Chapter 3: Natural Selection
Variability & Selection in Natural Populations of Wood Lice

BEFORE this lab
A. **Design a table** to record your data to be collected during the lab; include columns for repeated measurements for 30 individuals. Be sure to indicate the appropriate units of measurement. Bring TWO (2) copies—give 1 copy to your TA at the beginning of lab and keep the other copy to record your data during lab. Designing this table will help you think about the experiment and prepare for the lab in a meaningful way.

B. **Write out the definitions of the list of key terms** Use this exercise to see if you understand the main concepts illustrated in this chapter.

C. **Answer Pre-Lab Questions** below. Use these to test yourself and prepare for the lab. Compare your ideas with other students. These questions are not easy—see what ideas you come up. For background information use the lab description, course lecture notes and text. Several answers are possible for each question.
   1. How much variation (none, some, a lot) should you expect to see in each of the traits you are to study? Why might some traits be more variable than others?
   2. What might be the relationship between the amount of variation in a trait and the intensity of selection on that trait in the past? What might be the relationship between the amount of variation and the opportunity for selection in the present?
   3. For one of the traits you will measure in the lab, state a hypothesis about whether or not the trait will confer a survival advantage in the simulated predation experiment. Briefly describe how you will decide whether the trait confers such an advantage.

Summary
Many traits vary considerably in natural populations; other traits do not vary at all. Variation in a trait is necessary for that trait to evolve through natural selection, and the amount of variation can influence the rate at which the trait evolves. In this lab, we will measure the amount of variation in a natural population of terrestrial wood lice (Class Crustacea, Order Isopoda) and then determine which traits are subject to selection by predators by performing a simulated predation experiment.

Goals
*By the end of this exercise, you should be able to:*
- Construct a table to record data for this type of experiment.
- Collect and record a large number of data in an organized fashion.
- Construct a table to summarize results in a meaningful way (which is not the same as the table to record data) & present your data in graphs
- Draw a frequency distribution of sample data.
- Calculate a mean, standard deviation, and start to understand how to calculate and use a t-test of significance.
- State and evaluate hypotheses about which traits confer a survival advantage in a simulated predation experiment.
In this experiment, we will investigate 1) variation in several traits of wood lice a common terrestrial crustacean (Figure 1), 2) whether and how some traits confer a survival advantage in the presence of simulated foragers and 3) whether such survival advantages depend on the kind of forager.

**Figure 1.** External anatomy of a European wood louse, *Oniscus asellus*. (From Ruppert and Barnes, 1994, p. 742).

**Key Terms** To help study for this lab and future tests, write out the definitions and try to construct a concept map showing relationships between the following terms.

- Fitness
- Heritable
- Natural selection
- Phenotype
- Selection-directional, disruptive, stabilizing
- Variation
Materials

Per Group (half bench or 3-4 students):

- electronic balance
- plastic spoon
- plastic fork
- large forceps
- medium to fine forceps
- 30 wood lice
- 30 capped vials
- 1 ruler marked in centimeters
- 1 dissecting microscope with light
- 1 stopwatches
- 1 racetracks with paintbrushes
- 1 predation arena with refuges
- 1 release ring
- 2 plastic cups with lids labeled survivors or victims

Procedure  Work in teams of 3-4 students (half bench)

A. Simulated predation experiment

For the first part of today's exercise, you will be the predator on your population of prey isopods.

1. Assign one person in your group to be the artificial predator and decide which tool (i.e. morphological adaptations) this predator will have: spoon, fork, or forceps. Other members of the group should be responsible for counting animals as they are caught and making sure none escape the arena.

2. Assemble the predation arena as demonstrated by your TA. Divide your 30 isopods evenly into the release ring at the center of the arena. Allow the animals to recover for about one minute, then when the “predator” is ready, release the 30 isopods simultaneously. Using only the chosen tool, the predator should pick up isopods without injuring them and place captured prey in the ‘victim’-marked plastic cup. Collect the isopods until 15 have been captured; you may need to repeat the predation trial if many isopods escape to the refuges. Transfer the remaining isopods to the ‘survivor’-labeled cup. Be sure to keep the victims and survivors in separate cups.

B. Measuring traits

Since it is difficult to mark wood lice in a manner that does not interfere with their behavior, the first person in line should transfer each animal from its holding container (labeled VICTIM or SURVIVOR) to a clearly numbered vial after recording data on that animal. Randomize the numbering—don’t just put all victims in vials numbered 1-15. However, it is very important that the other students NOT know whether a given animal was a victim or survivor as this knowledge may bias their recording of other traits. Be sure to write out the status (victim/survivor) for each numbered vial and give this information to the rest of the team after the traits are measured.
Each person measures one variable and then passes each animal to the next person.

The following measurements should be made in whatever order you think will be most efficient.
1. Measure animal length: place it on cotton in a Petri dish. (Be sure that the cotton is slightly damp - not soaked!). When the dish is covered, the cotton will hold the animal in place for observation under the dissecting microscope. Measure the total length in millimeters using the ruler.

2. Measure sprint speed (two people are needed) One person should release an animal behind the starting line of the race track and prod it gently with the paint brush. As the animal crosses the starting line, the second person should start the timer. Record the time and the distance to the finish line (either 20 or 40 cm, depending on the individual animal). Repeat this a second time for each animal and compute the mean burst speed in cm/second. You are strongly advised to practice this procedure on non-experimental animals before actually running your tests.

3. Choose one additional character that can be measured easily and quickly on all 30 animals. (Why is the number of appendages not a good character to measure?)

C. Data analysis Due next lab; necessary background is in the Appendix. Be sure you have data for all thirty individuals.

1. For each of the three characteristics you measured, calculate the mean and range (high & low values). Enter these values at the bottom of each column of your data table.
2. Make three frequency distributions, one for each characteristic measured. Be sure to label the distribution with a title and label the axes. For the x-axis, you will need to establish an appropriate number of bins, each of the same range, in which to place the values for each character. For example, for speed you might have five bins, each with a range of 5 cm/second (0-5, 6-10, 11-15 cm/second, etc.). You may have to decide through trial and error on the number and width of the bins.
3. Evaluate your hypothesis about the survival advantage conferred by one trait of your choice by comparing the distributions of those traits in the survivors vs. the victims. Compare the means of the two distributions by performing a t-test (See the Appendix on Biometrics in this lab manual.) Report the mean and variance of the survivors and victims separately, the value of t, the degrees of freedom, and the associated probability.

Evaluation: 40 points (4%)
- 5 points Pre-lab Table to collect data due at the beginning of this lab (bring 2 tables, one to hand in and one to use during the lab)

The following are due at the beginning of the next lab:
- 15 points Summary table and graphs for the 3 traits
- 20 points For one of the traits evaluate survival advantage:
  - (10) Determine the extent (strength) of selection of one trait in this simulation. See the Appendix especially the last page for an example of how to tabulate and graph selection pressure and fitness results.
(10) For this trait is there a real difference between survivors and victims? Do the Student’s t-test statistic to see if this difference is significant (see the explanation of the t-test in the separate package on Biometrics). Show your calculations.

Literature Cited

References


APPENDIX 1 BACKGROUND on Variation in a Population

A population of organisms almost never consists of individuals that are all exactly alike. For some traits there is considerable variation among individuals in a population and this variation is biologically very important. Darwin was the first to understand the importance of such variation in organisms. He suggested that differences we observe between species (that is, their average properties) might arise from variation in those properties within species.

The mean and variation of a population are easily seen by graphing the number of individuals that have a trait of a given value. Suppose you measured the sizes of 100 apples and sorted the fruit into seven different size classes. You would probably find some large apples, some small ones, and more of intermediate size. A graph of the numbers of apples in each size class (Figure 2) is called a frequency distribution. In this case the distribution is symmetrical (bell-shaped) and so the mean value would lie close to the middle of the graph. The amount of variation about the mean is indicated by the breadth of the distribution.

![Figure 2: Size distributions for a sample of 100 apples](image)

Natural Selection

Ever since Darwin, it has been known that variation in a trait is absolutely necessary for that trait to evolve through natural selection. Natural selection is simply defined as variation in survival and reproduction that is associated with variation in a particular trait. Many different forms of selection occur in the wild.

Darwin proposed that over time the net effect of the various forms of selection acting on a population of organisms can result in the evolution of new species. For example, the famous Galapagos finches vary considerably in bill shape and size. This variation among species seems to have evolved in response to the distribution and abundance of different kinds of seeds among the islands of the Galapagos archipelago (Grant, 1986). Deep billed individuals within a population survive better when they have access to large seeds, while small-billed individuals survive better when they have access to small seeds. Over time, this form of selection has resulted in different species with very
different bill shapes. Presumably, the distribution and abundance of different finches has also generated complicated patterns of selection on seed size and shape.

Figure 3. An analogy between Galapagos finch bills and various pliers. (Grant, 1986, p. 114.

ROW 1 Geospiza Heavy Duty Linesman’s Pliers Platyspiza Parrot-head Gripping Pliers
ROW 2 Camarhynchus High Leverage Diagonal Pliers Pinaroloxias Curved Needle Nose Pliers
ROW 3 Cactospiza Long Chain Nose Pliers Certhidea Needle Nose Pliers

Fitness and Selection Intensity
A way of characterizing a selection event that involves some degree of directional selection is by measuring the intensity of a selection pressure. This is simply the difference between the mean value for some phenotypic state (e.g., body size) before and after selection. It can be calculated by taking the mean value for some phenotypic state of the survivors of selection and subtracting from it the mean phenotypic state of the original population. In the hypothetical selection event graphed below (Figure 4), the selection differential is 1.71 of whatever units we use to measure phenotypic value (10.71-9.00=1.71).
Figure 4. The selection differential as a result of this directional selection event is “1.71” of whatever units the phenotype is measured in. This is calculated by taking the mean phenotypic value following selection (10.71) and subtracting the mean phenotypic value of the population before the selection event (9.00).

The probability of survival for individuals of each phenotype may be estimated by taking the percent survival of individuals of that phenotype. For example, in the above example graphically represented in Figure 4:

a) None of the individuals with phenotypes of 5 or less survived. Thus, percent survival for each of these phenotypes is zero.

b) Similarly, for individuals with phenotypes of 12 or higher, the percent survival is one hundred percent.

c) Individuals with phenotypes between 6 and 11 are intermediate between 0% and 100% survival.

The raw data used to draw Figure 4 is presented below (Table 1). These data may be presented in another way (Figure 5) by a line plot of percent survival compared to phenotypic state on the x-axis to give an indication of ‘fitness’.
Table 1. Data are provided for phenotypic states 2 through 16. For each state, the numbers of individuals before selection and after selection are indicated as well as the percent survival of individuals of the state.

<table>
<thead>
<tr>
<th>Phenotypic State</th>
<th>Number of Individuals Before Selection</th>
<th>Number of Individuals Surviving Selection</th>
<th>Percent Survival</th>
<th>Phenotypic State</th>
<th>Number of Individuals Before Selection</th>
<th>Number of Individuals Surviving Selection</th>
<th>Percent Survival</th>
</tr>
</thead>
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<tr>
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<td>0</td>
<td>0.00</td>
<td>10</td>
<td>38</td>
<td>32</td>
<td>84.21</td>
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<td>2</td>
<td>0</td>
<td>0.00</td>
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<td>34</td>
<td>32</td>
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<td>0</td>
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<tr>
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<td>12</td>
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</tbody>
</table>

Figure 5. The fitness function for the selection event portrayed in Figure 6 (Table 1) is drawn by plotting the percent survival of each phenotypic state on the y-axis and the phenotypic state on the x-axis.