BioQUEST Notes

Volume 11 Number 2 *A publication of the BioQUEST Curriculum Consortium* Fall 2001

Items Of Special Interest In This Issue:

Workshop participants examining biofilms after field collection

A Report from the 2001 BioQUEST Summer Workshop

Microbes Count: Problem Posing, Problem Solving and Persuading Peers in Microbiology Education

This year's BioQUEST Curriculum Consortium Curriculum Development Workshop was big ... and very, very small. Thirty-two college and university professors along with 14 workshop faculty and 4 Beloit College students worked together for 9 days from June 16-24, 2001 to develop new problem solving activities for microbiology courses. They adapted BioQUEST simulations and bioinformatic approaches to fit with classrooms in large universities, small colleges and for distance learning. The workshop theme, Microbes Count: Problem Posing, Problem Solving and Persuading Peers in Microbiology Education, complemented the BioQUEST Curriculum Consortium's initiative to develop thinking activities and simulations to accompany the American Society for Microbiology's video series, Unseen Life on Earth. Professors **Marion Field Fass** and **John R. Jungck** of Beloit College chaired the workshop.

There were many highlights in the 9 days of the Microbes Count workshop. **Ken Anderson** of California State University led a collecting trip to Turtle Creek for stream organisms that yielded amazing diversity. **H. T. Odum** of University of Florida-Gainesville, **Betty Odum** of Santa Fe Community College, Gainesville, FL and **Vanja Klepac** of Massachusetts Institute of Technology demonstrated how to model the role of microorganisms in ecosystem energy balance. **Robin Greenler** and **John Greenler** of Beloit College and BioQUEST presented the many and varied ways to study and

continued on next page

continued from page 1

analyze Kimchee in the context of microbiology- their explorations became the subject for 3 participant projects. **Peter Lockhart**, visiting from Massey University in New Zealand, explained the intricacies and the rewards of phylogenetic tree building.

During the first weekend at the BioQUEST Curriculum Consortium workshop, professors took on the role of students and explored microbial ecology, techniques of visualization and analysis, and bioinformatics. They worked in small groups to explore questions they posed such as "What are the fractal dimensions of viral envelopes?", "Does diversity of HIV clones increase when CD4 count falls?", and " Does the growth of bread mold follow an exponential curve?" A poster presentation concluded this section of the workshop.

The second section of the workshop provided participants with the opportunity to explore BioQUEST Curriculum Consortium activities that accompany *The Unseen Life on Earth* video series and to generate activities for their classrooms in collaboration with faculty from similar institutions. Presentations on Investigative, Case-Based Learning, on Microbiology in Context and on Assessment provided a background for activity development. **Ethel Stanley** of the BioQUEST Curriculum Consortium discussed an overview of case-based learning while **Katayoun Chamany** from Eugene Lang College shared her new long-term classroom case study of Botulinum Toxin. **Karen Oates** of George Mason University linked our discussions of pedagogy to the research literature, and **Leleng To** from Goucher College described how she teaches microbiology through the lens of historical events that have been strongly influenced by the microbial world. **Marion Fass** linked course reform with institutional change as she reviewed a non-majors course on Emerging Infectious Diseases at Beloit College. **John R. Jungck** of Beloit College engaged the group with a presentation of toys that model the topographical characteristics of DNA and other complex biological concepts, and demonstrated the value of concrete models to enhance our understanding of mathematical concepts in biology. On the final day of formal presentations, **Jean Douthwright** of Rochester Institute of Technology

continued on page 12

Exploring Microbial Ecology with Kimchee

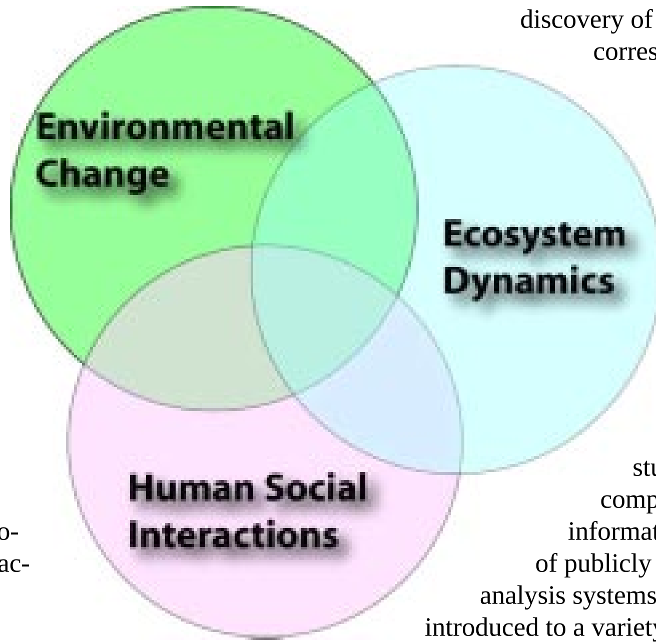
BioQUEST is cooking up some new activities with Kimchee! Kimchee is a traditional, fermented Korean food that can offer rich opportunities for hands-on student inquiry in microbiology (see report on BioQUEST's 2001 summer microbiology workshop).

Extensive research on the biochemical, microbiological, and nutritional aspects of kimchee provides a rich base for student-led exploration while real time data acquisition systems allow for rigorous quantification and data collection of experimental results. By constructing and monitoring kimchee fermentation

chambers in the classroom, students can measure changes in pH, turbidity, CO_2 production, O_2 consumption, microbial populations, sugars, and vitamins. The BioQUEST computer simulation, *Sim Chee*, (currently under development) will allow students to bridge the gap between wet-lab data collection and model construction and callibration.

Watch for more information on these new explorations in a future issue of BioQUEST Notes.

BioQUEST Workshop-June 15-23, 2002
Biocomplexity in Undergraduate Education: Integration of Biology, Society, and the Environment



Next summer's BioQUEST Curriculum Development Workshop will be held from June 15-23, 2002 and will focus on the integration of biocomplexity into undergraduate education. Biocomplexity is the study of the interrelations of biotic, social and global environmental systems. It encompasses the interdependencies of these systems; the dynamic and frequently non-linear responses to the corresponding interactions; and the contemporary importance of these interactions.

Key to the study of biocomplexity is teamwork that has both horizontal and vertical integration, and that includes representatives from broad areas of scientific study ranging from the biological specialties, to geochemistry, to sociology and economics. As Rita Colwell, Director of the National Science Foundation, states in her discussion of biocomplexity: "We must.... reach beyond, to discover the complex chemical, biological and social interactions in our planets' systems. From these subtle but very sophisticated interactions and interrelationships, we can tease out the principals of sustainability."

The integrated aspect of biocomplexity provides a wealth of opportunities for melding the domain of research with that of education. Many undergraduate students are already engaged in multiple areas of study and primed for the discovery of interrelationships and the corresponding synergies of understanding. Biocomplexity is a prime opportunity for students to bring together their frequently disparate course load.

Participants in the BioQUEST Summer-2002 workshop will be introduced to a diverse collection of tools used for Biocomplexity related studies. These will include computer-based geographic information systems (GIS), utilization of publicly available data sets, and field analysis systems. Participants will also be introduced to a variety of computer-based simulations and analysis tools from the BioQUEST software library.

Workshop participants will have the opportunity to collaboratively develop and share biocomplexity related problem-solving curricular materials for use in their schools. There is no need to have extensive background knowledge in biocomplexity to participate. Funding for room, board and registration is provided from a grant from the Howard Hughes Medical Institute. Detailed information on this workshop (including presenters, workshop dates, and application) will be in the Winter-2002 edition of *BioQUEST* Notes.

graphic courtesy of Dr. Rita Colwell, National Science Foundation

BioQUEST Presentations and Representation

BioQUEST has been well represented in the Education Reform Community

January

- Society for Integrative & Comparative Biology, *Commonalities among Comprehensive Curricular Reform Efforts across the Sciences,* Chicago, IL

February

- All Hands Meeting, EOT-PACI, San Diego, CA
- American Association for the Advancement of Science, San Francisco, CA
- *Integrating Science and Technology into Science Education: Investigative Case-Based Learning,* Morehouse College, Atlanta, GA
- Ed Grid Meetings, University of Illinois at Urbana-Champaign, IL

March

- National Association of Science Teachers, St. Louis, MO
- *Bringing Bioinformatics to Biology Education: A Hands-on Workshop to Develop Labs for Introductory and Advanced Courses,* Morehouse College, Atlanta, GA

April

- Symposium on Science Education in a Twenty-first Century University, *College and University Science and Mathematics Reform Movements: What Do They Share in Common? Why Are Such Communities So Important for Achieving Systemic Change?* Quinnipiac University, CT
- Department of Biology Seminar Series on Science Education, *Informing Biology Education By Examining The Nature Of Evolutionary Inquiry*, and *Bioinformatics/ BIRDD Workshop*, University of Delaware
- American Society for Biochemical/Molecular Biology, Orlando, FL

May

- 2001 Alliance All-Hands Meeting, <u>Cyberinfrastructure for the 21st Century,</u> *Bioinformatics Problem Solving, Bioinformatics in Your World*, University of Illinois at Urbana-Champaign. IL

- EdGrid Project Leaders Team Meeting, NCSA ACCESS Center, Washington, DC
- *LifeLines OnLine Workshop for Community College Faculty*, Southeast Missouri State, MO
- *Teaching Evolution by Inquiry,* sponsored by Oklahoma Teacher Education Collaborative, University of Oklahoma, Norman, OK
- American Society of Microbiology, *From Video to Computer: Using "Unseen Life on Earth" to Stimulate Student Problem-Solving with BioQUEST Simulations* and *From Frankenstein to "Frankenfoods": Exploring the Social Implications of Biotechnology* Orlando, FL

June

- Society for the Study of Evolution, University of Tennessee, Knoxville, TN
- Association for Biology Laboratory Education (ABLE), *Exploring Important Concepts Using Biology Workbench, a Suite of Bioinformatics Tools*, University of Chicago, IL

July

- Project Kaleidoscope Summer Institute, *Computational Science Across the Curriculum,* Snowbird, UT
- Annual Meeting of the Society for Mathematical Biology, <u>in silico</u> *DNA, RNA, Protein Sequence, and Structure Analysis: Theory and Practice,* and *Evolutionary Basis of Bioinformatics Education: Phylogenetic Profiling to Investigate Evolutionary Traffic in Genes Complementary to Protein Trafficking in One Cell with Three Genomes*, Hilo, Big Island, HI

August

- Alliance Center for Collaboration, Education, Science, and Software, *Biology Student Workbench: A Workshop about Integrating Bioinformatics into Biology, Science Education, Teacher Education, and Educational Technology Courses,* ACCESS Center, Arlington, VA
- National Research Conference, Biology 2010 , *College and University Science and Mathematics Reform Movements: What Do They Share in Common? Where are they Going?*, Snowmass, CO
- Gordon Research Conference, *Evolutionary Basis of Bioinformatics Education: Phylogenetic Profiling to Investigate Evolutionary Traffic in Genes Complementary to Protein Trafficking in One Cell with Three Genomes*, Tiltion, NH
- Science Education for New Civic Engagements and Responsibilities (SENCER), SENCER Summer Institute, Santa Clara University, San Jose, CA

September

- Pew Midstates Workshop in Mathematical Biology, *Biological Aftermath: Weaving Mathematical Modeling into Biology Major Programs*, University of Chicago, IL

October

- American Public Health Association Annual Meeting, *Engaging Activists: Teaching Global Perspectives on Health and Social Inequalities at the Undergraduate Level*, Atlanta, GA
- North Central Branch of the American Society for Microbiology, *Microbes Count: Strategies and Projects to Increase Student Engagement in Microbiology*, UW-LaCrosse, WI
- Association of College and University Biology Educators, *Biology in the Light of Evolution*, University of Nebraska-Kearney

A Course in Evolutionary Biology: Engaging Students in the "Practice" of Evolution

Cynthia Passmore, Jim Stewart
National Center for Improving Learning and Achievement in Mathematics and Science and the
Department of Curriculum and Instruction,
University of Wisconsin–Madison

The preparation of this manuscript has been supported, in part, by the National Center for Improving Student Learning and Achievement in Mathematics and Science (funded by the Educational Research and Development Centers Program as administered by the Office of Educational Research and Improvement, U.S. Department of Education), and by the National Science Foundation (Grant No. REC-9554193). Any opinions, findings, or conclusions are those of the authors and do not necessarily reflect the views of the supporting agencies.

Recent education reform documents have emphasized the need for students to develop a rich understanding of evolution's power to integrate knowledge of the natural world (American Association for the Advancement of Science, 1993; National Research Council, 1996). However, in spite of the efforts of science education reformers in publicizing the importance of evolution, a recent book on teaching evolution (National Academy of Sciences, 1998) lamented that, "many students receive little or no exposure to the most important concept in modern biology, a concept essential to understanding key aspects of living things—biological evolution" (p. viii).

In general, in education literature, the understanding of evolution has been limited to the understanding of individual concepts (e.g., variation, differential survival, natural selection, adaptation). Although the importance of understanding these concepts should not be downplayed, it is equally important for students to be able to use these concepts to think about evolutionary change. Such a level of understanding can be achieved by students' participation in instruction that mirrors aspects of the practice of evolutionary biology. Our approach to promoting understanding—engaging students in realistic inquiry—has formed through years of curriculum development and research into student learning, problem solving, and reasoning (see Cartier, Stewart & Johnson, BioQUEST Notes, Winter 2000).

In this article, we describe a 9-week high school course designed to help students understand evolutionary biology by engaging them in developing, elaborating, and using Darwin's model of natural selection. The first section provides an overview of some of the aspects of evolutionary biology that informed the design of our curriculum and is followed by a description how this view was translated into a 9-week high school course. Finally, to provide a feel for the way the curriculum was implemented, we describe three major components of the course.

Evolutionary Practice

We start with the assumption that students need to learn the key knowledge claims of a discipline as well as the processes by which such claims are generated and justified (see Kitcher 1993 for an elaboration of the concept of a scientific practice). We have found that a fruitful way to help students develop greater understanding of scientific practice (science "content" and broader nature of science issues) is to engage them in realistic inquiry. We recognize that different disciplines inquire in unique ways, and, therefore, careful consideration of the disciplinary context under study is an important step in curriculum development work.

On a general level, the practice of evolutionary biology is concerned with reconstructing how life on Earth has changed and with proposing mechanisms that account for the ways those changes might have occurred. The first of these goals, the reconstruction of the past, creates challenges for evolutionary biologists because, unlike many disciplines that focus on directly observable and replicable processes, evolutionary biology is concerned with processes and events that span a significant amount of Earth's history. This extended temporal span necessitates a historical view, one that has, in large part, resulted from biologists' acceptance of Darwin's writing on descent, with modification. Because organisms are now recognized to be related through a common ancestry that has a many-million-year history, a primary activity of evolutionary biologists is to make inferences about past speciation events in order to establish phylogenetic relationships for the "tree of life."

In addition to working with extensive periods of history, evolutionary inquiry also leads to the second goal of

continued on next page

continued from previous page

evolutionary biology, the creation of explanatory models that can account for patterns observed in the historical reconstructions. These models serve both as a way of explaining natural phenomena and as a framework to guide additional inquiries. In order to serve their explanatory function, these models interact with two distinct domains (a) the empirical phenomena for which the model purports to account and (b) the existing structure of evolutionary practice, which includes among other elements, related models, disciplinary specific language, methodological norms, and metaphysical assumptions about the natural world. Any particular model is deployed to explain and/or explore a limited empirical domain and is itself embedded in a context of practice that is in many ways unique to the model.

Although evolutionary biologists utilize an array of explanatory models there is one that is central—Darwin's model of natural selection. Natural selection is a mechanistic model that can be used to explain the changes in the heritable characteristics of populations over successive generations. This model interacts with a family of related models, including models of speciation as well as those in population genetics and is based on a set of shared assumptions about the natural world (e.g., belief in a naturalistic mechanism that acts on existing variation among individuals in a population) championed by Darwin and accepted by evolutionary biologists since Darwin.

Another key aspect of evolutionary practice, and one that sets it apart from other disciplines in biology, is the form that acceptable evidence takes. Because many evolutionary phenomena do not lend themselves to easy manipulation, what counts as appropriate evidence in the field is different from what is acceptable in highly experimental fields like genetics and physiology. Much of the evidence available to evolutionary biologists is necessarily indirect as it is often impossible to make predictions about evolutionary events and then run experiments to confirm those predictions. Instead, evolutionary explanations depend on historical data and the probabilistic nature of its explanatory models. Therefore, the evidence for evolutionary change comes from the fossil record, examination of homologous structures, and (increasingly in recent years) molecular information—all indirect sources of evidence.

Although the preceding is a limited account of the practice of evolutionary biology, we do believe that in order to develop a course on a subject, consideration of what goes into the practice of that discipline is essential. The recognition that the cognitive goals of evolutionary biology include both historical reconstruction and the modeling of observed patterns has important implications for evolution education, as does the recognition that the evidence considered acceptable is often indirect.

Curricular Approach

The practice of evolutionary biology sketched above provided the basis for designing our 9-week course. Because it is impossible to include all aspects of the practice of evolutionary biology in an introductory course, we focused on introducing students to the reasoning patterns of evolution by engaging them in developing, using, and extending Darwin's natural selection model. By focusing on natural selection, we were also able to provide a setting in which examination of argumentation, language use, and methodology would occur naturally as students collaborated to explain phenomena.

On a general level, our approach was to provide cases that "serve as realistic contexts that define a problem space and help students organize their learning of a body of known information" (Waterman, 1998, p. 4). Because evolutionary phenomena do not lend themselves to manipulation by high school students, the use of case materials (which included readings and data that could be used to build explanations and which defined the phenomena for student discussions) was instrumental. Through the use of cases, students were involved in extended explorations, each designed to promote understanding of particular aspects of evolutionary biology. The first set of cases involved students in an examination of the disciplinary context of evolutionary biology by providing them with materials about three explanatory models. The second case provided a large set of data from which an evolutionary explanation could be constructed using natural selection. The two final cases provided rich scenarios that required students to extend the natural selection model.

Course Description: Major Components

The first days of class were dedicated to establishing norms of classroom discourse in order to provide students with a common language and the analytical tools with which to examine and critique arguments. Students first participated in activities designed to help them distinguish between observations, inferences made from those observations, and the underlying assumptions that affect inference making. The students then used these distinctions to examine and critique knowledge claims made during this activity and throughout course.

continued on next page

continued from previous page

Students were then given activities that supported students' exploring the metaphysical assumptions of models proposed by Paley, Lamarck, and Darwin. By examining these models, students compared and contrasted Darwinian and non-Darwinian assumptions and gained a stronger working knowledge of the strength of Darwin's model. They then spent the remaining weeks of class applying Darwin's model of natural selection in order to explain phenomena in a hypothetical, but data-rich case and extending it to explore two other real-world data-rich cases.

Examination of Models: Paley, Lamarck, Darwin
This portion of the class involved students in the analysis of three models (Paley's model of intelligent design, Lamarck's model of use inheritance, and Darwin's model of natural selection), each of which, in its own way, accounted for species diversity. These models were chosen (a) because they were based on disparate assumptions and, therefore, lend themselves to comparison on that level and (b) because the models of Paley and Lamarck relate to common student misconceptions.

In order for students to compare the underlying assumptions of these models it was necessary for them to be familiar with the models. Students were asked to read an edited version of the author's original work and participate in class discussions in which the proposed mechanisms were elaborated. Students also experienced the phenomenon that inspired each author's model. For example, they examined fossils discussed by Lamarck, dissected an eye to examine the structure/function relationships that so fascinated Paley, and were visited by a pigeon breeder who brought several of the pigeon breeds described in Darwin's *Origin of Species.*
Once students had developed an understanding of each author's proposed mechanism and the observations on which it was based, they worked to identify the underlying assumptions of each argument. The first set of assumptions concerned the authors' view of species—Did the author view species as fixed or malleable, and what role did he attribute to variation within species? The second assumption concerned the author's view of the "force" responsible for production of new species. In this instance, students needed to consider what that force acted on, whether it was internal or external, and whether organisms played a conscious role in their own evolution.

Following this discussion, the comparison of models began. First, students assessed the explanatory power of each model: They used each model to explain phenomena

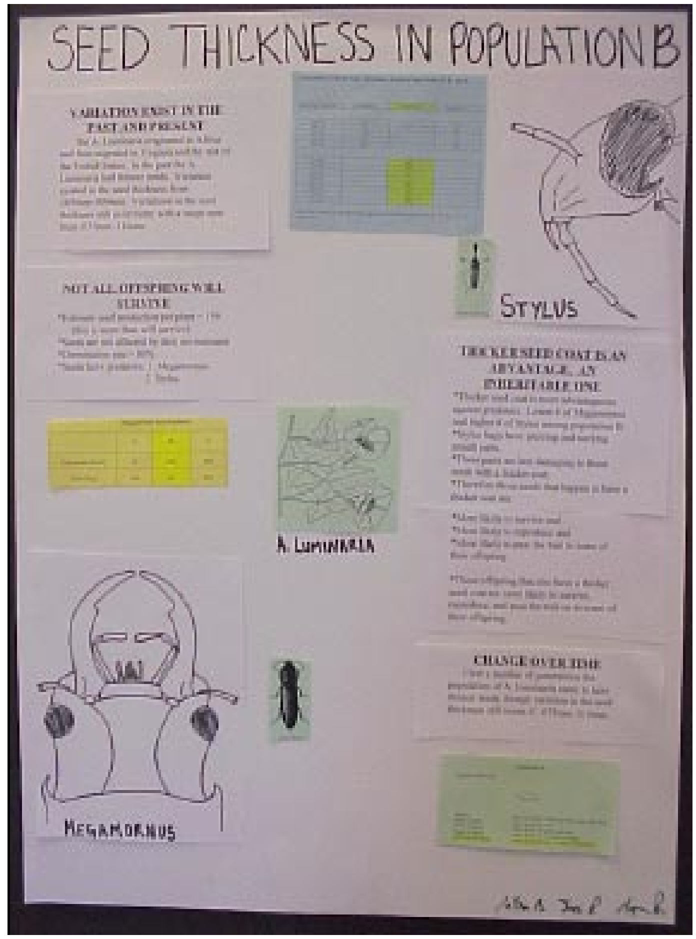


Figure 1A. Sample Case Materials

other than that described in the original paper. For example, they used Paley's model to explain the presence of fossils, and they used Lamarck's model to explain the structure of the eye. In some cases the model could easily account for new phenomena; in others, the students recognized the model's limitations.

Second, students were asked to compare and critique the authors' underlying assumptions, allowing students to understand that it is possible good scientific practice to critique a model based on the assumptions made by the author even if that model could account for diverse phenomena in its own context. Comparison of the assumptions of the three models enabled students to distinguish those beliefs that underlie the model of natural selection (that a naturalistic mechanism of species change acts on existing variation among organisms) from those that underlie Paley's model (notions of supernatural influence) and those that underlie Larmarck's (notions of individual need).

continued on next page

continued from previous page

Elaboration of the Darwinian Model

Once introduced to natural selection, students developed a Darwinian explanation (a narrative that describes variation in the population, a description of the selective advantage of a trait, and a discussion of the role of inheritance in accounting for changes that occurred in the frequency of particular traits) for a simple adaptation. After composing Darwinian explanations and explicitly considering the components of an appropriate explanation, students were given a data-rich case to explore. This case was designed to provide a scenario in which students could investigate a change in a trait over time, use the natural selection model to explain that change, and support their argument with appropriate evidence.

The case materials were based on hypothetical organisms, for which a large amount of data was supplied. The phenomenon to be explained was the change in a seed-coat characteristic in different populations of a hypothetical plant. Students were given descriptions of the ancestral population, natural history information on contemporary populations, predation information, and data that allowed them to establish the heritability of the trait. Sample case materials are shown in Figure 1.

The students worked in groups to create a scientific poster that used the natural selection model to explain the change in one of two traits (seed-coat thickness or number of seed-coat spines) over time. Students were asked to develop an explanation using the natural selection model as well as to tie data from the case materials to each component of the model. The case ended with a poster session during which students presented their posters and critiqued each other's explanations. Sample posters are shown in Figure 2.

Extension Cases

The cases used in these activities were similarly data rich, but they differed from the seed case in that these were based on real organisms and that the range of available data was constrained (e.g., no description of an ancestral population). These two cases were intended to push students into extending their understanding of the applicability of the natural selection model by asking them to construct explanations for situations in which the selective advantage of the trait in question was not immediately clear. The first case required students to explain the similarity in color between viceroy and monarch butterflies. What quickly became an issue for students was the lack of explanation for the bright coloration in the monarch. The second case asked them to explain differences in coloration between male and female ring-necked pheasants. Applying the model of natural selection to these less than straightforward cases necessitated a rich understanding of the model and the assumptions upon which it is based.

This portion of the class provided students with opportunities to work in groups and to meet periodically with other groups to compare explanations and present preliminary ideas. The culminating activity for the monarch/viceroy case was a round-table discussion, and the final work on the pheasant case was organized into a research funding competition.

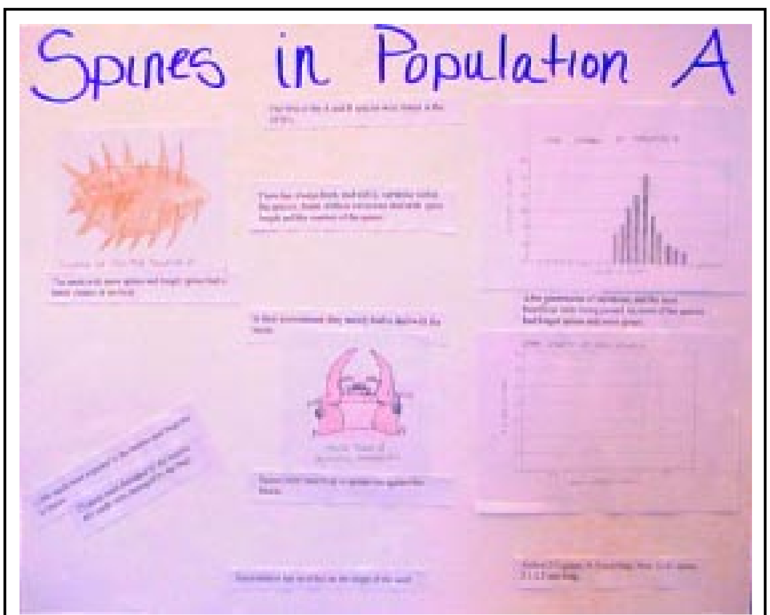


Figure 1B. Sample Case Materials

Monarchs and viceroys.

Once the students had finished writing their explanations for the monarch/viceroy case, they read and critiqued one other group's explanation. Students then met as a large group to discuss the case generally, describing the overall arguments and citing specific pieces of data to support their claims. At the beginning of their discussion about a general explanation for the similarity in color between the monarch and viceroy there seemed to be agreement that the viceroy was brightly colored to gain the advantage of resemblance to the poisonous monarch. There was a consensus that the monarch's habit of eating milkweed plants as a caterpillar resulted in toxicity of the adult butterfly.

continued on next page

continued from previous page

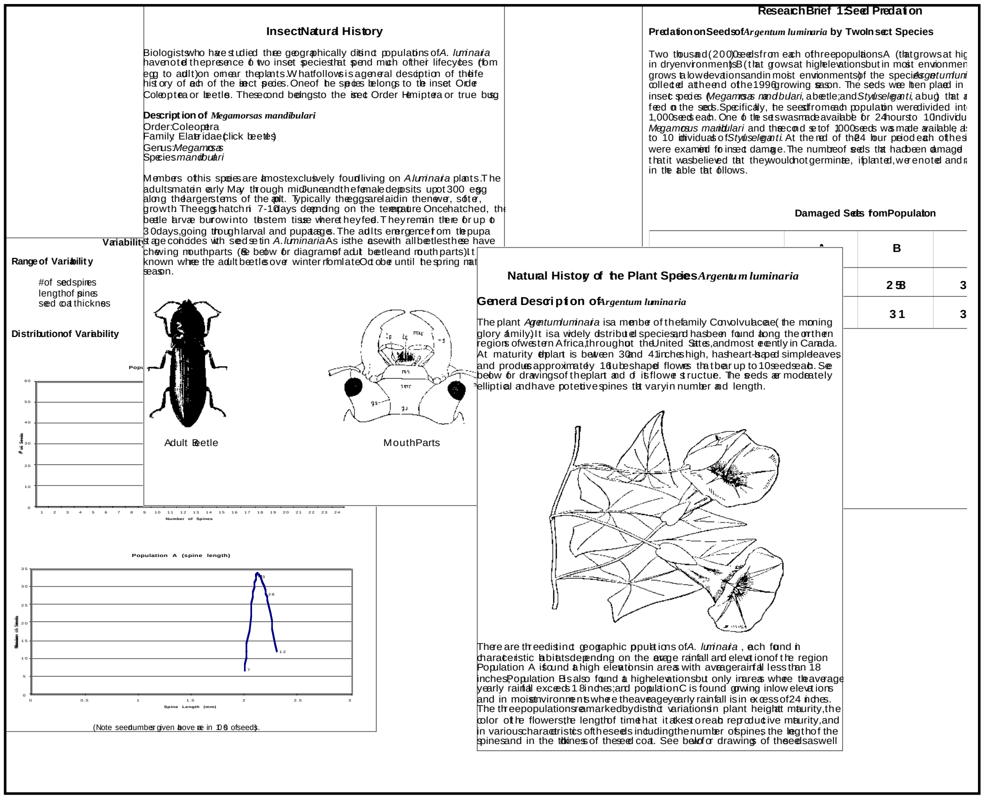


Figure 2. Examples of Student Posters

As the discussion progressed and students began to address the types of data that different groups brought to bear on their explanations, the interactions became more interesting: Not everyone assigned equal importance to pieces of data. For example, the case contained information on the habitat, range, and population densities of the monarch and viceroy in a meadow. This range map showed that the distribution of the monarchs and viceroys overlapped and that there were larger numbers of monarchs than viceroys in this area. The discussion students had about the relevance of this data provides interesting insights into their thinking about natural selection:

Linda: I thought it was very important, about how we talked about the density of the monarchs and the viceroys because if there, it said there was only .3 individuals per square meter of the viceroys and 2.2 individuals per square meter of the monarch and if it were, like for example, if the number of viceroys were higher or the monarchs were lower, then the blue jays wouldn't necessarily learn that the monarchs were poisonous and the coloring the way the monarch looked wouldn't act as a warning. It would act as more of, like, an attraction. you know, 'cause they wouldn't know the difference between the viceroy and the monarch.

Jasmine: So, you're saying there wouldn't be as many monarchs, so they wouldn't have the chance to eat as many and find out and experience.

Andrea: Well, yeah, if there were more, like, viceroy instead of monarchs, they wouldn't learn as quickly that the monarchs are poisonous because if they were the same color, the color would attract them instead of repelling them 'cause there's more monarchs, which is important 'cause they learn that the monarchs are poisonous, you know.

This discussion shows sophisticated reasoning about selective advantage. The focus on population density data appeared to be useful to some students in imagining how predators would begin to associate bad taste with bright coloration. Later, the students had an extended conversation about blue jay's ability to learn and remember. It was clear that they were concerned with the apparent disadvantage of bright coloration in terms of predation for individual monarchs, but they could imagine how bright coloration could be advantageous to the population as a whole if the predators began to associate brightness with distastefulness. This differentiation between an advantage for an individual organism versus an advantage for the entire population is central to evolutionary reasoning.

The students also dealt with issues of species interaction when they recognized the potential problem for the monarchs if there were more harmless viceroy mimics: "They'd just keep eating them" (the brightly colored butterflies) if it were "the other way around" (there were more harmless butterflies than harmful). This appreciation for the complexity of species interactions in evolutionary terms indicates a high degree of understanding of explanations for evolutionary phenomena using the Darwinian model.

The following day the students discussed the origin of bright coloration. They began their discussion by consid-

continued on next page

continued from previous page

ering how the trait could be advantageous before it was widespread throughout the population. Jen noted that "I don't see how in the beginning bright color could be an advantage."

This led one student to consider how the variation might have looked in the past in terms of the population as a whole:

Mark: Well, I don't think you can think of it as just one, one butterfly either, I mean even if it [evolution] is slow it is, I mean there's probably a lot, I have no idea, but—
Doug: Because butterflies have a lot of offspring.

These students went on to note that initially there could have been multiple butterflies that were "brighter" in color: Even if the trait of brightness originated with one pair of butterflies, butterflies lay so many eggs that there would potentially be several brighter butterflies in a batch of eggs. These questions of the initial advantage of the trait led them to further consider the ancestral population and question how to define the starting point of evolutionary change:

Anna: What about, I feel like we're saying that everything had to evolve from a dull color, what if it originally was bright, that just how it was. Just like every species has variation that was just that's what it was, it was bright for no particular reason.
Mark: But it had to evolve from something.

Here they began to talk about other animals and what they knew about ancestral traits. Mark brought the conversation back to defining starting point:

Mark: But it had to evolve from something sometime.
Rob: Do you think monarchs were always poisonous?
Mark: As long as they've been eating milkweed.
Rob: You think they always laid their eggs on milkweed?
Tim: They had to develop the ability to eat poisons without dying and pass on that trait to their offspring.
Doug: Well, how do you define a monarch? That's the question.

The class became very animated at this point—students were debating ways to define a population in the past in order to describe a change that occurred. Again the interactions described here would not have been possible without a clear understanding of the natural selection model. These two transcripts indicate that students are capable of sophisticated reasoning about evolutionary events when they work from a well-articulated model.

Pheasants. The pheasant case was organized as a research funding competition. Students were given the task of developing a Darwinian explanation for the bright coloration of the male ring-necked pheasant supported with evidence drawn from the case materials. Once they had formulated an explanation, they were asked to develop a research question that would allow them to investigate some component of their explanation. They then presented their explanations and research questions to the class in a competition for research funds. The other groups acted as judges and interacted with the presenting groups in an attempt to understand the proposal.

All but one of the Darwinian explanations the students developed for the bright coloration of the male pheasant were consistent with sexual selection. The one group that did not present a sexual selection explanation attributed the bright coloration of the males to an increased ability to protect the nest: Bright-colored males could distract predators better than dull-colored males; therefore, their offspring would be more likely to survive. These explanations, *developed by the students themselves*, required them to extend their knowledge of the Darwinian model. In contrast to traditional evolution instruction, which often presents mimicry, warning coloration, and sexual selection to students as additional concepts to be memorized, this instruction encouraged students to grapple with phenomena themselves, create plausible explanations, and, in so doing, develop deep understanding of the explanatory power of natural selection.

With each of the research questions proposed, the students attempted in some way to establish the selective advantage of the trait and to devise a wide variety of ways to test the advantage. Three groups proposed exploring the role of female choice in conferring a reproductive advantage to brightly colored male pheasants. Another group wanted to investigate the possible linkage of bright coloration to other advantageous traits, such as increased fertility or immunity to common disease. A fifth group wanted simply to establish the exact developmental timing of the acquisition of bright plumage. They thought that if they could establish a correlation between timing of sexual maturity and development of bright plumage, their idea that bright coloration aided in courtship would be supported. If, however, they found that these two events occurred at completely different times, the students realized that their sexual selection idea would need to be revised: They believed that the disadvantage of bright coloration in terms of predation could only be outweighed

continued on next page

continued from previous page

if the development of bright plumage coincided with the mating season, thereby providing a reproductive advantage. As in the discussion surrounding the monarch case, students interacted in sophisticated ways while defending their research proposals.

We argued earlier that an important goal of evolutionary biology is to infer historical or phylogenetic relationships. In the pheasant case, students were using an established phylogeny to support their claims about the way pheasants might have changed over time. They used this information on closely related species in order to determine a likely scenario for the way the ancestral population might have appeared—slight differences between the sexes. The instrumental use of this phylogenetic information illustrates one way in which students can use historical reasoning and thus bring this important feature of evolutionary thought to bear while creating explanations for natural phenomena.

Summary

When students are given opportunities to use their knowledge to explain interesting and appropriate evolutionary phenomena, the potential for their meaningful understanding of evolutionary concepts is enormous. In this article, we have described a course designed to engage students in the use of natural selection model, which provided a rich context for students not only to reason about evolutionary concepts such as variation and differential survival, but also to use those concepts to explain changes in populations over time. In describing this course, we attempted to redefine the expectations for students in evolutionary biology and to provide a picture of what curriculum designed with these goals in mind could entail. Students in this course were able to reason and argue from data, to develop their own explanations for natural phenomena, and to evaluate the hypotheses of their peers—a sharp contrast to students in traditional courses who often leave with a mental list of memorized facts and an "understanding" of evolution as a belief system rather than as reasonable scientific explanation of phenomena and species change.

References

American Association for the Advancement of Science. (1993). Benchmarks for science literacy: Project 2061. New York: Oxford University Press.

Cartier, J., Stewart, J., & Johnson, S. (2000). "A modeling approach to teaching high school genetics. BioQUEST Notes. Vol. 10 (2). 1-12.

Kitcher, P. (1993). The Advancement of science: Science without legend, objectivity without illusions. New York: Oxford University Press.

National Academy of Sciences Working Group on Teaching Evolution. (1998). Teaching about evolution and the nature of science. Washington, DC: National Academy Press.

National Research Council. (1996). National science education standards. Washington, DC: National Academy Press.

Waterman, M. (1998). "Investigative Case Study Approach for Biology Learning." Bioscene: Journal of College Biology Teaching. 24(1). 3-10.

Author Note

The preparation of this manuscript has been supported, in part, by the National Center for Improving Student Learning and Achievement in Mathematics and Science and by the National Science Foundation (Grant No. REC-9554193). Any opinions, findings, or conclusions are those of the authors and do not necessarily reflect the views of the supporting agencies. We thank Andrea Barton, Susan Carpenter, Jen Cartier, Sam Donovan, Susan Johnson, John Rudolph, and Fae Dremock for providing valuable comments on the manuscript.

BioQUEST workshop participants utilize visualization techniques to study microbial interactions within the phyllosphere.

Report from the 2001 BioQUEST Summer Workshop

continued from page 2

challenged participants to consider the impact of racism and sexism in microbiology practice and education.

The excitement builds in every BioQUEST workshop as participants develop their own projects. Participants came to project building at the Microbes Count workshop with shared interests in Microbiology, but from they came from very different educational settings. The projects they developed reflected the needs of their institutions and student populations. Curriculum projects explored microbial growth, bioinformatics and microbial evolution, and the use of case studies to drive investigations in microbiology.

Microbial growth activities

Christina Strickland of Clackamas Community College in Oregon City, Oregon, **Kyle Hammon** of Lane Community College in Eugene, Oregon and **Marian Hill** of St. Petersburg Junior College in St. Petersburg, Florida built an extensive set of investigative projects on Kimchee fermentation that demonstrated the range of activities that can be generated from this rich (and pungent) source, limited supplies and unlimited imagination. Their project identified seven variables that may be quantified throughout the time period required for kimchee production and that can be done in the lab or at home as part of a distance learning course. **Karen Fulford** of Morris Brown College in Atlanta, Georgia, **Susan Gibson** of South Dakota State University in Brookings, and **Ian Johnston** of Bethel College in Minneapolis, Minnesota extended the Kimchee model with activities to enhance the scientific problem solving skills of students with little science background. Their activities were designed to introduce students to cause and effect in the study of metabolism. They designed their basic experiment to make use of the Vernier system for data collection as well as use of olfactory, visual, and tactile means to monitor the fermentation process. **Peg Heimbrook** and **Josephine Ebomoi** of the University of Northern Colorado at Greeley, **Lawrence Bradford** from Benedictine College in Atchison, Kansas, **Betty Juergensmeyer** of Judson College in Elgin, Illinois and **Priscilla Peterson** of Janesville, Wisconsin developed a set of investigative projects for upper level students. Their activities enable students to design their own studies to explore the process of ecological succession in a microbial culture, and to study competition (inhibitory substances) and cooperation within the microbial culture.

Julyet Benbasat from University of British Columbia in Vancouver, **Frank Percival** from Westmont College in Santa Barbara, California, and **Jean Douthwright** from Rochester Institute of Technology in Rochester, New York developed a spread sheet model of the growth of bacteriophages. The model provides students with opportunity to explore some of the factors that affect phage production in the laboratory and start working with models of different complexity.

Bioinformatics and microbial evolution

Bev Brown of Nazareth College of Rochester in Rochester, New York, **Sam Fan** of Bradley University in Peoria, Illinois, **Leleng To** of Goucher College in Towson, Maryland, and **Min Ken Liao** of Furman University of Greenville, South Carolina developed a project to introduce students the study of evolutionary relationships

continued on next page

continued from previous page

through the construction of phylogenetic trees of eubacteria and archea. Their project combined the structure necessary to use Biology Workbench simulation with open-ended challenges that lead students to test evolutionary hypotheses.

Erica Suchman, from Colorado State University, in Fort Collins and **Mark Gallo**, of Niagara University in Niagara Falls, New York developed an activity involving the use of Biology WorkBench to explore the origins of West Nile Virus in the United States. Students produce and interpret phylogenetic trees using CLUSTALW and then use this information to predict the origins of the virus that was responsible for an outbreak in the eastern United States in 1999. Students also explore the biology of the vector organism, and implications for the epidemiology of the disease.

Judy Kandel of California State University in Fullerton, **Bob Simon** from State University of New York -Geneseo and **Kathy Takayama** from the University of New South Wales in Australia developed an investigative project for advanced students using microarrays of gene expression data available on the internet. The project addresses the following general questions through collaborative learning activities:

• What is the value of knowing an organism's genome sequence? (How does one utilize it; what does it tell you about the organism?)

• What methods can be used to learn both: (1) how the thousands of genes in an organism interact with each other and (2) the relationship at the genetic level of an organism to its environment?

Case studies in microbiology

Roberta White from Seward County Community College in Liberal, Kansas and **Patricia Schneider** from Queensborough Community College in Bayside, New York developed collaborative, problem-solving activities based on antibiotic resistant tuberculosis. Their activities are designed to engage beginning students, often in allied health fields, who often have poor backgrounds in science and math. They provided experiences with data organization and graphing and linkages to both wet labs and the BGuILE Project's *TB Lab* simulation, part of the BioQUEST Library.

Tony Slieman of Morningside College in Sioux City, Iowa, **Katayoun Chamany** of Eugene Lang College in New York City, **Bruce Patterson** of the University of

Participants collect a water sample

continued from previous page

Arizona in Tucson, and **Charles Dailey** of Sierra College in Rocklin, California developed a set of case studies on bioterrorism. Their cases are designed to motivate and engage students in learning about the microbiological agents that might be employed in attacks, the strategies used for defense, and the social and ethical implications of diverting resources to the production of offensive or defensive approaches to biological weapons.

Participants examine biological diversity from Turtle Creek, Beloit, Wisconsin

Finally, **Kathleen Jagger** from DePauw University in Greencastle, Indiana, **Joyce Cadwallader** from Saint Mary of the Woods College in Saint Mary of the Woods, Indiana and **Linda Crow** of Montgomery College in Conroe, Texas developed a case study simulation called "Languishing Legumes". This is an interrupted, investigative case involving infection of a major U.S. agricultural crop, soybeans (*Glycines max*), with a virus, Soybean Mosaic Potyvirus, to which the plant had been previously resistant. The vector for transmission of the virus is an invasive species of Asian aphid, *Aphis glycines*. Six major directions are identified all of which can use the introductory case scenario. The case can be used to teach students the scientific method in a realistic context, asking them to pose and modify hypotheses as new information becomes available. The case can also be used to develop an energy model using the environmental decision making software.

Participant evaluations of this year's workshop, Microbes Count: Problem Posing, Problem Solving and Persuading Peers in Microbiology Education were uniformly positive. Several participants commented that this was the best workshop that they had ever attended. **Kyle Hammon** of Lane Community College wrote, " I am changed both personally and professionally. Personally in that I learned much about my responses to others in teams, and professionally in my exposure to new material and to pedagogy." **Julyet Benbasat** noted that "I came with the intent to connect with others in my field who are also interested in curricular change. I'm leaving having learned a lot about collaboration and teamwork, and with a set of 3-4 new tools I can use with a little effort… The atmosphere of sharing and collegiality you have been able to generate here drives home the message that each of us has supported in curriculum reform. Feeling this cooperation is important in renewing our enthusiasm which is often dampened by financial crises and the apparent indifference of our colleagues." **Bob Simon** concluded, "I never expected the time to be filled with so many interesting and useful activities… Long live Kimchee. "

BQ Library, Volume VI Has Been Released!

This newest volume contains over 75 software simulations, tools, datasets, and other supporting materials from many areas of biology and includes several new modules for both Macintosh and Windows.

Volume VI of The BioQUEST Library can be purchased in packages for single and multiple users. Packages are available in three different sizes:

- **An individual package for <u>one</u> user**: $149.95 + tax
- **A three package lab-pack**: $295.00 + tax
  Valid for use by up to <u>three</u> individuals at the same time;
- **A ten package lab-pack**: $695.00 + tax
  Valid for use by up to <u>20</u> individuals at the same time.

Networked or distributed learning users should make a good faith estimate of the maximum number of <u>simultaneous</u> users and buy the appropriate number of packages. Special licensing terms can be arranged for institutions with more than 60 simultaneous users.

For additional information about *The BioQUEST Library*, please visit the BioQUEST Curriculum Consortium website at **http://bioquest.org** or contact Virginia Vaughan at vvaughan@hamilton.edu.

CONTACT INFORMATION FOR PURCHASES:

<u>To purchase an INDIVIDUAL COPY</u>

Jackie Tumahai
407-345-2566 or 1-800-321-5068 Ext 2566
jtumahai@harcourtbrace.com

<u>To purchase ONE OR MORE LAB-PACKS</u>
send email to textbook@acad.com OR
contact your regional representative below

CENTRAL U.S. & CANADA (Illinois, Indiana, Iowa, Kansas, Michigan, Minnesota, Missouri, Nebraska, North Dakota, Ohio, South Dakota, Wisconsin.; Canada: Manitoba, Ontario)
Marc Chambers
Telephone: (888) 864-7547 x 237
e-mail: mchambers@mkp.com

WESTERN U.S. & CANADA (Alaska, Arizona, California, Colorado, Hawaii, Idaho, Montana, Nevada, Oregon, Utah, Washington, Wyoming. Canada: Alberta, British Columbia, Saskatchewan.)
Wendy Westgate
Telephone: (800) 894-3434 x 6826
e-mail: wwestgate@acad.com

SOUTHERN U.S. (Alabama, Arkansas, Florida, Georgia, Louisiana, Kentucky, Mississippi, New Mexico, North Carolina, South Carolina, Oklahoma, Tennessee, Texas, Virginia, Washington DC, West Virginia.)
Deborah Kramer
Telephone: (800) 894-3434 x 6319
e-mail: dkramer@acad.com

EASTERN U.S. & CANADA (Connecticut, Delaware, Massachusetts, Maryland, Maine, New Hampshire, New York, New Jersey, Pennsylvania, Rhode Island, Vermont. Canada: New Brunswick, Newfoundland, Nova Scotia, Prince Edward Island, Quebec)
Christine Dewhurst
Telephone: (760) 720-6264
e-mail: cdewhurst@mkp.com

INTERNATIONAL
Harcourt Publishers
Telephone: 020 8308 5700 (this is in the UK)
e-mail: cservice@harcourt.com

For more information about the activities of the BioQUEST Curriculum Consortium, to contribute to the newsletter or to subscribe to *BioQUEST Notes*, please contact us:

BioQUEST Curriculum Consortium
Biology Department
Beloit College
700 College Street
Beloit, WI 53511

Phone: (608) 363-2743
email: bioquest@beloit.edu
BQCC web site: http://BioQUEST.org

Major support for BioQUEST development and activity has been provided by the Howard Hughes Medical Institute, the Annenberg/CPB Project and the Division of Undergraduate Education at The National Science Foundation, with additional support from Apple Computer Inc., The Foundation for Microbiology, and The Center for Biology Education at the University of Wisconsin-Madison. Any opinions, findings and conclusions or recommendations in these materials are those of the author(s) and do not necessarily reflect the views of the National Science Foundation or other funding sources.