**Genetic Drift Simulation**

## **Background:**

In addition to natural selection, one of the mechanisms of evolution is genetic drift. Genetic drift is the change of the frequency of alleles in the gene pool due to random sampling. This simulation will explore how sample size can influence the effect on genetic drift on the gene pool using different types of beans to represent individuals in the population.

**Materials:**

100 beans: 40 popcorn kernels, 30 medium white beans, and 30 black-eyed beans, one cup (to hold your beans)

**Pre-lab Questions:** Read the procedures before you answer the pre-lab questions.

1. Define genetic drift:
2. Could genetic drift lead to evolution of a population? Explain.
3. Predict: Will the effects of genetic drift on the gene pool differ with sample size? Explain.
4. Why should you take random samples? Would you be illustrating genetic drift if you selected the individuals non-randomly?

**Procedure**

* Each group will do two simulations each with *three separate trials.*
* You will need to fill a cup to create your 100-bean population: 40 popcorn, 30 white, 30 red beans.
* Read the procedure carefully before starting your trials.

**Simulation I (Large Sample)**

1. Under original population write the phenotypes (types of beans), the number of each phenotype and their percentages. Count out the numbers of each phenotype in your large population (beans in your cup). Determine your *phenotypic ratio* (as percentages, eg 40red/100 total = 40 %).
2. Trial 1: Randomly take a sample handful containing 40 beans from the original population (cup).
3. Determine the ratio in the sample (eg 5 red/40 = 12.5%) - did any of the allele frequencies change?

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| 100 beans | Original Population | | Trial # 1 (random 40) | | Trial # 2 (random 40) | | Trial # 3 (random 40) | |
| Phenotype | #Beans | Ratio % | #Beans | Ratio % | #Beans | Ratio % | #Beans | Ratio % |
| Popcorn | 40 | 40% |  |  |  |  |  |  |
| White | 30 | 30% |  |  |  |  |  |  |
| Black-Eyed | 30 | 30% |  |  |  |  |  |  |
| Total Beans | 100 | | 40 | | 40 | | 40 | |

1. Repeat two more times - returning the sample back to your main population to 'restock' each time.

**Simulation II (Small Sample):**

* Follow the same procedure as simulation I but use a smaller sample size of **10 beans**.

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|  | Original Population (10) | | Trail # 1 (random 4) | | Trial # 2 (random 4) | | Trial # 3 (random 4) | |
| Phenotype | #Beans | Ratio % | #Beans | Ratio % | #Beans | Ratio % | #Beans | Ratio % |
| Popcorn | 4 | 40% |  |  |  |  |  |  |
| White | 3 | 30% |  |  |  |  |  |  |
| Black-Eyed | 3 | 30% |  |  |  |  |  |  |
| Total Beans | 10 | | 4 | | 4 | | 4 | |

* Record your data in the table below.

**Post-Lab Questions**

* 1. Compare your results from simulation I and II. Did genetic drift have more of an effect on the allele frequencies in the larger or smaller samples? Why?
  2. An environmental change gave one phenotype an *adaptive advantage* over the others, increasing its *fitness.* This would cause a shift in *allele frequencies* as the fittest beans are best able to survive and reproduce. Would this be an example of *genetic drift?* Why or why not?
  3. Types of genetic drift: Bottlenecks and the Founder Effect.
     1. What type of genetic drift are you simulating if flood changes the allele frequency of the population?
     2. What type of genetic drift are you simulating if your sample leaves the main population and becomes reproductively isolated?