# Chapter 4

# A Laboratory on Population Genetics and Evolution: A Physical Model and Computer Simulation

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## Contents

## Introduction

The focus of this laboratory is the genetic basis of evolution — population genetics. Students use a physical model (bean seeds of two types in a paper bag) to simulate genetic equilibrium between allele and genotype frequencies in a population existing under Hardy-Weinberg conditions. Students then use a computer program called *Population Genetics Simulator* (*PGS*) to model genetic equilibrium using the same conditions they employed with the physical model. Several example simulations are studied with *PGS* in order to illustrate some important evolutionary phenomena and introduce students to the features of the program. Students now design a biologically realistic simulation to be studied with *PGS*. The simulation study can be done in class or later, and a short report summarizing the results and conclusions of the study along with graphical printouts from the program can be turned in to the instructor for evaluation.

This laboratory is useful because it gives students hands-on experience with a host of important biological concepts that many teachers consider lecture-only topics. Through involvement with physical and computer models of Hardy-Weinberg genetic equilibrium, students can investigate the genetic basis of evolutionary change and evaluate the importance of the various Hardy-Weinberg conditions. The computer program illustrates the role that computer simulations can play in modelling biology phenomena. A library of illustrative example simulations introduce students to many key evolutionary ideas, such as genetic drift, selection, gene flow, bottleneck effect, founder effect, etc., and provide students with ideas for designing their own simulations.

## Materials

### Physical Model

The small paper bags and beans needed for the physical model can be obtained in any grocery store. Black-eyed peas and black beans seem to work best. The slight size difference between these two seeds can lead to some unexpected results that provide an invitation to discussions of selection, as considered below.

### Information on *PGS*

*PGS* can be used to test ideas in evolutionary biology by setting up and running simulations. *PGS* is a stochastic simulation (a simulation based on random events) of genetic equilibrium in sexually reproducing populations of organisms, as described by the Hardy-Weinberg model. You can test important ideas in evolutionary biology by designing simulations where one or more of the Hardy-Weinberg conditions are violated. You set up a simulation in *PGS* by specifying the simulation conditions. Based on the initial allele frequencies and gene pool size, *PGS* establishes and randomly samples from a gene pool in the computer's memory. After each sample, *PGS* adjusts

the gene pool for the next generation based on the allele frequencies in the sample.  Two independent gene pools can be established in this manner.  Treatments, such as selection and mutation, can be turned on and off at specified generations.  Gene flow can occur between gene pools, or a founder pool can give rise to a new, emigrant pool at a specified time.  In most cases, you can specify both the magnitude of simulation parameters and the timing of events to simulate quite complex phenomena.  Because of the stochastic nature of *PGS*, re-running the simulation may give somewhat different results.

The *PGS* user interface is window-based and highly interactive so you can easily set up a simulation, run it, modify a condition, re-run the simulation, and compare the results.  Or, you can pause a running simulation, modify a parameter, and continue the simulation run under the new conditions.

*PGS* can be obtained at a nominal price by writing the author at the address on the title page of this chapter.  The *PGS* package includes the program, a library of example simulation files, and one copy of the User's Guide. The User's Guide can be duplicated for distribution to students.  Registered users will be notified of new versions of the program when they become available.  *PGS* runs on IBM PC, XT, AT, and PS/2 computers and other IBM compatibles with a minimum of 256KB memory and a graphics monitor.  A Macintosh version of this program will be available in 1994.

## Notes for the Instructor

### Physical Model

You may want to discuss how the bean model meets the Hardy-Weinberg conditions:

1.  The bag represents a physically isolated allele pool (no gene flow).

2.  The beans represent two different alleles for a gene. They do not change color (no mutation).

3.  The allele pool is maintained at 100.  Sampling is done with replacement so that allele frequencies do not change (emulates large population size).

4.  Survival and reproduction is random (selection for phenotypes is not occurring).

Assign student pairs different beginning allele frequencies.  Each group will draw out 50 offspring, two beans at a time (replacing them each time), and record genotypes in Table 4.1 (see Student Outline).  From these numbers, students compute genotype frequencies and allele frequencies in the new generation.  Each group should perform a chi-square test comparing their observed numbers of offspring to those predicted using the Hardy-Weinberg binomial and the initial allele frequencies.  Table 4.2 (see Student Outline) is a worksheet for this test.

In many cases, students may find that the observed frequency of the *A* allele (white bean) was significantly greater and the frequency of the *A′* allele (black bean) significantly less then the frequencies predicted by Hardy-Weinberg.  This is probably related to the slight size difference between the beans which may make it easier to pick up the somewhat larger white beans than the black beans (or perhaps the smaller black beans settle to the bottom of the bag more readily?).  A wonderful lead-in to the concept of natural selection!

## Computer Model

To provide some continuity with the physical model of genetic equilibrium, set up *PGS* with the same conditions used with the bean/bag model.  Use a single population with a gene pool size of 100 alleles, a sample size of 50 individuals, and two alleles with initial allele frequencies set to 0.5.  Run the simulation for 25 generations.  This will illustrate that a fair amount of genetic drift occurs with a sample size as small as 50 individuals.  Running the simulation several times will show that the allele frequencies diverge substantially from the expected equilibrium values of 0.5 and that the results can differ markedly from one run to the next.  These are the hallmarks of *genetic drift*.  Show students how to observe the results of chi-square tests in *PGS* by selecting *D)isplay* and then *option 2* for observing a table of the allele frequencies from the most recent run.  Whenever you observe "($\alpha \leq .05$)" next to a generation number, statistically significant differences exist between the observed allele frequencies and the initial allele frequencies.  This is a good criterion for deciding when the population is not in genetic equilibrium.

If you increase the sample size to about 500 individuals (you must first increase the allele pool size to at least 1000 alleles), genetic drift essentially disappears, although running the simulation for an extended time period (> 25 generations) may still result in some drift.

You can use the example simulation called PKU.*PGS* to illustrate selection.  (This will also show students how to load simulations from disk).  This simulation shows that recessive lethal alleles do not disappear but are maintained in the population within heterozygous individuals.  However, if the population is small, (< 50 individuals) then by chance all recessive alleles may occur in homozygous individuals and the allele will be eliminated.  Since natural selection acts on phenotypes, to study selection you must first define phenotypes.  Demonstrate how phenotypes are entered and assigned to genotypes, and how selection coefficients are entered.  *D)isplay* menu options can be used to look at graphs and tables of alleles, genotypes, and phenotypes for the most recent run of the simulation.  Also, show them how they can pause a simulation, return to the simulation information window, modify a parameter, and resume the same simulation run.

Other aspects of selection can be demonstrated by modifying the PKU simulation.  For example, you can modify this simulation to show the results of selection against the phenotype representing the homozygous dominant and heterozygous genotypes.  (You will want to change the allele designations and phenotype labels and assignments.)  This will show why dominant lethal alleles are not maintained in populations.  Now change the phenotypes and their assignments to reflect intermediate inheritance (*A* and *A'*?) and set up selection coefficients to demonstrate selection for the heterozygous phenotype.  Selection for the heterozygote leads to the maintenance of equal allele frequencies (*A* = *A'* = 0.5), because this maximizes the frequency of the heterozygous class in the population.  This is best illustrated if you start with quite different allele frequencies (i.e., *A* = 0.9 and *A'* = 0.1).  You might also illustrate absolute selection against heterozygous individuals.  Typically, this type of selection leads to homozygosity within the population because the least frequent allele is always over-represented in the heterozygote class.  Even if you start with equal allele frequencies (*A* = *A'* = 0.5), one allele will be eliminated because one allele will eventually, by chance, be over-represented in the heterozygote class.  Running this simulation several times shows that the final outcome (which allele survives) varies randomly.

At this point in the lab, we divide the class into pairs and each pair works through one of the example simulations provided with the program.  You may wish to develop additional example simulations to illustrate aspects of evolutionary biology you consider important.  Students usually need about 1 hour to work through their simulations and organize a short oral presentation on their results and conclusions to be given to the rest of the class.

*PGS* **Example Simulations**

**Drift.***PGS* – This simulation, looking at flower color in snapdragons, examines the effects of genetic drift by comparing two populations differing in the number of individuals upon which future generations are based. Compare this simulation with the one contained in the file "Italian.*PGS*".

**Moth.***PGS* – This simulation examines the peppered moth (*Biston betularia*) story in England and shows how quickly allele frequencies can change in a population when fairly strong selection pressures are at work. Note that the initial low frequency of the *b* allele depended on the operation of Hardy-Weinberg equilibrium to maintain it. If the population had been too small, the *b* allele might have disappeared before the environment changed and natural selection had a chance to favor it.

**SickCell.***PGS* – This simulation shows a more typical example of selection where the selection pressures are not absolute but relative. The $Hb_s$ allele is selected against when in the homozygous state, but has an advantage over the $Hb_a$ allele due to the malaria resistance it confers on the heterozygote. Obviously, in malaria-free areas, this advantage is never realized and the $Hb_s$ allele becomes more and more rare. In malaria infected populations, an equilibrium state will develop in the pool for the two alleles, based on the relative selection pressures exerted against the three phenotypes by the environment, specifically, the severity of the incidence of malaria in the area.

**GeneFlow.***PGS* – In the real world, gene flow between populations subjected to different selection pressures is common and can influence the direction of evolutionary change in a population. This simulation illustrates a situation that has been found to occur in peppered moth populations in certain areas of England.

**ABO.***PGS* – This simulation, examining the "Dunkers" community in Pennsylvania, should be run several times to show that the resulting equilibrium allele frequencies in the emigrant pool can differ widely from the parent population, and from other emigrant populations for different runs of the simulation.

**Italian.***PGS* – This simulation looks at a documented case of genetic drift in the Parma Valley of Italy, again looking at a selectively neutral characteristic – blood group determination. Two populations with only 40 and 80 reproductive individuals are compared through time and from one simulation run to the next.

**Seals.***PGS* – This example simulates the bottleneck that the northern elephant seal population went through due to over-hunting. It uses the founder effect option to randomly create a small population from a larger population (this simulates the random destruction of most population members) and then to follow both populations through time. This allows you to examine allele frequency changes in the small population after the bottleneck with the original population had the bottleneck not occurred.

**MutSel.***PGS* – This simulation shows that a realistically small mutation rate by itself will not lead to evolutionary change in a population. However, if the mutant allele is selectively advantageous, its frequency will quickly increase in the population. This leads to the idea of mutation as creator of raw material upon which natural selection can act. *Note:* In simulations involving mutation, students should be reminded that at each generation mutation occurs before selection or any other treatment is exerted.

**Giraffe.***PGS* – The results of this simulation can best be studied by using a feature of *PGS* that allows you to view histograms of phenotypes at each generation. This feature is available if you are studying two or more genes and have defined phenotypes. This makes it especially easy to examine the effect of selection on the distribution of phenotypes for a characteristic whose inheritance is determined by multiple genes (polygenic inheritance).

**Snail.***PGS* – This simulation looks at selection for phenotypes based on the interaction of two different genes, using what is known about predation on *Cepeae* land snails. Shell coloration and banding are the characteristics and the relative fitness values of the different phenotypes differ seasonally, so students must pause the simulation, change fitness values, and resume the simulation.

## *PGS* **Project Suggestions**

You may wish to discuss the following general recommendations when students are ready to design their own simulations:

1. Projects should be fairly simple in design and test only one or possibly two related variables.

2. Because of the stochastic nature of *PGS* simulations, several simulation runs should be completed before conclusions are formed.

3. Most simulations will work fine with a sample size of 500, unless you are studying genetic drift. Larger sample sizes take more time and can lead to frustration. Also, most simulations do not need to be run for more than 20–25 generations. Longer run times also waste time and cause genetic drift to become a more important extraneous variable.

4. Printouts of the simulation information and allele, genotype, or phenotype graphs, as appropriate, can be included as data to support the conclusions presented in their report.

### **Student Outline**

## **Laboratory Synopsis**

In this laboratory, you will use a physical model and a computer simulation to examine simple biological situations where one of the Hardy-Weinberg conditions is not met and evolutionary change occurs. You will use these same concepts to investigate a more complex simulation of a biological phenomenon using the microcomputer program *Population Genetics Simulator*. The results and conclusions from your simulation will be presented to your instructor as a short written report.

## **Laboratory Objectives**

1. Define the terms population and gene pool, and relate them to the concept of evolutionary change.

2. Explain the Hardy-Weinberg genetic equilibrium between allele frequencies and genotype frequencies and relate it to the expression $(p + q)^2 = p^2 + 2pq + q^2$.

3. Describe the four conditions necessary for a population to be in Hardy-Weinberg genetic equilibrium.
4. Explain how the physical model provides the necessary Hardy-Weinberg conditions.

5. Use the microcomputer program, *Population Genetics Simulator*, to model a biologically realistic situation where evolutionary change might occur.

6. Explain the evolutionary phenomena described by the terms mutation pressure, genetic drift, genetic fixation, founder effect, bottle-neck effect, gene flow, natural selection, and genetic load.

**Pre-Lab Questions**

1. What are the four Hardy-Weinberg conditions?

2. Which of the Hardy-Weinberg conditions are usually valid for most populations?

3. Which of the Hardy-Weinberg conditions are usually *not* valid for most populations?

4. If a population is in Hardy-Weinberg equilibrium and you know that the proportion of individuals with the genotype *aa* is 0.16, can you determine the expected proportions of *AA* and *Aa* genotypes? If yes, what are they?

5. If a population is in Hardy-Weinberg equilibrium, and you know that the proportion of individuals with the genotype *Aa* is 0.48, can you determine the expected proportions of *AA* and *aa* genotypes? If yes, what are they?

6. What do the concepts genetic drift, founder effect, and bottleneck effect have in common? How do they differ?

7. How can the Hardy-Weinberg equilibrium principle be used to determine if evolution has occurred?

8. In the physical model for Hardy-Weinberg genetic equilibrium you will use today: (a) What do the bean seeds represent? (b) What does the bag holding the bean seeds represent? (c) What does the person picking the beans out of the bag represent? (d) What would constitute an evolutionary change?

**Introduction**

The process of evolutionary change occurs at the level of the population. A *population* is a group of interbreeding individuals located in the same area and separated physically from other populations of the same species. The genotype of a population is called its *gene pool* and consists of all of the alleles present in the population members for all of the genes found in that species. Evolutionary change occurs when there is a measurable change in the population's genotype through time. The smallest unit of evolutionary change is an alteration in the allele frequencies for a single gene in the population through time. In 1908, G. H. Hardy and W. Weinberg independently showed that evolutionary change will only occur when certain conditions within a population are violated. If these conditions are not violated, *genetic equilibrium* will be maintained within the population.

Hardy and Weinberg developed a model expressing the equilibrium between the allele frequencies for a single gene and the genotype frequencies among population members for that gene as an expansion of the binomial $(p + q)^2$, or:

$$\begin{array}{ccc}
\textit{allele} & & \textit{genotype} \\
\textit{frequencies} & & \textit{frequencies} \\
(p+q)^2 & = & p^2 + 2pq + q^2
\end{array}$$

For example, for a single gene with two allelic forms ($A$ and $A'$), if you know that the population frequency of allele $A = 0.6$ and $A' = 0.4$, then you can say that

$$p = \text{frequency of allele } A = 0.6$$
$$q = \text{frequency of allele } A' = 0.4$$

The Hardy and Weinberg model predicts that the genotype frequencies in a population can be estimated by the expression.

$$p^2 + 2pq + q^2$$

Specifically,

$$p^2 = \text{frequency of } AA \text{ genotype} = (0.6)^2 = 0.36$$
$$2pq = \text{frequency of } AA' \text{ genotype} = 2\,(0.6)\,(0.4) = 0.48$$
$$q^2 = \text{frequency of } A'A' \text{ genotype} = (0.4)^2 = 0.16$$

Further, the Hardy and Weinberg model states that unless certain conditions are violated, these allele and genotype frequencies will be maintained through time (Figure 4.1).

The so-called Hardy-Weinberg conditions are the following:

1. Mutation must not occur or if it does there must be mutational equilibrium (i.e., rate of $A \rightarrow A' =$ rate of $A \leftarrow A'$).

2. Migration (immigration or emigration) must not occur in the population.

3. Population size must be large.

4. Survival and reproductive success of population members must be random and independent of their genotypes.

The Hardy-Weinberg conditions within the population are necessary to insure that gametes, and their alleles, combine *randomly* to produce new individuals in the next generation. If the way in which gametes combine is random, then knowing the allele frequencies, $p$ and $q$, allows us to calculate the genotype frequencies as the products of the independent probabilities for each allele. For example, if $q = A' = 0.4$, then the probability that a particular individual has a single $A'$ allele is 0.4, and the probability that it has two $A'$ alleles (i.e. has the $A'A'$ genotype) is $0.4 \times 0.4$ or $(0.4)^2$. The other two genotypes are predicted using the same reasoning. The Hardy-Weinberg conditions are considered in more detail in the following paragraphs.
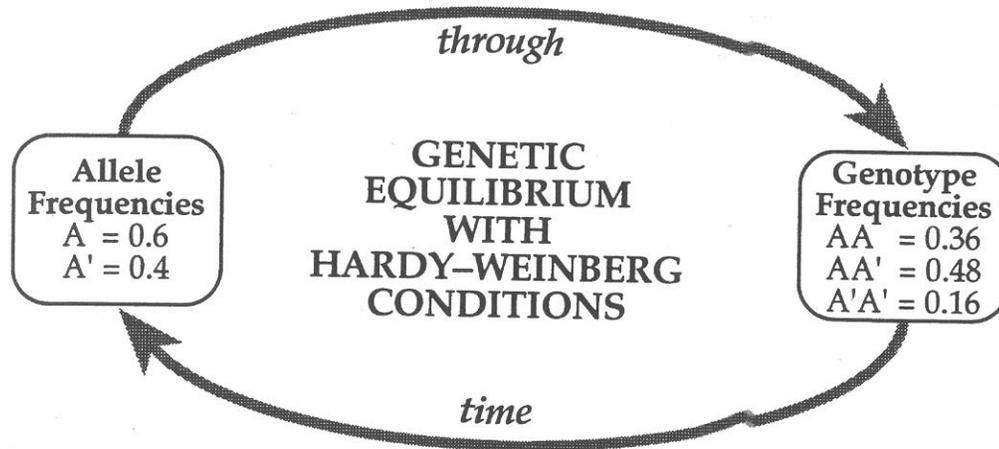
**Figure 4.1.** Genetic equilibrium within a population under the Hardy-Weinberg conditions.

*Mutation*

Mutation is an on-going process and seldom is there an equilibrium in forward and back mutations for a given gene. An imbalance in the mutation rate for a gene creates a *mutation pressure* that tends to favor one allele and cause the population to deviate somewhat from Hardy-Weinberg equilibrium. However, the rate of mutation is very small (perhaps 1 in 10,000 meiotic divisions for a specific gene) and, unless there is a concomitant selection pressure (see below) for the mutant allele, mutation *per se* has little effect on genetic equilibrium.

*Migration*

The exchange of members between different populations, due to emigration and immigration, results in *gene flow* that can produce significant changes in allele frequencies, providing the populations involved differ genetically.

*Population Size*

Several of the Hardy-Weinberg conditions are necessary because they insure that the combining of gametes and their alleles to form the genotypes of the next generation is random. For example, population size (specifically, the population of breeding individuals), must be large or chance events will cause deviations from expected results. In small breeding populations, where a single population member may be a significant fraction of the whole population, whole alleles may disappear due to chance events. *Genetic fixation*, a condition in which genes are represented by only one of two or more possible alleles and many individuals are homozygous for many genes, is characteristic of small populations. Change in allele frequencies in small populations due to chance events is called *genetic drift*.

Frequently when a small population emigrates from a large parent population and becomes established in a different area, its gene pool may become significantly different than that of the parent population. The so-called *founder effect* occurs because the original small group of emigrants was not, by chance, representative of the larger population.

Like founder effect, the *bottleneck effect* is another random evolutionary change that can occur within a population, in this case if the population is reduced to a small number of individuals due to a natural or man-made disaster. If, by chance, the initial survivors were not genetically

representative of the original population, when the population recovers to its previous size, it may be genetically quite different than the pre-disaster population.  Typically, the result of the bottleneck effect is a reduction in genetic variability within the population since many alleles may be lost when the population is very small.

*Natural Selection*

Natural selection, the non-random survival and reproduction of population members, is the major cause of evolutionary change in most populations.  Natural selection works through the organism's environment which exerts specific *selection pressures* that favor certain individuals and act against others, based on their phenotypes.  The environment is, in a very broad sense, any factor that influences population members in any way, including both physical (weather, temperature, photoperiod, etc.) and biological factors (predators, parasites, inter- and intraspecific competition, etc.).

If a certain genetically determined characteristic is deleterious to an individual's survival in a given environment, individuals possessing that characteristic are *selected against* (subject to a *negative selection pressure*).  This means that, due to their less adaptive phenotype, these individuals have a lower survival rate (i.e., they do not live as long) and, consequently, they contribute proportionally fewer progeny to the population.  Therefore, their alleles become less frequent in the population's gene pool.  Individuals that possess an advantageous phenotype are *selected for* (subject to a *positive selection pressure*).  Individuals with an advantageous phenotype live longer and contribute proportionally more progeny to the population.  Therefore, their alleles become more frequent within the population's gene pool.  In this way, due to natural selection, the population's phenotypic characteristics change to become more like the individuals that are selected for and less like the individuals that are selected against.  The following paragraphs describe several examples of evolutionary change due to natural selection.

Recessive lethal alleles exist in the gene pools of every species and represent what is called the species' *genetic load*.  By definition, when recessive lethal alleles are present in a homozygous condition, the individual dies.  *Phenylketonuria* in humans is a genetic disease caused by a recessive lethal allele.  With absolute selection against a recessive lethal allele, how long do you think the allele will be maintained in the population's gene pool?

The British biologist H. B. D. Kettlewell collected evidence to show that the changes in the frequencies of light and dark morphs of the moth *Biston betularia* were due to a negative selection pressure against the less cryptic morph by bird predation.  In polluted woodlands, with darkened, lichen-free tree bark surfaces, the light morph is less cryptic.  In unpolluted woodlands with clean, lichen-covered tree bark surfaces, the dark morph is less cryptic.  Differential selection in these two environments led to large phenotypic changes in the moth populations in a period of less than 50 years.  The polymorphism in coloration in these moths is caused by a single gene with two allelic forms, the allele causing pigment production (*B*) being dominant to the allele (*b*) causing no pigment production.  Therefore, dark morphs are *BB* or *Bb*, while light morphs are *bb*.

The genetic disease, sickle-cell anemia, illustrates a case where an allele has both positive and negative selection pressures associated with it.  Sickle-cell anemia is caused by a mutant allele $Hb_s$ which, when present in the homozygous condition, causes the production of abnormal, sickle-shaped erythrocytes.  These erythrocytes do not carry oxygen efficiently and also clog capillaries.  The wild-type allele ($Hb_a$) produces normal erythrocytes. Individuals with the genotype $Hb_sHb_s$ die of severe sickle-cell anemia before reaching reproductive age.  Individuals who are $Hb_aHb_a$ are normal, while heterozygotes, $Hb_aHb_s$, suffer a mild form of sickle-cell anemia (their RBCs are only moderately deformed) that is not fatal.  Because the $Hb_s$ allele is lethal in the homozygous condition, biologists were surprised to find that it is a fairly common allele in certain

populations, particularly in equatorial Africa. It is now known that heterozygous individuals show a marked resistance to the blood disease malaria. Thus, the $Hb_s$ allele is subject to negative selection pressure (lethal if the individual is $Hb_sHb_s$), as well as positive selection pressure (enhanced resistance to malaria in the heterozygote).

Today, you will use both a physical model and a computer simulation of Hardy-Weinberg genetic equilibrium in order to investigate the causes of evolutionary change.

## Physical Model

The model represents the gene pool for a single gene with two allelic forms. It consists of beans of two colors in a paper bag. The two colors of beans represent the different alleles. The size of the allele pool is determined by the number of beans placed in the bag and the initial allele frequencies are the proportions of total beans that are black and white. A key idea in population genetics is that if the allele frequencies for a gene in a population are known, then we can predict the genotype frequencies *directly* without being concerned about actual matings of population members. In the physical model, you randomly select pairs of gametes from the pool by drawing out of the bag two beans at a time. Each pair of gametes is a new individual in the next generation.

1. Add sufficient white and black beans to the bag so 100 in total are contained in the proportions assigned to you. The 100 beans represent the gametes for a population of 50 diploid individuals. Black beans represent gametes with the A allele, white beans represent gametes with the *A'* allele.

2. To form an individual of the next generation, reach into the bag and, without looking, randomly pull out two beans. Record the genotype of the individual represented by the two beans (*AA*, *AA'*, or *A'A'*).

3. *Return* the two beans to the bag and *shake* the bag to randomize the gene pool. Now, reach in and *select* the next individual. Replacing beans before you select each new individual insures that the allele frequencies do not change due to sampling, and creates the effect of a larger population than just the 50 individuals you have in the bag.

4. Continue sampling with replacement until you have recorded the genotypes of 50 new individuals. Record the numbers of the three genotypes in Tables 4.1 and 4.2.

5. Calculate the frequencies (proportions) of the three genotypes and the *A* and *A'* alleles in the new population of 50 individuals. Record these numbers in Table 4.1.

6. Use your original A and *A'* frequencies and the expression $p^2 + 2pq + q^2$ (where $p$ = frequency of *A*, and $q$ = frequency of *A'*) to calculate the *expected* genotype frequencies based on the Hardy-Weinberg genetic equilibrium. These frequencies times 50 will give you the number of expected individuals of the three genotypes. Record these values in Table 4.2.

7. Use the chi-square test to compare the observed and expected genotype numbers (*not* frequencies) for the new population recorded in Table 4.2.

*Questions*

1.  For the model to accurately simulate genetic equilibrium it must meet all of the necessary Hardy-Weinberg conditions.  Does it?  Consider each condition and explain how the model meets it.

2.  Is there any evidence that natural selection, as previously defined, may be at work in the physical model?  If so, what is the nature of the selection pressure involved?

**Table 4.1.**  Observed genotype and allele frequencies in a new population produced by the physical model from an allele pool with 100 alleles.

| **Error! Bookmark not defined.**Parent population Allele frequency | | New population Genotype number (frequency) | | | Allele frequency | | $X^2$ |
|---|---|---|---|---|---|---|---|
| A (black) | A′ (white) | AA | AA′ | A′A′ | A | A′ | |
| | | ( ) | ( ) | ( ) | | | |
| | | ( ) | ( ) | ( ) | | | |
| | | ( ) | ( ) | ( ) | | | |
| | | ( ) | ( ) | ( ) | | | |
| | | ( ) | ( ) | ( ) | | | |
| | | ( ) | ( ) | ( ) | | | |

**Table 4.2.**  Chi-square test of the results from the physical model while simulating Hardy-Weinberg conditions.

| **Error! Bookmark not defined.**Genotype | Observed number | Expected number | (O - E) | $(O - E)^2$ | $(O - E)^2 \div E$ |
|---|---|---|---|---|---|
| *AA* | | | | | |
| *AA′* | | | | | |
| *A′A′* | | | | | |
| Tabular statistic ($\alpha = 0.05$, d.f. = 2) = 5.99  $X^2 =$ | | | | | |

*Population Genetics Simulator* (*PGS*)

This microcomputer program is designed to allow you to investigate evolution using a computer simulation based on random sampling from an "allele pool" maintained in the computer's memory. In this regard, *PGS* works in a way analogous to the physical model you have just used.

During the laboratory, your instructor will demonstrate how the program works and you will then work in groups to study one of several example simulations.

As an independent project, you will use *PGS* to study a simulation of a biologically realistic situation. You will have time in class today to design a simulation and discuss your plans with the instructor. If time permits, begin data collection for the project in class. You will need to visit the course's PC Room later in the week to complete your project.

**Answers to Pre-Lab Questions**

1. Large population size, no migration, no mutation or else mutational equilibrium, and no selection (equal reproduction and survival for all!).

2. Mutation and population size requirements are met by many populations.

3. Migration and selection requirements are met by few populations.

4. Yes. Since $q^2$ = frequency of the *aa* genotype, $q = \sqrt{0.16} = 0.4$ and $p = 1.0 - 0.4 = 0.6$, so $p^2$ (frequency of *AA* genotype) = $(0.6)^2 = 0.36$ and $2pq$ (frequency of *Aa* genotype) = $2(0.6)(0.4) = 0.48$.

5. No. You must be able to estimate the frequency of at least one allele; since the heterozygote frequency is the product of both doubled, you know neither.

6. All three result because of chance events due to too small a population size. Genetic drift is random fluctuations in allele frequencies of a small population through time; founder effect refers to a non-representative assortment of alleles among a small group of founders; bottleneck effect is the reduction in genetic variability due to a marked reduction in population size.

7. Yes. If you can estimate the allele frequencies from the genotype frequencies, you can see if genotype frequencies differ significantly from the expected values predicted by $p^2 + 2pq + q^2$. If they do, evolution has occurred.

8. (a) Beans = alleles for a gene. (b) Bag = the barriers isolating the population genetically from others. (c) Person = the fickle finger of fate (a stochastic process determining the genetic composition of the next generation). (d) Observing a significant shift in the frequency of the beans from one generation to the next.

**Suggested Reading**

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