

Discussion-Oriented Exercises on Two Hot Topics: Global Warming and Tropical Deforestation

Jane M. Beiswenger and Neil Snow

*Departments of Zoology and Botany, University of Wyoming
Laramie, WY 82071*

*Department of Biology, Washington University
St. Louis, MO 63130*

These exercises focus on two issues of global importance: global warming (the “greenhouse effect”) and tropical deforestation. We hope that by doing these exercises and through class discussions, the students will develop an understanding of the biological phenomena related to each issue. They should then, as world citizens, be able to form intelligent, fact-based opinions as these issues evolve and new information becomes available.

Climatic data for the past century suggest that the earth's atmosphere is warming and that this is due to the build up of heat-retaining gases, such as carbon dioxide. These gases are by-products of industry and are released through the use of fossil fuels. While the burning of fossil fuels adds increasing amounts of carbon dioxide to the atmosphere, the fast pace of deforestation in the tropics is decreasing the removal of CO₂ by plants during photosynthesis. As a result, the CO₂ concentration is rising. Carbon dioxide, and other atmospheric gases, retain much of the longer-wavelength energy that is radiated from the earth and this increases the temperature of the atmosphere. This is much like heat retention within a greenhouse.

The exercise concerning the “greenhouse effect” asks the students to predict biological responses to a given change in climate. They first consider the responses of a variety of species to changes in temperature and precipitation. Next, they evaluate the confounding effect of migration rates, soil preferences, and other parameters that determine species habits.

Tropical deforestation is another global issue. This topic provides an avenue for the discussion of many subjects, all of which are at least tangential to biology. These include political science, economics, sociology, medicine and public health, agriculture, and biodiversity. The exercise is intended to foster an understanding of the causes and consequences of tropical deforestation and to illustrate the complexity and multidisciplinary nature of land management decisions.

Prior to each exercise we recommend showing a series of slides or video to provide background information and to explain the basis of each problem.

Why Do Mendel's Peas Wrinkle?

Thomas Fogle

*Department of Biology, Saint Mary's College
Notre Dame, IN 46556*

Students have difficulty imagining how the genotype, operating at the primary level of organization to produce a polypeptide, can effect higher order phenotypic expression. One reason for the difficulty is that hierarchical complexity of cell, tissue, and organ system interaction is skirted when a genotype is correlated to a complex trait (as, for example, R = round, r = wrinkled). This exercise explores the biological basis for a classic genetic trait, round versus wrinkled peas, by investigating the multiple (pleiotropic) effects that the gene product, starch branching enzyme, has on metabolism, shape of the starch grain, and osmotic potential.

The RR seeds contain two forms of starch branching enzyme, one that activates early in seed formation and the other late. In wrinkled seeds, rr , only the late acting form is present. Without the starch branching enzyme in early development, sugar precursors are converted to straight chain polysaccharides (amylose) rather than branched polysaccharides (amylopectin) by the enzyme starch synthase. Fewer branches means fewer sites to bond sugars to growing polysaccharides and, therefore, an accumulation of sugar molecules. This, in turn, increases osmotic pressure, increases water accumulation as the pea seed grows, and causes greater water loss when the pea dehydrates by the completion of development. A shriveled (wrinkled) seed results. Bhattacharyya et al. (1990) cloned the gene and discovered the r allele contains an 0.8 kb insertion of a transposable element not found in the R allele. The insertion alters the protein sequence.

Students are given dehydrated peas of three types (Early Alaska [EA], Thomas Laxton [TL], and Little Marvel [LM], available from Carolina Biological Supply Co.) and asked to determine which are round [EA] and which are wrinkled [TL, LM]. Several peas of each strain, hydrated in water overnight, are ground with mortar and pestle containing 10 ml of water. Wet mounts reveal that EA produces kidney bean-shaped starch grains; those of the other two strains resemble a sand dollar and are often fragmented. Extracts are centrifuged at 2500 rpm and the supernatant dropped onto agar plates prepared with glucose-1-phosphate (5 g G-1-p, 20 g agar, 1000 ml water). After 30 minutes, the plate is flooded with IKI and observed for starch production (positive for LM, TL) that reflects enhanced starch phosphorylase activity. The latter, which is not coded by the r gene, is likely an indirect metabolic effect of starch branching enzyme. Finally, students compare the wet and dry weight of peas to determine the percent difference in water content (highest for LM, TL).

Bhattacharyya, M.D., A.M. Smith, T.H. Noel Ellis, C. Hedley, and C. Martin. 1990. The wrinkled-seed character of pea described by Mendel is caused by a transposon-like insertion in a gene encoding starch-branching enzyme. *Cell*, 60:115–122.

Use of a “DNA Cookbook” to Demonstrate Transcription and Protein Synthesis

Marsha E. Fanning

Biology Department, Lenoir-Rhyne College, Hickory, NC 28603

Students often have trouble visualizing the processes of transcription and translation that lead to the formation of proteins. As such, a simulation using the analogy of a cookbook containing instructions for making lemonade was developed. This simulation was designed to help students see the relationship between DNA in the nucleus containing the code (the cookbook), mRNA (a note card) which carries the code in a slightly different language from the nucleus to the ribosome, and tRNA (a cup) which functions to hold a specific amino acid (ingredient) and to properly line up the amino acids by matching anticodons (on the cup) to codons (on the note card). The protein product is represented by the mixture of all of the ingredients (the drink). By changing a base pair in the DNA, the student can see the effect of mutations. A change in the DNA results in a change in the mRNA which then requires different tRNAs (cups) containing different amino acids (ingredients) to contribute to the product (drink). What started out as a tasty drink becomes unpalatable, or a different color, or has a different taste. As in nature, most “mutations” are worse than the original.

There are unlimited possibilities as to the products that can be made. Depending on one's creativity, many different combinations are possible. In the simulation presented, coding from a 12-base pair piece of DNA resulted in a four amino acid product: lemonade.

