

Genetic Drift Lab

Small population sizes are more strongly influenced by random events than large populations. This means that the genetic frequencies of alleles in small populations are more likely to vary from one generation to the next from the original population. Often, genetic variation is rapidly lost in small populations and random events can create rapid genetic changes or microevolution in such cases.

Populations may be subject to this random genetic drift (rapid movement of allele frequencies) by one of two events that reduce population size.

1. Bottlenecks - an incident reduces the overall number of individuals in a population and only a few survive to produce the next generation. Evidence of bottlenecks have been discovered in many species, such as cheetahs and the northern elephant seal.

2. Founder effect - a small number of individuals disperse and colonize new habitat, founding a new population. Organisms colonizing new habitats, such as islands, or migrating to new areas are also common.

In both cases the surviving or founding individuals will often vary in genetic frequency from the parental populations (original sources). Also, small subsequent population size plays a big role in additional changes to the gene frequencies.

I. Simulation of random events (coin tosses):

Each student flips a coin 10 times.

What are the expected number of heads for 10 flips?

How many heads did you obtain for your 10 flips? _____

students in your class _____

times heads appeared out of 10 trials for all students:

0 _____ 1 _____ 2 _____ 3 _____ 4 _____ 5 _____

6 _____ 7 _____ 8 _____ 9 _____ 10 _____

How many total times did the replications meet the expected

number of heads _____ How many times did the replications not meet this? _____

II. Simulation of genetic drift.

1. From a population of 10 beans (black and white), representing two allele frequencies (two forms of the same gene) collect at random the following: 5 individuals (2 beans per individual = 2 allele forms of one gene, starting with 50%, or a .5 frequency for each allele), 10 beans total and list their frequencies. Replace the bean colors (alleles) removed from the population **each time** you collect two for a 'new' individual.

2. Using your new population of 5 individuals (10 bean alleles) place them into the cup and begin to form a second generation of individuals, again select 5 individuals, 10 beans total, and place them in a new container. Make sure you replace beans, by adding from an original stock as you pull them out. You should have 10 beans in each container now, by random chance each, will be different. Place remaining beads from second container back into stock container. Count the frequencies in 3rd generation.

3. Repeat above step, using the third generation to pull alleles for the fourth generation and so forth, up through 10 generations.

Record # of each allele in the populations

Population with

#	10 beans (5 ind)	
Generation	# white	# black
Start	5 (.5)	5 (.5)
1	_____	_____
2	_____	_____
3	_____	_____
4	_____	_____
5	_____	_____
6	_____	_____
7	_____	_____
8	_____	_____
9	_____	_____
10	_____	_____

Graph the ratios of black allele frequencies for each generation.

What were the final allele frequencies in your population?

What were the frequencies of the 10th generation for the black allele in other student populations?

Yours _____ Others _____

Did fixation (elimination of one allele type) occur in any populations?

How many populations were distinct from each other, due to random genetic drift?

What would you expect in a wild population with a low population in terms of genetic drift and genetic diversity?

