

Evolutionary Biology 30305 Fall 2017

Topics for the 1st Exam

This list is not meant to be totally inclusive. We have covered other topics and many examples not listed. You are responsible for all the material covered in the lectures and in the assigned readings.

Readings

- Bowler, P. J., 2009. Darwin's originality. *Science* 323:223-226.
- Padin, K., 2008. Darwin's enduring legacy. *Nature* 451:632-634.
- Chapter 1 all sections
- Chapter 2 all sections
- Chapter 3 sections 3.4 – 3.7
- Chapter 5 all sections
- Chapter 6 all sections

Review Questions from the Book Chapters

- Chapter 1: Multiple Choice 1-3, 5-8; Short Answer 1-5.
- Chapter 2: Multiple Choice 1,3-6; Short Answer 1,3-6.
- Chapter 5: Multiple Choice 5-9; Short Answer 3-6.
- Chapter 6: Multiple Choice 1-10; Short Answer 1-3, 5. Q4 uses the average fitness of an allele and we won't cover that equation shown in Box figure 6.5.1).

Intro to Evolutionary Biology

Practical Applications
Goals of Evolutionary Biology
Names: Dobzhansky

Historical Development of Evolutionary Theory

Properties of Evolving Systems
Elements of Evolution by Natural Selection
Timeline for History of Evolutionary Thought
Lamarck's hypothesis
Historical Context for the Theory of Evolution by Natural Selection
Darwin's Observations and His 4 Theories of Evolution
Evidence for Evolution: Homology, Common Descent, and Vestigial Traits, Fossil Record, Experimental Evidence and Direct Observation
Names: Plato, Aristotle, Linnaeus, Buffon, Lamark, Ussher, Steno, Hutton, Smith, Lyell, Cuvier, Annig, Darwin, Malthus, Wallace

Origin of Variation

Types of Mutations
Mutation Rates
Drake's Constancy Hypothesis
Luria-Delbruck Experiment
Adaptive Mutation
Mutational Effects
Mutation Accumulation Experiments
Names: McClintock, Luria & Delbruck, Drake, Fisher (first time of many!)

Mendelian Genetics

Mendel's Laws

Calculating Gene (Allele) and Genotype Frequencies
 Hardy-Castle-Weinberg Law
 Assumptions of H-W Equilibrium
 Post-Darwinian Controversies
 The Modern Synthesis – What was it, and what were the outcomes?
 Measuring Genetic Variation in Natural Populations
 DNA Polymorphism and Forensic Analysis (The Product Rule)
 Change in Allele Frequencies by Mutation
 Measuring Fitness (Relative vs. Absolute Fitness)
 Analysis of Single Locus Selection
 Rate of Increase of a Favorable Allele
 Selection against a Partially Recessive Lethal
 Selection Coefficient (s) and Dominance Coefficient (h)
 Heterozygote Advantage (Overdominance)
 Heterozygote Disadvantage (Underdominance)
 Single Locus Adaptive Landscapes
 Frequency-Dependent Selection
 Evolution of Sex Ratio
 Selection-Mutation Balance
 Migration
 Migration-Selection Balance
 Genetic Drift
 Coalescence Theory
 Loss of Heterozygosity in Finite Populations
 Effective Population Size (N_e)
 Inbreeding
 Inbreeding Coefficient (F) and Identity By Descent (IBD)
 Inbreeding depression
 Population Subdivision (F_{st})
 Relationship between F_{st} and N_m
 Genome Scans
 Names: Mendel, Hardy, Castle, Weinberg, Ford, Fisher (again), Haldane, Wright, Kettlewell

Origin of Life

Fundamental Characteristics of Life
 Origin-of-life Research
 Panspermia
 RNA-DNA-Protein First?

Evolution of Early Life Formst

Fossil and Molecular Time Line for the Origin of the Domains of Life and Major Evolutionary Events
 LUCA
 Evolution of Genome Size
 Prokaryotes/Eukaryotes and the Origin of Organelles
 3 Domains of Life

Useful Equations to know for Population Genetics:

Gene frequencies:

$p + q = 1$, where $\text{Freq}(A) = p$ and $\text{Freq}(a) = q$ (this is for a single locus with 2 alleles but can easily be expanded for a single locus with multiple alleles)

Genotype frequencies:

$p^2 + 2pq + q^2 = 1$, where $\text{Freq}(AA) = p^2$, $\text{Freq}(Aa) = 2pq$, $\text{Freq}(aa) = q^2$

This equation also describes the Hardy-Castle-Weinberg proportions of genotype frequencies.

Allele frequencies from known genotype frequencies:

$$p' = p^2 + \frac{1}{2}(2pq)$$

Equilibrium gene frequency under mutation:

$$\hat{p} = \frac{v}{(u+v)}, \text{ where Freq(A) = } p \text{ and Freq(a) = } q, u \text{ is the mutation rate from A} \rightarrow \text{a, and } v \text{ is the back mutation rate from a} \rightarrow \text{A}$$

Population mean fitness:

$$\bar{w} = p^2W_{AA} + 2pqW_{Aa} + q^2W_{aa}, \text{ where } W_{ij} \text{ is the absolute fitness for a particular genotype}$$

Average excess fitness of an allele:

$$a_A = [p \times (W_{AA} - \bar{w})] + [q \times (W_{Aa} - \bar{w})]$$

Equilibrium gene frequency with heterozygote advantage and disadvantage models of selection:

$$\hat{p} = \frac{t}{(s+t)}, \text{ where } t \text{ is the selection coefficient associated with the homozygous aa genotype and } s \text{ is the selection coefficient associated with the homozygous AA genotype, and Freq(A) = } p. \text{ This equation describes the equilibrium gene frequency for either model of selection. The major difference is that under heterozygote advantage the equilibrium is } \textit{stable} \text{ and under heterozygote disadvantage the equilibrium is } \textit{unstable}.$$

Mutation-Selection Balance – The equilibrium frequency of a recessive deleterious allele is given by:

$$\hat{q} \cong \sqrt{\frac{u}{s}}, \text{ where } u \text{ is the mutation rate to the deleterious allele and } s \text{ is the selection coefficient against that allele. For a dominant allele } \hat{q} \cong \frac{u}{s}, \text{ and for a partially recessive allele } \hat{q} \cong \frac{u}{hs}$$

Migration-Selection Balance - The equilibrium frequency of an allele on the island (p_i) with migration from the continent that is under selection is given by:

$$\hat{p}_i \approx \frac{mp_c}{s}, \text{ where } m \text{ is the migration rate, } p_c \text{ is the allele frequency on the continent and } s \text{ is the selection coefficient against the allele on the island.}$$

Loss of Heterozygosity – The loss of heterozygosity after 1 generation with an effective population of size N_e is given by:

$$H_1 = \left[1 - \frac{1}{2N_e}\right] * H_0, \text{ for multiple generations } H_t = \left[1 - \frac{1}{2N_e}\right]^t * H_0 \cong H_0 e^{-t/(2N_e)}$$

Genetic effective populations size N_e is given by:

$$N_e = \frac{4N_m N_f}{N_m + N_f}$$

Genetic effective populations size N_e across multiple generations with varying population size is best described by the harmonic mean:

$$\frac{1}{N_e} = \frac{1}{t} \left(\frac{1}{N_0} + \frac{1}{N_1} + \dots + \frac{1}{N_{t-1}} \right)$$

Heterozygosity in a partially inbred population is given by: $H_{obs} = 2pq(1 - F) = H_{exp}(1 - F)$

Estimating F from observed and expected heterozygosity: $F = (H_{exp} - H_{obs}) / H_{exp}$

Population Subdivision - The level of population subdivision is given by:

$F_{ST} = \frac{(H_T - H_s)}{H_T} = 1 - \left(\frac{H_s}{H_T} \right)$, where H_s is the average expected heterozygosity within subpopulations and H_T is the total expected heterozygosity across all populations.

Relationship between F_{ST} and the number of migrants is given by:

$$F_{ST} = \frac{1}{1 + 4Nm}$$