

1-Alfred Wallace spent many years traveling among the small, isolated islands of Southeast Asia. One of the taxa that he was particularly interested in was land snails. Suppose that he observed that in the Aru Archipelago, almost all shells of one snail species had banding patterns on some islands but checkered patterns on other islands. Wallace, a co-discoverer of natural selection, would probably have postulated that the color pattern differences were caused by the effects of color pattern on survival in different island environments. You offer an alternative explanation.

- a. What is the alternative explanation?
- b. Explain how it accounts for both lack of variation within populations and high variation among populations.
- c. If you are correct, what other predictions would you make about these island populations?

2-You are sampling different populations of a spider that lives on mountain tops in the Appalachian Mountains. You determined the genotype frequencies for 5 different populations last summer. Because the spiders are on mountain-tops their populations are relatively small compared to those found in valleys, there is no migration and mating is random within each population.. This summer you are planning on determining the genotype frequencies of the same 5 populations. You know that there have been no differences in the environment this year. Do you expect the genotype frequencies to be the same this summer as they were last summer? Why or why not?

3- There are only less than 2,500 individuals of the endangered Giant Panda Bear alive in the wild. Is this a relatively large or small population? Is this a large or small population compared to the Panda Bear's close relative the Polar Bear (about 22,000 individuals in the wild)? What effect does population size have on the genetic diversity of the Giant Panda Bear population?

Here is the link to the Genetic Drift Simulator:

<http://pandasthumb.org/archives/2009/03/population-gene.html>

Click on Start Red Lynx Simulator

4- Run the simulator 10 times for each of the following trials (Approximate Population Size, Generations, and Num Allele A) then answer the following questions. Do not change any of the other options provided (Dominance, Fitness of AA, etc.) The simulator is slow with the largest population size, so be patient when it runs.

Trial	Population Size	Generations	Num of Allele A
1	100	1000	100
2	100	1000	20
3	500	3000	500
4	500	3000	200
5	10,000	10,000	10,000
6	10,000	10,000	4,000

- a. Calculate the frequency of A for each of the trials. (Hint: Every individual has 2 alleles)
- b. What is the average number of generations until one of the alleles (A or the other allele that isn't shown) is fixed or lost in a population for each of the above trials?
- c. Does genetic drift only affect smaller populations?
- d. What happens to genetic diversity within populations because of genetic drift?
- e. How do the effects of genetic drift change with population size?
- f. What happens to an allele if it starts with a low allele frequency? (like 0.2)

5- Set the simulation to 500 generations and change the Population Size and Num of Allele A settings so that as you change the Population Size, the frequency of the A allele stays at approximately 0.5. Run the simulator multiple times for every Population Size you use.

- a. Roughly, how big does a population have to be to have a 50% chance of retaining both alleles after 500 generations?
- b. Set the Population Size to the answer for the above question, then set the Num of Allele A setting so that the frequency of the A allele is 0.25. Run the simulator again a few times. Are both alleles still retained or does one get fixed in the population?

6- Run the simulator for 20 times with a starting population size of 100, and an Allele frequency of 0.1. Run the simulator 20 times with the same population size and a A allele freq of 0.8. Can you predict if the A allele will be fixed or lost based on its initial frequency?

### **Questions from material that has not been covered in lecture yet:**

7- It is estimated that every individual human carries 3-5 recessive lethal alleles (i.e. alleles that cause death in the homozygous state) in their genome of ca. 30,000 loci. Use this information and what you know about the effects of inbreeding to explain the observation that inbred individuals (of many species) are on average less likely to survive than individuals that result from random matings.

8- Populations of sand lizards (*Uma notata*) live in large, isolated sand dunes in the southwestern United States. Herpetologists studying these lizards in Imperial County, California found that the frequency of the *Fringe-toed* allele was 0.88 in an eastern dune population and only 0.12 in a western dune population. Suppose that a brutal windstorm comes along and blows enough sand around to create a corridor in which some of these lizards can boldly migrate from the eastern dune to the western dune. After the storm is over, 279 individuals are collected from the western dune, 37 of which are from the eastern dune in the last generation.

- i) Calculate the migration rate into the western dune.
- ii) What would the frequency of the *Fringe-toed* allele be in the western sand dune after one generation of migration?
- iii) Use this example to explain why a population experiencing migration is NOT in Hardy-Weinberg equilibrium.

9- Monarch butterflies over winter in the Trans-Mexican Volcanic Belt pine-oak forests of Mexico. For populations east of the Rocky Mountains, monarch butterflies migrate starting in the spring as far north as Canada before starting their southward migration back to Mexico in the fall. Would a population geneticist regard this movement as migration?

10- A population of 350 water snakes live on an island off the coast of Lake Erie. At a particular locus involved in determining color patterning, this population has a frequency of 0.54 for the E allele and 0.46 for the F allele. Assume that this is an ideal population (none of the genetic drift assumptions are violated  $N=N_e$ )

a. What is the probability that the E allele will become fixed in the population? What about the F allele?

b. How many generations do you predict will pass before there is a loss of genetic diversity?

11- Captive breeding is a way of increasing the population size of endangered species in captivity. When researchers breed endangered species in captivity they exchange animals from around the world to mate. Why is this so important?