

### Molecular Clocks

- **Molecular clocks:** the average rate at which species' genomes accumulates **neutral mutations** over time.
  - A linear rate is often easy to establish.
  - Used to measure evolutionary divergence.

### Nonrandom Mating

- ▷ **Inbreeding:** production of offspring from closely genetically related individuals.
  - Results in homozygosity, which can increase chances of offspring being affected by deleterious or recessive traits.
  - **Inbreeding depression:** the reduced fitness in a given population due to inbreeding.
    - Usually caused by population bottlenecks or the founder effect.
  - Can also result in purging of deleterious alleles through purifying selection.
  - Can allow for the expression of advantageous phenotypes, which if outweighs the disadvantages, then could potentially lead to speciation.
  - **Coefficient of inbreeding:** the probability that two alleles at any locus in an individual are identical by descent.
  - Nonrandom mating does not alter allele frequencies and not a mechanism of evolution.
    - Can alter the frequencies of genotypes, changing the distribution of phenotypes in a population, which can alter patterns of natural selection.
- ▷ **Assortative mating:** mating based on phenotypic factors.
  - Can play a role in sympatric speciation.
  - A form of sexual selection.
  - Can be either positive or negative, selecting for similar or different phenotypes respectively.



## 8 Evolution at Multiple Loci

### Linkage Equilibrium and Disequilibrium

- ▷ **Linkage equilibrium:** when the genotype of a chromosome at one locus is **independent** of its genotype at another locus.
- ▷ **Linkage disequilibrium:** the non-random association of alleles at different loci in a given population.
  - Occurs when frequency of the association between loci's different alleles is higher or lower than expected.
- ▷ **Haplotype:** a group of alleles in an organism that are inherited together from a single parent.
  - Used to mean the collection of specific alleles that represent a phenotype and likely to be conserved.
  - Also can be used to mean a set of linked single-nucleotide polymorphism alleles that are associated statistically.
- ▷ Factors that influences disequilibrium: selection, rate or genetic recombination, mutation rate, genetic drift, system of mating, population structure.
  - Understanding linkage disequilibrium in a genome can be a powerful signal of the population genetic processes that structure it.
  - Selection, genetic drift and population admixture act to **create disequilibrium**.
  - Recombination and outbreeding (sexual reproduction) act to **reduce disequilibrium**.
- ▷ Level of linkage disequilibrium can between *A* and *B* can be quantified by the **coefficient of linkage disequilibrium,  $D_{AB}$** .
  - Formula:  $D_{AB} = P_{AB} - P_A P_B$
  - $P_{AB}$ : the frequency with which both occur together on same gamete, or the frequency of the *AB*haplotype.
  - $P_A P_B$ : product of the probabilities give the probability they occur together.
  - When there is a difference, the magnitude of the coefficient rises, indicating linkage disequilibrium.

### Recombination's Effect on Disequilibrium

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## Adaptive Significance of Sex



## 9 Quantitative Genetics

### The Nature of Quantitative Traits



### Heritable Variation



### Measuring Differences



### Predicting Evolutionary Responses

















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