AP BIOLOGY · UNIT 7 · TOPIC 7.4

Population Genetics

Learning objective 7.4.A Explain how random occurrences affect the genetic makeup of a population, and 7.4.B describe the role of random processes in the evolution of specific populations.

Name: Date: Period:

Use the tool **Small Numbers, Large Consequences**. Parts 1 and 2 use **How big is the population**, Part 3 uses **A crash and a founding**, and Parts 4 and 5 use **Which process was it**. Topics 7.1 to 7.3 all had something doing the choosing: an environment or a breeder. Nothing chooses anything in this topic. Allele frequencies still change, because the alleles that get into the next generation are a **sample** of the ones in this one, and a sample is not the same as what it was drawn from.

Part 1 · Four population sizes, no selection at all

Every population starts at an allele frequency of **0.5** and runs for **100** generations. There is no fitness difference between the alleles. Record the four rows from the summary table on the second panel.

Population size	Average final frequency	Spread of outcomes	Fixed or lost	Variation left
N = 10				
N = 50				
N = 500				
N = 5000				

1. Describe genetic drift.

2. Using the Average final frequency column of the Part 1 table, explain what the data indicate about the direction of genetic drift.

Part 2 · Why size is the whole story

Open the panel headed **Checking the simulation against the standard prediction**. Population genetics predicts that the variation held under drift falls by a factor of (1 − 1/2N) each generation. The simulation was never given that formula.

Population size	Variation left, simulated	Variation left, predicted	Do they agree?
N = 10			
N = 50			
N = 500			
N = 5000			

3. Explain why genetic drift has a larger effect in a small population than in a large one.

4. A student claims that genetic drift “pushes rare alleles toward extinction.”
(a) Describe what is correct about the student's claim.

(b) Using the Part 1 table, explain what is incorrect about the student's claim.

5. The simulated values in the Part 2 table were produced without the formula, and the predicted values were calculated without the simulation. Explain why the agreement between the two columns is stronger evidence than either column alone.

Part 3 · A crash, and a founding

Go to **A crash and a founding**. The source population holds four alleles: **A1 55%, A2 30%, A3 12%, A4 3%**. Survivors are chosen entirely at random; nothing about any allele affects which individuals live. Click each button in turn, from 4 survive to 250 survive, and record the readouts.

Survivors	Alleles still present (avg)	Crashes that lost the rare allele	Crashes that lost the commonest
4			
10			
50			
250			

6. (a) Describe how a bottleneck and a founder effect are similar.

(b) Describe how a bottleneck and a founder effect differ.

7. In the Part 3 crashes, the survivors were chosen at random, yet the rare allele was lost far more often than the commonest allele. Explain why.

8. A rare disorder occurs in about 1 in 4,000 people worldwide but in about 1 in 58 on one small group of islands. Using the founder table in the panel The same sampling, told as a founding, explain how the disorder could become this common on the islands without natural selection favoring the allele.

Part 4 · Which process was it?

Go to **Which process was it**. Forty populations, all starting at **0.35**, under one process at a time. Click each of the three process buttons (Drift only; Selection, 6% advantage; Migration, 4% per generation) and fill in the table from the readouts.

Process	Average endpoint	Spread	Populations that rose	Range of endpoints
Drift only				
Selection				
Migration				

9. The frequency of an allele in a population has increased over thirty years. Using the Part 4 table, explain why this increase alone does not show that natural selection caused it.

10. Describe data that would allow a researcher to conclude that natural selection, rather than genetic drift, caused the increase in question 9.

Part 5 · Gene flow, and mating that is not random

Two populations, one at 0.90 and one at 0.10, exchange members each generation. Record the table in the panel Gene flow, on its own. Then look at the non-random mating table below it, and compare the allele frequency column with the genotype columns.

Migration rate	Difference after 60 generations	Fraction of the difference left
0% per generation		
1% per generation		
5% per generation		
15% per generation		

11. (a) Using the Part 5 table, describe the effect of gene flow on the difference in allele frequency between two populations.

(b) Predict the effect of stopping gene flow on the allele frequencies of the two populations over many generations. Justify your prediction.

12. In the non-random mating table, the genotype frequencies changed over 10 generations but the allele frequency p did not. Explain why.

13. On its own, mutation takes about 1,000 generations to bring a new allele to a frequency of 1%. Explain why mutation is still important to the evolution of populations.

What the model simplifies

Generations do not overlap and every individual has the same chance of contributing gametes. Real populations have overlapping generations and unequal contributions, which makes the effective population size smaller than the number of individuals you can count, often much smaller, so real drift is stronger than a headcount suggests.

One locus is followed and it is unlinked to everything else. Real genomes drift as blocks: an allele can rise because it sits beside something being selected, which at the locus you are watching is indistinguishable from drift.

The gene-flow panel is deterministic: the two populations are treated as large enough that drift can be ignored, so that the closing of the gap measures migration and nothing else. An earlier version kept them finite, and drift closed part of the gap even with no migration at all; true of real populations, but it made the panel a poor measurement of gene flow.

Non-random mating is modeled as a preference for one's own genotype. Real assortative mating acts on phenotypes, which for a recessive trait groups heterozygotes with one homozygote class and changes the numbers, though not the conclusion.

Mutation is treated as one-way at a constant rate. Real mutation goes both ways at rates that differ by site, and most new mutations are lost to drift within a few generations of appearing, whatever their effect.