

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. Define genetic drift.

2. Look at your second column. Explain what it shows 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 says genetic drift “pushes rare alleles toward extinction.” Using your Part 1 table, explain what is right about that and what is wrong.

5. The simulation and the formula are two independent routes to the same numbers. Explain why their agreement is worth more than either result on its own.

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 who lives.

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

6. Distinguish between a bottleneck and a founder effect.

7. Explain why rare alleles are the ones most often lost, given that nothing selected against them.

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 tool, explain how this can happen without the islands favoring the allele in any way.

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. Fill the table from the readout for each of the three buttons.

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

9. A population's allele frequency has risen over thirty years. Explain why this alone does not show that natural selection is responsible.

10. Describe evidence that would let a researcher conclude selection rather than drift was acting.

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

Two populations at 0.90 and 0.10 exchange members each generation. Then look at the assortative-mating table below it — watch the allele-frequency column and the genotype columns **separately**.

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

11. Explain what gene flow does to two populations, and what happens when it is cut off.

12. In the assortative-mating table the genotype frequencies changed but the allele frequency did not. Explain why.

13. Mutation takes about a thousand generations to bring a new allele to 1% on its own. Explain why mutation still matters to everything in this topic.

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.