

Aim: How do we explain speciation in populations?

Leading question: 5 points: Distinguish between adaptation and acclimation.

Correction: The tree on Audesirk 351 is testable, while Towle 346 is not. The concept above is testable. Anything encased in the AMNH itinerary is testable. The regents that shall not be named is a source for evo and graphing questions. Cladistics is testable. The state lab we just did is testable.

Cladistics Wrapup:

All 5 critical forms of structural and molecular evidence we discussed in class must agree to help conclude how a species formed. We stand by our molecules, but the fossils of extinct forms have to line up with the extant organism data too, to form a full picture. The sum total of all of these data (homology, vestiges, development, molecules, and fossils) are built into a character matrix.

Cladograms are the branch diagrams or phylogenetic trees for kingdoms, plants, and animals. Taxonomy and classification allows us to turn keys into trees. Cladistics analyzes the evolutionary relationships between organisms that form a group. Forks in a cladogram represent differences between organisms that possess or lack a certain character. When character traits are different enough, an outgroup forms. Outgroups group organisms by similarity to each other and differences with an organism from which they diverged. As we showed in class, the numbers of similarities help with grouping. Character numbers or types specified at the branches of a phylogenetic tree show where the group change occurred. The more similarities a group of taxa have, the further back in evolutionary time they are related. See board for example.

The types of speciation mechanisms that cause phylogenetic trees to emerge are complex. Building trees from keys is methodical and depends upon a great deal of data.

Hardy-Weinberg equilibrium:

This is an idealized explanation of shifts in allele frequency that occur in populations of organisms (see previous handout for allowances and exclusions). The reason it is idealized is that selective pressures in environments are almost unavoidable, yet there are some selected traits, such as sickle cell anemia mutation and certain disease resistances, that behave closely according to Hardy-Weinberg predictions. Sickle cell in fact meets all H/W conditions but selection and random mating.

- populations have traits that vary
- variation is a function of heredity and environment
- h/w allele frequencies in the gene pool deal with a stable population, 2 alleles
- assume there are 2 forms of a hypothetical allele. Both exist in a population. Use phenotype frequencies of parents to determine the genotypes and phenotypes of a second generation. The distribution of offspring follows a binomial expansion. There is that pesky math again!
- Given the frequency of one homozygous combination (ex pp or p^2), you can calculate the other frequencies (q^2 , then $2pq$). See board for alleles, relationships, and example.

Mechanisms of Speciation or Adaptation over time:

Coevolution: 2 species develop to coexist intimately in the same niche.

Convergent evolution: 2 species independently evolve to look the same.

Divergent evolution: 2 species become more and more dissimilar over time.