UMSL Bio. 3302: Introduction to Evolution
Study Guide
Population Genetics
Molecular markers
Conservation Genetics

Important Terms and Concepts

AFLP
Allele
Allozymes
Assortive mating
Biosphere Reserve
Bottleneck effect
Cline
Co-dominant
Deme
Dispersal
Directional selection
Disruptive selection
Dominant
Edge effects
Effective Population Size
Ex-Situ Conservation
F statistics
Extinction Vortex
Fitness
Fixation of allele
Founder effect
Fst
Genetic Equilibrium
Gene flow
Gene frequencies
Gene pool
Genetic Drift
Genetic load
Genotype
Habitat fragmentation
Hardy-Weinberg equilibrium
Heterozygous
Heterozygosity
Heterozygote advantage
Homozygous
H_S
H_T
Inbreeding
Inbreeding depression

Industrial Melanism
ISSR
Local population
Macroevolution
Microevolution
Microsatellites
Migration
Monomorphic gene
Mutation
Mutationist
Natural Selection Agents
Neo-Darwinian
Nonrandom Mating
Peppered Moth example
Phenotype
Polymorphism
Proportion polymorphic loci
Population
RAPD
Recessive
Reintroduction
Self-fertilization
Sexual Selection
SLOSS
SNP
Stabilizing Selection
Structure
Subpopulation
UPGMA
Wright's Fixation Index

Discussion Questions

1. Under what conditions are gene frequencies conserved under the Hardy-Weinberg equilibrium? (What are the assumptions?)

2. How can we derive gene and genotype frequencies in a diploid population when we only know the frequency of recessive homozygotes?

3. Natural populations do not usually fit the Hardy-Weinberg Equilibrium model. What does this tell us about most natural populations?

4. What is genetic drift and why does it matter? What are the population or genetic parameters that influence the effects of drift in a population?

5. Explain how a bottleneck can lead to a reduction in genetic variation. Contrast with the founder effect. Give examples.

6. Describe and diagram the three type of selection that are recognized. Which type of selection is most common in nature? Give some examples of directional selection.

7. In stabilizing selection, what categories of phenotypes is selection removing from the population?

8. What is evolution? What is evolution by natural selection?

9. What are 5 sources of variation in a gene pool? Which is most important in the long run? Why?

10. What are three general solutions to preserving biotic diversity? Which is best in the long term?

11. What is the effect of habitat fragmentation on population size, and how might this be related to the long term survival of species?

12. Explain the difference between expected and observed heterozygosity. Discuss why the sample size matters.

13. Does genetic diversity really matter in species conservation? Why or why not?

14. To what extent can human population growth be directly blamed for the conservation crisis?

15. Can zoos, hatcheries, and similar ex situ species sanctuaries harbor enough specimens to provide the genetic diversity their species need to survive until they can be reestablished in the wild?

16. What are the best ways to design nature preserves if maximizing genetic diversity and gene-flow are considered important? If a single large preserve is not possible, what are some other alternatives? Describe the SLOSS alternatives.

17. You are monitoring a population of endangered turtles, and find that allele frequencies differ from Hardy-Weinberg expectations. What could you conclude about your population as a result of this finding and how might it inform your conservation decisions?

18. You are trying to pick a molecular marker to study variation in populations of morel mushrooms. If you get your grant you can pick any marker you want. If you don’t get funded you have to pick some economical. What markers would you choose in either case, and why?

19. What are some characteristics of a good molecular marker for population genetic studies? Give some examples.

20. Which molecular markers are codominant, allowing the researcher to see the alternate forms of the alleles directly? Why is this important?

How does genetic drift differ from natural selection, both in how it works and in its evolutionary consequences?

When trying to make sure that a very rare species doesn't go extinct, conservation biologists and zookeepers do several things to manage the rate that that species evolves. What evolutionary phenomenon are they most worried about? Why? And what can they do to minimize the problem?

Invasive species often go through bottlenecks. What is the genetic consequence? How might this reflect their rate of evolution in a new environment?

Attempts to restore populations of the greater prairie chicken by increasing habitat availability alone were unsuccessful. Researchers suggested they had fallen into an ‘extinction vortex’ Briefly explain, using text or diagrams. Please try to stay inside the box!

Collared lizards in the Ozark Mountains seemed to be falling into an ‘extinction vortex’. Use a diagram / illustration to briefly explain what this means. What practical solution turned out to be most effective in the conservation of these lizards?

Why is the Hardy-Weinberg principle important, since genetic equilibrium seldom occurs in nature?

Distinguish genetic bottleneck from founder effects.

Consider two species of plants. One has wind-dispersed seeds, the other has squirrel-dispersed seeds. In which species would you expect to find more among-population variation in allele frequency? Explain. Note - assume that wind-dispersal is more effective than dispersal by squirrels. "Among-population variation" means differences among population, not within populations.

In theory, inbreeding should be a serious problem in captive zoo populations. Yet in many cases, it is difficult to detect inbreeding depression in well-maintained captive populations. Why might this be?

Ecologists are already documenting significant environmental changes associated with global climate change. Some species will adapt and some will not. Of the four microevolutionary processes, pick your favorite two: how will these two processes play a role in survival vs. extinction?

We discussed a statistic to quantify population genetic structure. What is it and how do you interpret it?
The statistic FST is used to quantify population structure. Essentially it is a measure of how much allele frequency variation there is between populations. For example, in humans FST =

0.123, which means that approximately 12% of genetic variation in humans is due to differences between populations and 88% (1-FST) is due to differences among individuals within populations. Thus, the vast majority of genetic variation in humans is due to differences between individuals rather than populations.

A large population of prairie flowers contained two alleles for flower color, B and b. The allele frequencies were 0.6 and 0.4, respectively. After the prairie was plowed into farm fields, the plant was restricted to hedgerows and the original large population was split into several dozen small, isolated, populations. Assume that flower color is completely neutral and that there is no gene flow among the small populations.
What will be the likely frequencies of alleles in the small populations after many years of isolation?
After many many years, the subpopulations will become fixed for one allele or the other: either all BB or all bb. Because the probability of fixation of an allele is equal to p0, about 60% of the populations will be fixed for B and 40% will become fixed for b.