

Favorite Demonstration

Demonstrating an Interactive Genetic Drift Exercise

Examining the Processes of Random Mating and Selection

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The phenomenon of genetic drift is a powerful force in molecular evolutionary biology (Kimura 1983). Neutral alleles under the influence of drift, but not selection, likely account for a large part of the widespread levels of genetic polymorphism observed in natural populations. Purely advantageous or disadvantageous alleles would contribute little to polymorphism since these alleles are fixed or lost quickly within populations. Conversely, neutral alleles can drift in frequency for long periods of time before eventually becoming lost or fixed in a population.

Genetic drift is usually presented in very abstract terms in most texts. Many texts present graphs of computer simulation results showing an allele's frequency changing over time, perhaps at different speeds for different population sizes. The graphs are excellent, but they may not have an impact on a student who learns best using hands-on activities.

In general, students may have a hard time understanding how a frequency can change without selection, or they may not fully appreciate the effects of population size on the dynamics of frequency changes in populations. Supplementing such graphical depictions with a popu-

lation genetics computer program to simulate drift may not help students because they do not necessarily observe what happens in a potentially "black box" computer program.

The exercise presented here is a hands-on demonstration of the phenomenon of genetic drift in populations. In particular, it reinforces the random nature of drift and demonstrates the effect that population size can have on the mean frequency of an allele over just a few generations. The students will take on the roles of organisms (with genotypes) and they will choose mates and generate offspring themselves (on note cards). The frequency of each genotype in the population will be recorded over time. From this the allele frequencies for the population can be calculated. The students will see that by simply choosing mates using a random-mating system, they will generate allele frequency dynamics.

Materials

The following items comprise the materials for this demonstration:

- ♦ one note card per student
- ♦ one coin per student
- ♦ one pen per student

Procedure

The effects of population size are illustrated by performing the exercise twice, once with the entire class acting as a large, completely mixed population and once with the class partitioned into

smaller groups that must "mate" within their own groups. Although the larger population will show some fluctuation in allele frequencies, it should be more stable than some of the smaller populations, at least one of which will hopefully go to fixation/loss of an allele.

To start the exercise, each student is given a notecard with an initial genotype printed on it. The genotypes involved are A_1A_1 , A_1A_2 , and A_2A_2 . I suggest creating a starting set of cards designed so that the genotypes are in Hardy-Weinberg equilibrium with equal frequencies of each allele (approximately a 1:2:1 ratio of the genotypes). This way the starting frequency for each allele will be 0.5, the maximum polymorphism possible.

Each generation comprises the following events:

- ♦ Each student finds another student to "mate" with. The students are encouraged to mate at random.
- ♦ Each student then independently generates a new genotype by randomly selecting an allele from his or her genotype and combining it with a randomly selected allele from the mate. The students can flip coins (for example, heads for the first allele and tails for the second) or use some other technique. It is important that the technique for randomly choosing between the alleles be well known and influenced only by chance. This new genotype repre-

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sents an offspring of the mating between the two genotypes involved. Each student then records his or her new genotype on the note card below the previous genotype. This will be their genotype in the next generation. Each pair of students will mate twice to generate two new offspring, one per student.

- ◆ The instructor calls for a show of hands for each genotype and records this data on the board.

While the somewhat chaotic mating period is going on, the instructor can calculate the frequency of each allele from the genotypes and record this information on the board. Alternatively, the class as a whole can do these calculations.

These generations are repeated for an appropriate number of times (at least five or six) or until one allele has been lost or fixed. At the end of the trial, there will be a series of frequency values for each allele. The instructor should do a rough line plot of these values from the starting value of 0.5 to the final value. All fluctuations seen will have resulted purely by chance. Because the students did every step themselves, they will appreciate that there are no mysterious hidden factors that have influenced the allele frequencies. The remainder of the class time can be used to discuss what has just occurred.

Discussion

The following discussion topics start by reinforcing what the students have seen firsthand in the demonstration and continue on to more advanced concepts. The more advanced ideas are commonly seen scattered throughout texts. By discussing them after the demonstration, the students have a better opportunity to synthesize these ideas because the idea of drift is fresh in their minds. These points address many of the common misconceptions about drift and selection as they pertain to changing the frequencies of alleles in populations. Each point is prefaced by a question that the instructor can pose to the students to initiate discussion.

(1) Did the population size affect how

the frequencies changed? Even if all the smaller populations persisted, they should have shown more severe swings in frequency from generation to generation than the larger population.

(2) What do such effects of population size mean for wild populations? Since smaller populations are more likely to lose alleles at a locus, they will more quickly become homozygous for various alleles across their entire complement of distinct loci. This will reduce the pool of variation within the population that facilitates an evolutionary response to new threats or environmental conditions. A smaller population becomes much more vulnerable to extinction than a larger one. This has important ramifications for the conservation of organisms in the wild.

(3) Was the mating truly random? Most students interpret random mating to mean that they should never mate with the same student twice if they can help it. Truly random mating would have many instances of the same students mating. Preferential outbreeding (avoiding all relatives as much as possible) actually acts to increase the frequency of heterozygotes, but has no impact on allele frequency.

(4) If an allele disappears from a population, does that mean it was harmful? If the experiment went well, then at least some of the smaller groups lost alleles, presumably because of random effects, not because one was consistently bad. The loss of an allele from a population does not imply harmfulness of that allele, it may be lost purely due to chance.

(5) In the converse of (4), does fixation of an allele (it becoming the only allele in the population) prove that it is beneficial? Interestingly, this result means that an allele that is seen to increase in frequency in a population over time need *not* be beneficial. Students may want to provide ideas about how they would test for the possible benefits of a given allele if it is seen to increase in frequency.

(6) What would happen to the allele frequencies if each student with an A_2

allele got to mate more often than the students homozygous for the A_1 allele? The frequency of A_2 would very likely increase over time and the allele would go defined above in (topic 5) to fixation, since the starting frequency of the A_2 allele is so high that its loss due to random factors (topic 4 above) is remote. However, new beneficial mutations start in single mutant individuals.

(7) What would happen if all members of the population were A_1A_1 except for a single A_1A_2 mutant? A neutral A_2 allele would most likely be lost eventually (25 percent chance of loss in first generation alone if everyone gets to mate as described in this exercise). Even if it were beneficial, there is a real chance of loss for such an allele. Using population genetics theory, the chance of eventual fixation of such a beneficial allele from a single copy is approximately twice the selective advantage of the mutant allele in the heterozygote (for example, if heterozygotes with the allele have an average of one percent more offspring, the allele has a two percent chance of becoming fixed in the population as a whole). Kimura (1983) and Gillespie (1998) provide a summary of the relevant mathematics involved. The students may consider how many beneficial mutations have been lost because of random factors just after their formation by mutation.

Using this hands-on demonstration and these more advanced discussion topics, the instructor has the chance to make students really appreciate the randomness inherent in determining the frequencies of alleles in populations. The students will gain a feel for the processes of random mating and selection that are the cornerstone of much of the modern thinking in evolutionary biology.

References

- Kimura, M. 1983. *The Neutral Theory of Molecular Evolution*. Cambridge: Cambridge University Press.
- Gillespie, J. 1998. *Population Genetics, a Concise Guide*. Baltimore, MD: Johns Hopkins University Press.