Each group should submit a single Excel file (via e-mail) that includes all trait data (for both your selected trait & your correlated traits) for the initial, breeding, and offspring populations. Column headings in this file should be clearly labeled so that I can duplicate your calculations if necessary.

Each student will submit a written analysis of his or her group’s Brassica selection experiment due by 5pm on 31 October 2008. Reports should be typed and include all relevant data (see sections below) with figures prepared in Excel or a similar graphing program.

Introductory comments...

Your introduction should make clear the connections between the topics/terms you learned in lecture (e.g., quantitative traits, heritability, modes of selection & corresponding changes in mean/variance) and their relation to the assumptions and predictions of this laboratory. Also, provide enough background/detail such that someone not familiar with the assignment could understand the rationale for the experiment, the experimental methods [including details of the trait(s) you measured], and your interpretation.

Some examples of topics you might want to address in the introduction include: What was the goal in this laboratory and how did you set out to achieve your objective and evaluate your results? Be specific with regard to the trait your group measured and the direction of selection you invoked. What exactly was the trait you chose? How does it develop and what is its function in the plant? Perhaps include a picture or drawing of how you quantified this trait. Lastly, what traits did you hypothesize might be correlated or uncorrelated with your trait of interest and how were these traits measured? Why do you expect them to be correlated (or uncorrelated) with the trait of interest?

Results...

Use the sections below to help you organize the data you gathered for this experiment. Note that every figure and table should be accompanied by a legend that allows the figure (or table) to stand alone within the body of the written description of your results (see any journal article as an example here).

Initial population: Calculate measures of both the central tendency (mean, median, or mode) & the dispersion (variance, standard deviation) for your traits in the initial population. Typically, the mean and standard deviation are used, however, you will likely want to determine the variance in your populations as well (see below). Also, plot frequency distributions for the trait values in the initial population.

Breeding population: Indicate clearly those plants that were used as parents (i.e., the breeders) for the offspring generation. For example, it may be useful to include a table summarizing your crossing combinations and the number of offspring generated from each, etc. Determine how intense your selection was by calculating the selection differential (S) for your trait of interest.

Offspring population: Again, calculate measures of the central tendency (mean, median, mode) & the dispersion (variance, standard deviation) for your traits in the offspring population. Plot the frequency distributions for the trait values in the offspring population. Calculate the observed response to selection (R) for your selected trait.
**Heritability estimate:** Using the data for the parental crosses and the offspring generation, estimate the narrow-sense ($h^2$) heritability for your selected trait. Show your regressions of mid-parent and mid-offspring values. Given your estimate of heritability and the selection differential, what is the *expected response to selection*?

**Trait correlations:** Looking at the initial population, were your traits correlated and, if so, describe this correlation. Did the correlation hold true in the offspring generation as well? How can you test (given the data you collected) whether selection for trait x resulted in a change in trait y?

**Analysis...**

Start with a brief summary about your expectations for the experiment; restate the goal here. Did you succeed in changing your trait across the single generation of selection? If so, summarize the important pieces of data to emphasize this point or, if not, restate which aspects of your data support this conclusion. Do the changes in means and variances across generations make sense given the type of selection imposed in this experiment (see pp. 346-50 and your lecture notes)?

Given the trait you chose, the selection differential, and the estimated heritability, do your results for the offspring generation make sense? How does the predicted response to selection compare to the actual response you measured across generations? Why might the predicted and observed responses differ? Be specific about how any factor (contributing to variation in a quantitative trait) would affect your results. With how much certainty can you predict the response to selection for these traits (e.g., if you were to continue the selection over a third generation, given the same selection differential, what do you expect the trait values to be in the third generation?)

Given your selection differential ($S$) and the actual response to selection ($R$), what is the realized heritability in the experiment? What exactly is the realized heritability measuring & can you use it (compared to your estimate of heritability) to make any inferences about factors that contribute to a quantitative trait?

What are the assumptions of the experiment (i.e., the breeder’s equation and estimates of $h^2$; see Box 3.1, page 84 in your text to help you start thinking about complicating factors)? For example, this laboratory modeled a particular type of selection, and there is an expectation for changes in the mean and variance of traits under such selection. Also, recall the assumption that the trait under selection is a quantitative trait, why is this relevant? Lastly, do you have any evidence that maternal effects are operating in the system; how might you test for maternal effects (see Box 3.1 on page 84 and Galen's experiment on *Polemonium* on p. 342-3)?