Approach for Exercise 3

from emails from T Kittel and A Hoylman

Date: Fri, 02 Jun 2000 12:08:02 -0600
From: Tim Kittel <kittel@cgd.ucar.edu>

I'm intrigued by the possibility of demonstrating in a field exercise the role of genetic diversity of populations in their ecology.

As Anne has discussed, I'm not sure how posing this exercise in terms of heart vs periphery of range yet doing the exercise at a local scale is going to be fruitful. This is because it seems more likely that morphological variation in spp at any of the sites is primarily driven by plastic responses to environmental gradients (e.g. leaf size and LAI as a function of moisture availability; sun vs. shade leaves). Not to belabor the point too much -- this is a scale issue: the populations in the vicinity of a site are all likely to be either in the heart or the periphery of their range in the sense of Smith et al., and so not primarily expressing genetic differences as found for their full range.

On the other hand, I see this as a valuable exercise. My suggestion is to rephrase the exercise in terms of:

> (1) evaluating morphological (i.e. expressed) intraspecific differences along local environmental gradients
>
> (2) with a final goal of students generating hypotheses to explain these differences

Such hypotheses could be along the lines of:

> H1: Morphological differences along local environmental gradients are an expression of changes in genotypes along that gradient (ecotypes), or at least changes in population gene frequencies.
>
> H2: Morphological differences are an expression of phenotypic plasticity.

The main difference between this suggestion and the original exercise is that the question students are asked to address at the

start is "Do organisms exhibit morphological differences along local resource gradients?" and they end up with generating questions such as "Are the observed differences due to genetic differences, or do they arrive from phenotypic plasticity?"

The students are exposed to the same concepts of genetic variability, phenotypes, and environmental pressures as in the original exercise but are presented with a problem that is more tailored to working at the site level. This change in approach would mean that the ideas from Smith et al are de-emphasized in the Background section, and that the evaluation of morphological differences (e.g., in 'Your Question') is put in terms of local scale effects, rather than in regards to heart vs periphery of range. Students would still share results among sites to help evaluate morphological response to gradients and to formulate their hypotheses. The evaluation of local effects would a lead-in for the Abiotic section, but the emphasis here would be on intraspecific phenotypic and genotypic response and environmental selection.

An additional benefit is that at the end of the exercise the students will have gone through the process of question-hypothesis-observation-analysis-new question-new hypothesis. In future years, students could use allozymes to test the new hypotheses, and material from distant sites could be introduced as Anne suggests.

Date: Thu, 18 May 2000 11:51:46 -0700 (PDT)
From: Anne Hoylman <ahoylman@yahoo.com>

I've had a chance to look over the Intraspecific Vigor lab and give it some thought. I'm concerned that it will not work smoothly for several reasons. First, the translations of Smith et al's findings from a global to a local scale is a problem. Smith et al. were looking at variation across the entire geographical range of a species, not, as you have written the lab, within a local population. The focus on a very local scale dramatically changes some basic assumptions that are embedded in Smith et al., and makes it highly likely that any variation we find in plant morphology is environmental rather than genetic. For instance, dispersal (and thus gene flow) is likely occurring

across any resource gradient we identify (e.g. at black rock: tulip trees, blueberry, ferns, oak spp in a 1-2 km elevational or watershed gradient) - in fact for most plants dispersal is likely over the entire region (BRF) we are studying and this gene flow will certainly be enough to overcome extremely local selection (say within a 100 km2 region at the extreme of the gradient). This was not the case in the greenbul study.

Second, the allozymes, which you list as an additional tangent on this study. I talked to Matt (his background is in molecular ecology and he worked with Bob Wayne) about this, and he feels that it is unlikely to work smoothly in a short period of time because we don't know which isozymes are likely to be variable in advance for the species of interest quite a bit of equipment and reagents are needed, and waste products must be taken off site (cant flush these things at BRF - they have composting toilets!). The above difficulties can be overcome, but two other issues are more problematic. First, we are working in localized regions where gene flow is likely to be high and many plants may be related. Allozyme studies are known to be difficult in these scenarios. In other words, we are unlikely to find variability between localities along our resource gradient. Second, we would actually need fairly large sample sizes from each locality of interest on or resource gradient. It may not take long to do a handful of samples, but we would need more than a handful of samples to do this allozyme exercise well.

I suggest this:

1. Have students do the lab in the context of them choosing a species (I think it would be valuable to have teams of students pick their own species of interest - with our guidance of course), and deciding whether environmental or genetic change is a more likely explanation for the variation observed. This allows us to bring up a variety of topics such as the difference between the phenotype and genotype, and the

importance of gene flow and selection.

2. As for the allozyme angle, I think it is too much and should be left out of this lab. Perhaps in the future this could done as a separate molecular ecology lab that is well integrated with this lab, but could also incorporate samples from other regions, as well as a broader discussion of the pluses and minuses of different molecular techniques for answering different questions in ecology (allozymes, mtDNA, microsatellites, etc).

Let me know what you think about my comments. I still think we should do the lab, but just recognize the difficulty in discerning genetic versus environmental induced changes. Cox's Lab Manual, Ex 18 addresses this issue, maybe we could draw upon it some too.
