

Speciation - BIOL 7117
Fall 2025 - Exam 2 Review Material

Names and terms:

Felsenstein, Falconer, Waddington, Gould, Noor, Rieseberg
gradualism vs. saltationism
hopeful monster
Modern Synthesis (and associated names)
association mapping
forward genetics
Quantitative Trait Loci (QTL)
Genome Wide Association Studies (GWAS)
reverse genetics
outlier analyses
positive selection, d_N/d_S
regulation of gene expression
genomic architecture
genetic hitchhiking
structural variants
hybridization, introgression
primary vs. secondary contact
tension zone
allopolyploid speciation
transgressive phenotypes
migrant/archaic tracts
hybrid swarm, syngameon
standing variation, ancestral variation
combinatorial speciation
three domains of life: Eubacteria, Archea, Eukaryota
microbiome, holobiont, hologenome
lateral gene transfer
co-phylogeny vs. phyllosymbiosis
macroevolution
punctuated equilibrium, phyletic gradualism

Lecture Questions:

Compare and contrast QTL mapping and GWAS as means of identifying the number, strength of effect, and potential identity of genes underlying reproductive character divergence between incipient species.

What are regulatory genes? Distinguish between *cis*- and *trans*- regulatory elements. Why have Sean Carroll and others thought that the former play a special and disproportionate role in the evolution of morphological novelty? How are the results of Yusef et al. 2025 (BioRx)) consistent and/or inconsistent with Carroll's view?

What are genomic islands of differentiation? What four characteristics of genomic islands of differentiation have been noted in arguing that they are genomic islands of speciation? Explain how the way in which "differentiation" is measured (relative or absolute) can alter the interpretation of genome scans that have claimed to identify genomic islands of speciation.

Explain the logic underlying the ABBA/BABA test for introgression (as opposed to the sorting of ancestral variation) as the source of a particular allele.

Explain the pattern of genomic architecture seen by Rieseberg et al. (1996 Science 272: 741) in experimental sunflower hybrids and how it altered thinking about hybrid speciation.

Explain three reasons why ancestral variation may provide a better substrate for divergent selection leading to speciation than *de novo* mutations.

What gene region is used most commonly to survey microbial diversity? Explain three advantages for using it over hypothetical alternatives.

Compare and contrast the prevalence, specificity, localization (within the genome) and homology of genetic exchange among prokaryotes and among eukaryotes. Discuss the implications of these differences for the adaptive evolution of the hologenome.

Name and describe three aspects of evolutionary history that cannot be revealed without the fossil record.

Draw a phylogenetic tree of nine species with a **constant** diversification and construct a lineage-through time plot from that tree. Repeat for an **adaptive radiation** (a burst of speciation followed by a slow-down in diversification).

Distinguish between phyllosymbiosis and co-phylogeny.

From Discussion papers: These questions arose mainly from the papers we read. In some cases, relevant information appeared in the paper, but you may need to consult textbooks or other sources to get a satisfactory answer.

Describe Seehausen's combinatorial view of speciation. What evidence from Turbek et al. (2021) suggests that this view applies to the recent speciation of southern capuchino seedeaters?

Explain how Jensen et al. (2024) reasoned that introgression of the Y chromosome should be especially rare. What data of theirs most strongly argued that such introgression occurred in guenons?

What is the value of mapping short-read whole genomes sequences to a pangenome (a collection of genomes from the same species) over a single reference genome? How would the results of Lutgen et al. (2025) have been different if they had used just a single reference genome?

Explain the approach used by Meier et al. (2023, esp. Fig. 5) to infer that a common pool of ancestral variation provided some common genetic basis to the evolution of ecomorphs in different lakes.