In This Issue:

Microarrays and Data Analysis
David Kushner

Introductory Biology Discussion Group Evaluation
Marcy Peteroy-Kelly

Online Versus Onsite Bioinformatics Instruction
Kristina Obom and Patrick Cummings

Microbial Mats as Educational Tools
Carlos Rios-Velazquez, Lilliam Casillas-Martinez, and Pieter T. Visscher
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DNA Microarrays in the Undergraduate Microbiology Lab: Experimentation and Handling Large Datasets in as Few as Six Weeks

David Kushner

3-12

A Discussion Group Program Enhances the Conceptual Reasoning Skills of Students Enrolled in a Large Lecture-Format Introductory Biology Course

Marcy Peteroy-Kelly

13-21

Comparison of Online and Onsite Bioinformatics Instruction for a Fully Online Bioinformatics Master’s Program

Kristina Obom, and Patrick Cummings

22-27

Learning Geomicrobiology as a Team Using Microbial Mats, a Multidisciplinary Approach

Carlos Rios-Velazquez, Lilliam Casillas-Martinez, and Pieter T. Visscher

28-35

On the Cover

Dickinson College students John Sheridan and Matoli Vifansi, Biochemistry and Molecular Biology majors, class of 2007.

Photograph was taken by A. Pierce Bounds, Dickinson College photographer for the Dickinson College Office of College Relations. Photographs were submitted by David B. Kushner, Ph.D., Department of Biology, Dickinson College. Article begins on page 3.

“Rooted in microbiology and branching out to all of biology.” From our new logo to our new name the previous sentence says it all when it comes to the changes seen in the journal this year. The name has changed from Microbiology Education to the Journal of Microbiology & Biology Education (JMBE) and with it the scope has broadened to reflect what microbiology educators teach. While one might expect the educators in ASM to just teach microbiology, their actual classroom teaching duties extend to most of the subdisciplines of biology. We, on the Committee on Undergraduate Education, strive to provide a publication outlet for all members of ASM who are performing novel education scholarship in each of their subdisciplines. In addition, we aim to welcome other biology educators to publish their scholarly research in JMBE, thus providing additional examples of good scholarship and novel teaching methods for our members.

To carry this new theme of biology into this 8th volume is a paper by Peteroy-Kelly examining discussion groups in a large lecture-format biology course. Though this research was accomplished in a biology course the methods are directly applicable to large lecture-format microbiology courses. To entice those interested in the broad topic of genomics there are papers on microarray analysis (Kushner) and bioinformatics (Obom and Cummings). Finally, for those interested in “rock solid” microbiology there is a paper by Rios-Velazquez et al. on the use of microbial mats in learning geomicrobiology.

As always, JMBE stands ready to publish your scholarly research in the microbial and biological sciences.

Respectfully,

Jeffrey J. Byrd
Editor-in-Chief, Journal of Microbiology & Biology Education
DNA Microarrays in the Undergraduate Microbiology Lab: Experimentation and Handling Large Datasets in as Few as Six Weeks

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DNA microarrays have significantly impacted the study of gene expression on a genome-wide level but also have forced a more global consideration of research questions. As such, it has become critical to introduce undergraduate students to genomics approaches to research. A challenge with performing a DNA microarray experiment in the teaching lab is determining the time required for the study and how to handle the voluminous data generated. At an unexpectedly low cost, a 6-week, project-based lab module has been developed that provides 3 weeks for wet lab (hands-on work with the DNA microarrays) and 3 weeks for dry lab (analyzing data, using databases to help with data analysis, and considering the meaning of data within the large dataset). Options exist for extending the number of weeks dedicated to the project, but 6 weeks is sufficient for providing an introduction to both experimental genomics and data analysis. Students indicate that being able to both perform array experiments and thoroughly analyze data enriches their understanding of genomics and the complexity of biological systems.

It has been just over a decade since the first report about a DNA microarray was published (14). While the first few years of this period featured technical challenges and high costs, improvements have allowed for greater ease in performing experiments using DNA microarrays. Widespread use of this technology, its applications in numerous research areas, and connections to genomics and bioinformatics predicate the need to introduce this concept into the undergraduate biology curriculum. Several recent publications have addressed the benefits of incorporating microarray work into the lab curriculum (1–4; 6). Notably, the Genome Consortium for Active Teaching (GCAT) provides resources and information for faculty who teach microarrays to undergraduate students (1, 2, 4). In addition, as per the recommendations of BIO2010 (13), a microarray study can easily be an aspect of a project-based laboratory.

Challenges with a DNA microarray study include determining an appropriate course in which to incorporate it, the timeframe required to complete the study, and what types of data analysis to perform following the microarray experimentation. Trying to complete all of this can be daunting not just for the students, but also the professor. Nevertheless, these challenges can all be met, based on the goals one has for students performing the exercise. I have incorporated a DNA microarray experiment into an upper-level course in microbiology. Prerequisites for this course include 1 year of Introductory Biology or equivalent AP credit. Of the 68 students enrolled in this course between 2003 and 2005, there were 18 sophomores, 19 juniors, and 31 seniors with majors as diverse as biology, biochemistry and molecular biology, chemistry, physics, environmental science, psychology, and French. The 14-week course includes a weekly 3-hour lab meeting. Because other lab exercises (e.g. identification of unknowns using traditional staining and molecular methods, etc.) are important to include in a microbiology course, only about half of the semester is available for a DNA microarray experiment.

This study is based on three hypotheses and three goals. It was hypothesized that in a short time (half a semester) it is possible to perform both wet and dry aspects of a DNA microarray study, with student understanding of experimental design, execution of method, and data analysis involving the ability to consider large datasets. Second, it was hypothesized that students become invested in this extensive exercise based on its open-ended, project-based nature. Finally, it was hypothesized that DNA microarrays serve as an effective introduction to genomics and illustrate the complex biology resulting from a single change in a biological system. As for goals, the first was for students to perform a DNA microarray experiment for hands-on experience with array technology and to be introduced to genomic approaches to project-based research. Another goal was for students to analyze data from such an experiment to better understand how to work with a large amount of data. A final goal was to have students use databases so as to understand and appreciate their value as a scientific resource, and see how they can be used to help consider how parts of a large dataset may biologically connect—a foray into the realm of the complex biology of a system. In this report, I demonstrate that these hypotheses were validated and assess achievement of these goals.

MATERIALS
Saccharomyces cerevisiae DNA microarrays with DNA oligonucleotides (arrayed in duplicate), each representing a unique 70-nucleotide portion from each gene of the genome, were obtained from GCAT (www.bio.davidson.edu/projects/gcat/gcat.html). The 3DNA 900 kit (Genisphere, Hatfield, Pa.) was used for conversion of total yeast RNA to cDNA.
and the sequential hybridizations of cDNA and fluorochromes (Cy3 and Cy5 dyes) to the DNA microarrays. Microarrays were scanned at Davidson College. Microarray data were analyzed using MAGIC Tool (7) and Microsoft Excel. Various databases linked from the Saccharomyces Genome Database (www.yeastgenome.org) were employed during data analysis of genes found to have strongly altered levels of transcription. Details on working with S. cerevisiae (including media preparation for, growth of, transformation of plasmids into, and use of heated acidic phenol to extract RNA from) and on performing the microarray experiment can be obtained from the Yeast Resources portion of the Protocols section of the GCAT webpage (download document by Kushner and Tiede, www.bio.davidson.edu/projects/gcat/GCATprotocols.html#phenol).

**METHODS**

A significant challenge with setting up a DNA microarray experiment in the teaching lab is determining the amount of time that can be afforded for such work (without taking time away from other relevant, and important, lab exercises within a course), and therefore what elements of the study can be performed given time constraints. Work with arrays can be divided into four components: (i) experimental design, (ii) wet labwork (which in this study involved manipulation and growth of S. cerevisiae, RNA extraction, cDNA synthesis, and then sequential hybridizations of cDNA and fluorochromes to the microarray), (iii) determination of up- and down-regulated genes (which in this study primarily involved use of MAGIC Tool (7)), and (iv) working with large data sets (which in this study involved using information from databases to learn about the genes, analyzing that information, and proposing biological connections of gene products from within the dataset). One of the purposes of this report is to present an overview about the options for performing the aforementioned four components to microarray experimentation and to note the time required for each step. In my course, students performed components (ii) through (iv) with the bulk of the work taking 6 weeks (Table 1). In the lab, six groups of three to four students each used one microarray; for the second and third years I taught this lab, three of the six groups performed one of two different experiments, therefore each of the two experiments was completed in triplicate (an ideal setup). As noted in the Materials section, a detailed protocol for using S. cerevisiae and performing arrays can be found at the GCAT webpage; these approaches are applicable for model organisms other than S. cerevisiae.

(i) **Experimental design—multiple options for consideration.** Experimental design offers numerous options for the teacher and the members of the class. The key to designing a DNA microarray experiment is to ensure that only one variable will exist between the two conditions to be tested. In three separate offerings of my microbiology course (2003, 2004, and 2005), I designed the experiments to be performed, since I used these opportunities to ask questions that might be helpful for my research program. Although this removed the option of the students designing their experiment, the project was open-ended as the result was unknown at the onset of the study. As such, the students were intrigued to perform original research, there was immediate “ownership” of the experiment, and there was a time benefit in that no lab time was required for experimental design. Alternatively, several weeks prior to the experiment, but after an introduction to the theory underlying uses of microarrays, lab groups could have been given homework directing them to design a microarray experiment. Proposed experiments could have been discussed during a class meeting with no loss of lab time. Doing this several weeks in advance would allow the instructor time to obtain necessary materials and to help students modify their proposals to ensure they would be testable (include only one variable). Another option would be for students to mimic previously performed DNA microarray experiments, allowing students to compare their results to published results; an example of this is comparison of gene expression in steady-state log-phase yeast grown in the presence of glucose versus galactose (11).

### TABLE 1. Microarray timeline

<table>
<thead>
<tr>
<th>When conducted</th>
<th>Activity</th>
</tr>
</thead>
<tbody>
<tr>
<td>2 weeks in advance&lt;sup&gt;a&lt;/sup&gt;</td>
<td>Transform yeast with plasmids (30’ 2x during nonarray lab)</td>
</tr>
<tr>
<td>1 week in advance&lt;sup&gt;a&lt;/sup&gt;</td>
<td>Grow and harvest yeast (few days)</td>
</tr>
<tr>
<td>Week 1</td>
<td>Extract RNA from yeast (3 hr)</td>
</tr>
<tr>
<td>Week 2</td>
<td>cDNA synthesis (3 hr)</td>
</tr>
<tr>
<td>Week 3</td>
<td>cDNA and Cy dye hybridizations&lt;sup&gt;b&lt;/sup&gt;</td>
</tr>
<tr>
<td>Week 4</td>
<td>MAGIC Tool; gridding (3 hr)</td>
</tr>
<tr>
<td>Week 5</td>
<td>Identify induced and repressed genes (3 hr)</td>
</tr>
<tr>
<td>Week 6</td>
<td>Data analysis and database exploration&lt;sup&gt;c&lt;/sup&gt;</td>
</tr>
</tbody>
</table>

<sup>a</sup>Optional for students.

<sup>b</sup>Sequential; requires meeting over 2 days (see text).

<sup>c</sup>Additional nonlab time is required for lab report preparation.

(ii) **Wet labwork—3 weeks of lab.** In my microbiology course, the main aspects of this portion of the experiment were RNA extraction from yeast, cDNA synthesis, and sequential hybridizations and washes of cDNA and Cy dyes to the DNA microarray. This portion of the experiment required 3 weeks of lab time. However, in order for students to start at the point of RNA extraction, yeast cells were previously
grown and harvested. I preferred to grow and harvest the yeast, since I had time to carefully monitor the growth of the yeast so that all cultures of the cells were simultaneously harvested while at the same part of their logarithmic growth phase, reducing variability between samples (the theory underlying growth and division of unicellular organisms was discussed in lecture).

It should be noted that one way to create differences between populations of yeast cells is to transform yeast with a plasmid(s) that confers foreign gene expression (with parallel transformation of an “empty” plasmid(s) into the control yeast). This was done, as part of my labs, 2 weeks prior to the RNA extraction lab (Table 1). This provided time to grow and select yeast transformants on solid media, grow the yeast in liquid media, and harvest the cells prior to the lab where RNA was extracted. Benefits for the students included having time for me to introduce the long-term microarray project and learning how to transform competent cells. Of course, experiments could be designed not requiring transformations (e.g., reference 11).

Students in my course spent one 3-hour lab period extracting RNA from yeast using heated acidic phenol. Students learned principles of how phenol is used to separate protein and nucleic acid and, by default, how to carefully work with hazardous material. In cases where working with phenol is not ideal, the MasterPure RNA purification kit (Epicentre Biotechnologies, Madison, Wis.) can be used (C. J. Alvarez, personal communication; www.bio.davidson.edu/projects/GCAT/protocols/RNA/RNA_methods.html).

The second of the three wet lab weeks involved using the Genisphere 3DNA 900 kit to reverse transcribe the isolated RNA into cDNA. Each RNA was subjected to reverse transcription with either a primer for Cy3 or Cy5 to enable dye reversal (see next paragraph). The 2-hour incubation allowed for further explanation of the background and rationale behind the experiment and details of microarray technology.

The third week of wet lab work involved using the 3DNA 900 kit for sequential hybridization (described below) of the cDNA and Cy dyes to the DNA microarray. As each yeast DNA microarray obtained from GCAT has a top portion and a duplicate bottom portion, a dye reversal was performed on the single array (Fig. 1; www.bio.davidson.edu/projects/gcat/GCATprotocols.html#phenol) so that, in total, the control and the experimental samples were each ultimately labeled with either Cy3 or Cy5. This accounted for variability in strength of signal and is important since Cy5 signal is easily degraded in the presence of ozone (5).

In general, there are two approaches for hybridizing cDNA to the DNA microarrays. One option is to incorporate the fluorochromes into the cDNA as it is being synthesized, with subsequent hybridization of the fluorochrome-labeled cDNAs to the array followed by a series of washes. Use of the 3DNA 900 kit, with sequential hybridizations of cDNA and the Cy dyes, required some creativity in scheduling lab time. Students spent about 2 hours the evening before the scheduled lab period pretreating the DNA microarray, preparing the cDNA hybridization mixes, and adding the cDNA to the microarray for an overnight incubation. The next day, the students spent about 90 minutes washing the array, preparing the Cy dye hybridization mixes, and adding the Cy dyes to the washed array for a 4- to 5-hour incubation. Later that day, the students returned for an hour to wash and dry the slides. Since the nature of the work did not fit neatly into the scheduled afternoon lab time, in order to ensure each student gained hands-on experience with method, each student was asked to be present for at least one hybridization solution prep, hybridization of cDNA or Cy dyes to the array, and one series of washing. Since I am aware of these scheduling challenges as the semester starts, the class and I selected meeting times so that the greatest number of students were present during all of the steps. The students were willing to meet during the extra time since they had already spent a lot

FIG. 1. DNA microarray experimental setup. Control (ctrl) and experimental (expt) RNA were each reverse transcribed with Cy3 or Cy5 tagged primers (four total reactions) in week 2 of the wet lab work. Distinct pairs of cDNAs were hybridized to distinct portions of the microarray (as indicated in the figure). A sequential incubation with Cy dyes generated signal. The results of the dye reversal can be seen in the sample array image (right). The two yellow spots in the center and upper right of both halves of the sample array indicate similar expression of the gene in both conditions; no signal indicates no expression of the gene in either condition; expression of the two genes in the experimental condition is seen using both dyes via the dye reversal.
of time and energy on the project and were willing to put in the extra time with the aim of obtaining good array data.

(iii) Dry lab work—3 weeks of lab. The first week of data analysis employed MAGIC Tool (7) to determine the relative gene expression of each yeast gene under each of the two tested conditions (control versus experimental). First, students were introduced to MAGIC Tool by uploading sample red and green .tif image files which feature four grids from an array and then “gridding” the individual data spots (www.bio davidson.edu/projects/MAGIC/MAGIC.html). Students then uploaded their personal red and green .tif images into a new MAGIC Tool file. The yeast microarrays from GCAT (currently) feature 16 grids on each of two identical halves of the array; therefore 32 grids, encompassing 13,544 data spots, were generated. Working in groups of three or four, the students took turns gridding to complete this task in about 75 to 90 minutes. “Segmentation” of the gridded data was performed, generating red-green signal ratios for each spot on the array. Powerful computers with a lot of memory should be used; for example, Macintosh G5 computers segmented the data in 1 to 2 minutes, whereas older G4 machines required about 20 minutes. According to the MAGIC Tool program installation guide (www.bio davidson.edu/projects/magic/magic.html#down), MAGIC Tool runs on any operating system with Sun Java; 512MB of RAM is minimal and 1 to 2GB of RAM is optimal. Following segmentation, red-green ratios were saved for the second week of dry lab work.

The second week of dry lab entailed identifying genes with either enhanced or repressed expression on both halves of the array. This allowed one to account for different raw red-green ratios that were generated on each half of the array. Red-green ratios were \( \log_2 \) transformed; then using Microsoft Excel spreadsheets, the \( \log_2 \) transformed red-green ratios from each part of the array were normalized using the “standardize” function, which generates a normalized value based on a distribution characterized by the mean and standard deviation of the dataset. Therefore, for each half of the array, the genes in the experimental condition can be ordered from “most enhanced expression” to “most repressed expression.” Since the goal of the array is to identify the genes with the most enhanced or repressed expression in the experimental condition, 6.25% of the most enhanced genes from both halves of the array (about 422 genes from 6,552 nonmitochondrial genes (some genes are duplicated on each half of the array)) were compared. Genes on both lists were considered to be enhanced and were retained for further study (the same held true for repressed genes). In general, this resulted in groups needing to further analyze about 80 total enhanced and repressed genes.

The third week of dry lab featured two components. The first was to introduce students to some of the databases they could use to help with analysis of their genes (see part iv, below). The second was a short exercise (Table 2) to verify that the students understand how enhanced and repressed gene expression relates to the original experimental design.

<table>
<thead>
<tr>
<th>Question</th>
<th>Answer</th>
</tr>
</thead>
<tbody>
<tr>
<td>Originally, which samples were labeled green and red, and which green-red combinations were hybridized to each respective half of the array?</td>
<td>To verify that if the experimental cDNA was tagged with Cy5 (red) and added to array half “A,” that Cy3 (green)-tagged experimental cDNA was added to array half “B” (and the converse for the control sample).</td>
</tr>
<tr>
<td>For array half “B,” we did a dye reversal, but then “flipped” the red and green files when loading them into MAGIC Tool. What does this effectively do to Grid B in terms of what red and green represent?</td>
<td>MAGIC Tool only computes red-green ratios. Since a dye reversal effectively is a “flip” of the samples, MAGIC Tool needs to be instructed about this so that for array half “B” the raw red-green ratio is properly computed.</td>
</tr>
<tr>
<td>From the log transformed data, positive and negative numbers were obtained; ultimately, how were positive and negative numbers derived from red-green ratios?</td>
<td>Positive red-green ratios indicate that the signal from Cy5 (red) was greater than the signal from Cy3 (green); negative ratios indicate greater signal from Cy3 (green).</td>
</tr>
<tr>
<td>An array signal for a gene features strong red signals in array half “A” and strong green signals in array half “B” (and, similarly, weak green in “A” and weak red in “B”). In which yeast cell population (control or experimental) was the gene highly expressed?</td>
<td>Assuming that cDNA from the experimental cells was labeled with Cy5 in array half “A” (and Cy3 in “B”), then the gene expression was greatly enhanced in the experimental cells (also, the gene expression was repressed in the control cells).</td>
</tr>
</tbody>
</table>

(iv) Analysis of large data sets—incorporation into student lab report preparation. As an introduction to engaging students to think about the cell as a dynamic entity, that of a “system,” students used the Saccharomyces genome database (SGD; www.yeastgenome.org) and databases linked from SGD to obtain information about their genes and gene products. For example, gene name, open reading frame designation, and gene ontology information are provided on the SGD web page specific to each yeast gene. As for databases linked from SGD web pages that are specific to each yeast gene, the yeast GFP-fusion localization database (GFP DB
at UCSF; yeastgfp.ucsf.edu; available via the “Localization Resources” link) was accessed for protein localization information; the General Repository for Interaction Datasets (BioGRID; www.thebiogrid.org; available via the “Interactions” link) lists protein-protein interactions, etc. This information was used to help compose a table for a lab report listing each gene identified during the second week of the dry lab (Fig. 3). The table included gene name, ORF designation, gene ontology annotation, essential or nonessential gene, protein localization, and known protein-protein interactions. Students were encouraged to work on this as a team, since an enormous amount of information was generated. Information in the table was then used by the students as a vehicle to help them look for potential connections between genes with up-regulated expression and also between genes with down-regulated expression. Such connections were reported in the discussion section of lab reports.

RESULTS

Over 3 years of microbiology class, 18 groups of three or four students each utilized one array per group. Sixteen of the 18 groups (89%) obtained data that could be gridded and analyzed. Since array projects were generally performed in triplicate (as described in Methods), student groups who did not perform the array successfully used data from another group for data analysis, so that they could participate in that element of the laboratory exercise.

Assessment of student understanding was performed for various aspects of the lab exercise. The three main areas assessed were (i) understanding of experimental design, (ii) understanding trends in gene expression, and (iii) ability to propose connections between genes with either up- or down-regulated expression, as an initial exercise in considering biology of an entire system.

(i) Understanding of experimental design and general microarray use. Student understanding of general principles in design of microarray experiments was assessed through GCAT-based assessment tools and/or questions during an in-class exam. In 2003, the students (n = 22) were asked three questions (Table 3) at the start of the semester and again as part of an exam administered late in the term (students knew that any material from lecture or lab could be part of the exam). In response to how one could measure a genome-wide response to a virus, 20 students (91%), following their experience in lab, knew to employ a DNA microarray (the other two students suggested looking at immune response, which while a clue to virus infection, does not involve measuring genome-wide response) compared to only three students (14%) knowing this at the start of the term. When asked about controls to use, 17 students (77%) replied that, at the least, cells lacking virus should be used (two other students (9%) proposed other kinds of controls, but uninfected cells are best since this control directly tests the variable of the virus being present); only nine students (41%) thought of this before experimentation. In terms of technical limitations for microarray use, 19 students (86%) were able to list at least two potential issues for use of microarrays (common answers included needing to know the genome sequence of the organ-

TABLE 3. Assessment questions

<table>
<thead>
<tr>
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<tbody>
<tr>
<td>1</td>
<td>Design an experiment to measure the genome-wide response when a cell becomes infected with a virus.</td>
<td>You are interested in a bacterium that grows in high temperature conditions. One interesting observation is that it is green when grown at the normal high temperature, but colorless when grown at a temperature that is 20 degrees below the optimal growth temperature. Which of the following would be the best description of the way you could investigate this difference using microarrays? (Isolate total RNA from the organism grown at the two temperatures, reverse transcribe it with dyes to cDNA and incubate with the microarray)</td>
</tr>
<tr>
<td>2</td>
<td>What controls would you need for this experiment?</td>
<td>A smoker and a coal miner both got lung cancer. The cancers are histologically identical, but there might be functionally important differences in gene expression in the two cancers which would allow personalized treatment. Which of the experiments is the best design to determine appropriate treatment for the two lung cancers? (Compare the gene expression profiles of the two lung cancers to lung samples without cancer)</td>
</tr>
<tr>
<td>3</td>
<td>What are the technical limitations to the method(s) you chose?</td>
<td>You are investigating the changes in gene expression in cancer cells compared to normal cells by labeling of RNA samples. When you look at your entire microarray after performing the scan in both dye channels, you observe spots with several shades of green, but no red spots. Which of the following best explains the data? (Poor labeling of one of the samples)</td>
</tr>
</tbody>
</table>

* Correct multiple-choice answer provided after the question, in parentheses.
ism so the array can be generated, challenges with accurate quantitation of gene expression, and not knowing if changes in protein levels correlated with mRNA levels), when, at the start of the term, only two students (9%) described one technical limitation.

In 2004 and 2005, student understanding of microarrays was determined via a new online assessment tool designed by members of GCAT. Two multiple-choice questions on this assessment addressed application of knowledge in terms of experimental design (Table 3). In 2004 (n = 24 students; 22 students took both the pre- and posttests) for question 1, two of 22 students (9%) answered correctly on the pretest; for the posttest that improved to 16 students (73%). For question 2, four of 22 students (18%) answered correctly on the pretest; 10 students (45%) answered correctly on the posttest. In 2005 (n = 22 students; 14 students took both the pre- and posttests) for question 1, three of 14 students (21%) answered correctly on the pretest; 11 students (79%) did so on the posttest. For question 2, five of 14 students (36%) answered the pretest question correctly; 11 students (79%) did so on the posttest. Finally, a third question, asked each year, addressed what could have happened during the microarray experimental procedure to result in no red signal on the microarrays. Two of 22 students (9%; 2004) and two of 14 students (14%; 2005) knew the answer to this question prior to microarray work; after array work, 13 (59%; 2004) and 6 (43%; 2005) students answered this question correctly.

Because the assessment used to ascertain student understanding of experimental design changed after 2003, a two-way analysis of variance with Student-Newman-Keuls comparisons test (factors: pre- versus posttest and course year) was performed to determine (i) if, each year, there was a statistically significant increase in student understanding, and (ii) if this was independent of the year the students took the course (and which assessment was performed). The results are summarized in Table 4. The \( P \) value of <0.001 indicates that the improvement in understanding was significant. In addition, there was no effect due to the year the students took the course (and which assessment was performed) based on the \( P \) value of 0.128.

(ii) Understanding trends in gene expression data. In 2003, as described above, 22 students completed both the pre- and posttests. Here, a fictitious diagram (Fig. 2a) showing gene expression changes (via fold induction and fold repression) for each of six different genes over a 75-minute time course (time 0 and every 15 minutes thereafter) was provided, and students were asked to comment on any aspect of gene expression they chose. On the pretest, six of 22 students (27%) were able to apply the concept of the “map” of gene expression changes to accurately comment on gene expression changes of some or all of the six genes shown. After doing the experiment

<table>
<thead>
<tr>
<th>Year</th>
<th>Question(s)</th>
<th>Pretest (%)</th>
<th>Posttest (%)</th>
<th>( P ) value(^b)</th>
</tr>
</thead>
<tbody>
<tr>
<td>2003</td>
<td>Table 3 question 1</td>
<td>14</td>
<td>91</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>2004</td>
<td>Table 3 question 1</td>
<td>9</td>
<td>73</td>
<td></td>
</tr>
<tr>
<td>2005</td>
<td>Table 3 question 1</td>
<td>21</td>
<td>79</td>
<td></td>
</tr>
</tbody>
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<tr>
<th>Year</th>
<th>Question(s)</th>
<th>Pretest (%)</th>
<th>Posttest (%)</th>
<th>( P ) value(^b)</th>
</tr>
</thead>
<tbody>
<tr>
<td>2003</td>
<td>Figure 2a question</td>
<td>27</td>
<td>100</td>
<td></td>
</tr>
<tr>
<td>2004</td>
<td>Figure 2b question</td>
<td>18</td>
<td>45</td>
<td></td>
</tr>
<tr>
<td>2005</td>
<td>Figure 2b question</td>
<td>7</td>
<td>36</td>
<td></td>
</tr>
</tbody>
</table>

\( ^a \) Two-way analysis of variance with test interval and year as Student-Newman-Keuls pairwise comparisons; analysis performed using Sigmapstat 2.0.

\( ^b \) Pre- and posttest information for each set of questions was analyzed as a group via two-way analysis of variance; the \( P \) values shown are for the interval of learning. No significant year-to-year effect was observed (see text in Results).
and discussing graphical representation of array data, all 22 students (100%) accurately commented on several aspects of gene expression.

In 2004 and 2005, a different diagram was shown (Fig. 2B) and students were asked to consider potential relationships between the three genes shown. In 2004, at the start of the term, four of 22 students (18%) were able to correctly note that gene 2 likely induces expression of gene 1 (a specific answer from a panel of multiple-choice options); whereas 10 of 22 students (45%) did so at the end of the term. In 2005, one of the 14 students (7%) who took both the pre- and post-tests knew the answer at the start of the term, and five of 14 students (36%) did so at the end of the term. Of note, this style of data representation was not discussed at any time in the course.

As noted above, because the assessment design changed after 2003, a two-way analysis of variance was performed to determine (i) if there was a statistically significant increase in student understanding in trends in gene expression, and (ii) if this was independent of the year the students took the course (and which assessment was performed). The results are summarized in Table 4. There was a trend towards improvement in understanding ($P = 0.103$), yet there was no effect due to the year the students took the course (and which assessment was performed) based on the $P$ value of 0.26.

(iii) Working with large datasets: proposing biological connections between gene products. One of the greatest challenges for students performing microarrays is the sheer volume of data that is generated and knowing what to do with it. The discussion section of the lab report offered an opportunity for students to consider the entirety of the data and select some elements of it to discuss. Guidelines for the lab report included prompts such as “Discuss any genes that are functionally related...focus on gene ontology, localization, and protein-interaction information.” The goal was for each student to peruse the information in the table that their group generated (Fig. 3) and identify sensible biological connections between subsets of genes in the microarray analysis, as an initial foray into considering the complex nature of the cell. The ability of each student to do this was assessed upon reading the lab report. Fifty-eight of the 68 students (85%) in the course from 2003 to 2005 described several potential connections between subsets of genes that had been found to be enhanced or repressed in their expression levels on the microarray. Six students (9%) only noted one possible connection; two students (3%) listed groups of genes but did not explain the connections between them; two students (3%) simply did not attempt this part of the discussion section of the lab report.

DISCUSSION

Two factors that concern faculty in regard to introducing a DNA microarray experiment into a lab portion of their course are time required and cost of materials. I have described a protocol where wet and dry lab exercises require 6 weeks of lab (7 weeks if the option of transforming yeast with plasmids is performed; however, since it does not take much time this can be combined with another lab earlier in the term or, alternatively, could simply be performed by the lab instructor and students given cell pellets harvested from cultures of transformed yeast cells). Some students have noted that they would like more time to perform the microarray experiment and more time to spend with the data; while this would be ideal, the results from the assessment and, importantly, the lab report discussions suggest that an initial understanding of the main aspects of project-based genomics research and how microarrays can be used in that regard is obtained. At Dickinson College, since another faculty member in our department teaches a course on Genomics, Proteomics, and Bioinformatics, I can suggest that students enroll in this course for additional instruction in this and related areas. Admittedly, for some students, more time discussing arrays,
<table>
<thead>
<tr>
<th>ORF</th>
<th>Standard gene name</th>
<th>Feature type</th>
<th>Gene description</th>
<th>Molecular function</th>
<th>Biological process</th>
<th>Cellular compartment</th>
<th>Viability of a deletion strain</th>
<th>Protein localization</th>
<th>Protein-protein interactions</th>
</tr>
</thead>
<tbody>
<tr>
<td>YKR034W</td>
<td>DAL80</td>
<td>Verified</td>
<td>Negative regulator of genes in multiple nitrogen degradation pathways; expression is regulated by nitrogen levels and by Gln3p; member of the GATA-binding family, forms homodimers and heterodimers with Deh1p</td>
<td>Transcription factor activity</td>
<td>Regulation of nitrogen utilization; transcription</td>
<td>Nucleus</td>
<td>Viable</td>
<td>N/A</td>
<td>YLR110C, YER047C, YKR045W, YLR376C, YDR520C, YNL021W, YHR006W</td>
</tr>
<tr>
<td>YKR073C</td>
<td>N/A</td>
<td>Dubious</td>
<td>Unlikely to encode a protein</td>
<td>Unknown</td>
<td>Unknown</td>
<td>Unknown</td>
<td>Unknown</td>
<td>Viable</td>
<td>N/A</td>
</tr>
<tr>
<td>YKR105C</td>
<td>N/A</td>
<td>Uncharacterized ORF</td>
<td>Hypothetical protein</td>
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<td>Unknown</td>
<td>Unknown</td>
<td>Unknown</td>
<td>Viable</td>
<td>YDR135C, YJR091C</td>
</tr>
<tr>
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<td>Dubious</td>
<td>Hypothetical protein</td>
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<td>Unknown</td>
<td>Unknown</td>
<td>Unknown</td>
<td>Viable</td>
<td>N/A</td>
</tr>
<tr>
<td>YLR220W</td>
<td>BUR2</td>
<td>Verified</td>
<td>Cyclin for the Sgg1p (Bur1p) protein kinase; Sgg1p and Bur1p comprise a CKD-cyclin complex involved in transcriptional regulation through its phosphorylation of the carboxy-terminal domain of the largest subunit of RNA polymerase II</td>
<td>Cyclin-dependent protein kinase regulator activity</td>
<td>Mitotic sister chromatid segregation; transcription</td>
<td>Nucleus</td>
<td>Viable</td>
<td>N/A</td>
<td>YPR161C, YBR135W, YMR125W, YIL158C</td>
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<td>YLR236C</td>
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<td>Unknown</td>
<td>Unknown</td>
<td>Viable</td>
<td>N/A</td>
</tr>
<tr>
<td>YML099W-B</td>
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<td>Dubious</td>
<td>Hypothetical protein</td>
<td>Unknown</td>
<td>Unknown</td>
<td>Unknown</td>
<td>Unknown</td>
<td>Viable</td>
<td>N/A</td>
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<tr>
<td>YML080W</td>
<td>DUS1</td>
<td>Verified</td>
<td>Dihydrouridine synthase, member of a widespread family of conserved proteins including Smu1p, Dus1p, and Dus4p; modifies pre-rRNA (Phe) at U17</td>
<td>rRNA dihydrouridine synthase activity</td>
<td>rRNA modification</td>
<td>Nucleus</td>
<td>Viable</td>
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<td>Hypothetical protein</td>
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<td>Unknown</td>
<td>Viable</td>
<td>N/A</td>
</tr>
<tr>
<td>YML123C</td>
<td>PHO84</td>
<td>Verified</td>
<td>High-affinity inorganic phosphate (P) transporter and low-affinity manganese transporter</td>
<td>Inorganic phosphate transporter activity (IDA, IMP, ISS), Magnesu Ion Transporter activity (IMP)</td>
<td>Manganese ion transporter activity (IMP), phosphate transport (IDA, IMP, ISS)</td>
<td>Integral to plasma membrane (IDA, ISS)</td>
<td>Viable</td>
<td>N/A</td>
<td>YER125W, YDR388W, YDR523C, YLR238W, YNL061W, YNL116W, YJR091C, YDR200C, YGR040W, YOR181W</td>
</tr>
</tbody>
</table>

FIG. 3. Portion of a student’s table (from fall 2005) containing information obtained from online databases. The molecular function, biological process, and cellular compartment categories relate to gene ontology. Protein localization information came from the yeast GFP-fusion localization database, and protein-protein interactions information came via BioGRID. As seen in the gene ontology columns, traceable author statement (TAS), inferred from direct assay (IDA), inferred from sequence or structural similarity (ISS), and inferred from mutant phenotype (IMP) are evidence codes for how the annotation was generated.

how the data are generated (mathematical analysis thereof), and more ways the data can be analyzed would be beneficial and might enable improved scoring on the multiple-choice assessment tools, which stress application of knowledge. However, considering that this experiment is performed in a relatively short time, the hypothesis—that the compressed timeframe still allows students to clearly understand how to use microarrays and why one would do so—is supported.

The experiment is (potentially surprisingly) cost-effective. Since the dry lab aspects of the course are cost free (MAGIC Tool is shareware available via GCAT) and if reagents for general work with microbes are already available (in my case, solid and liquid media for growth of yeast, chemicals for transformation of plasmids into yeast, etc.), then the one-time-per-course costs come from the DNA microarrays (via GCAT, six yeast arrays cost $150) and the 3DNA kit (to generate the cDNA, hybridize the cDNA to the array, and add the Cy dyes to the bound cDNA, I use two kits, which cost about $700 with shipping). Therefore, a 6-week lab for six groups of three to four students only costs about $850.
Notably, the lab exercise described herein is not restricted to working with *S. cerevisiae*; parallel approaches can be taken with other species. Currently, GCAT can provide instructors of undergraduate students with DNA microarrays from 10 species, including *Escherichia coli*, human, mouse, and *Arabidopsis*. For data analysis, instead of the *Saccharomyces* genome database, the *E. coli* Genome Project (www.genome.wisc.edu/sequencing/k12.htm) can be accessed by students using *E. coli* arrays in the lab (e.g., to obtain gene annotation).

For the students, a challenge of the DNA microarray experiment is that it occurs over a long period of time. Therefore, being able to recollect details of the early parts of the project can be difficult. I stress to the students that it is important for them to keep good notes so that they are able to recall all elements of their work on the project. Also, in my Microbiology course the DNA microarray study is the second of two multiweek experiments, so a subset of the students may be helped by having experience in a lab project prior to the DNA microarray work.

Another challenge for the students is that, as designed in my course, the project-based lab lacks a “correct” answer—I like the open-ended nature of this work since it is analogous to real research experiences; others have also commented on the value of project-based labs (13). My observations of students becoming deeply engaged in the DNA microarray work and subsequent data analysis supports the hypothesis that, even with the half-semester timeframe for the study, this is a successful vehicle for students to experience an open-ended, project-based lab.

Another important concept for the students to appreciate is that generation of DNA microarray data is really only a starting point in what would be a more extensive study; for example, the microarray should only be considered to be a qualitative-semiquantitative assessment of changes in transcription and resulting levels of steady-state RNA. For quantitation of gene expression, genes from microarray studies would need to be analyzed by quantitative, real-time PCR. Following that, biological significance should be investigated to understand why changes in gene expression occurred. Furthermore, while I do not stress statistical analysis of the data in my course, other faculty may find this valuable; indeed, there are many dry lab exercises that could be performed following generation of the microarray data based on the goals that one has for his/her students.

The assessment performed makes it clear that doing an experiment using a DNA microarray helps the students understand how to perform an experiment on a genome-wide level. In addition, during informal conversations following completion of the microarray exercise, students often remark that while it is difficult to ponder the enormous dataset generated, looking for connections between genes in the dataset really helps them realize the complexity within the cell and helps them move away from consideration of genes and gene products functioning in isolation. This validates the hypothesis concerning the use of microarrays as a valid tool for engaging students in considerations of biological complexity. In some ways, this may be one of the most important results of the array work, since the genomic era forces us to think about biology in a more complex manner. Furthermore, several students gain interest in the computer science side of the project, from the power of databases to the realization that computer programs are invaluable in analysis of large data sets. Such realization spurs some students to appreciate that in order to help comprehend biological systems, approaches in systems biology, an emerging area of biology that relies on math and computer science (8–10; 12), will need to be pursued. This is a wonderful illustration of the need for collaborative, interdisciplinary science as we continue with investigation of complex biological questions. An experience working with DNA microarrays and microarray data therefore serves as an exceptionally effective introduction to this arena.

**ACKNOWLEDGMENTS**

This work was partially presented as a poster at the 2005 American Society for Microbiology Conference for Undergraduate Educators in Atlanta, Georgia (Kushner D. B. and B. J. Tiede, Microarray analysis in the microbiology laboratory: completing both experimentation and data analysis in as little as six weeks). I thank the GCAT community, especially A. Malcolm Campbell, Laurie Heyer, Todd Eckdahl, Laura Hoopes, Mary Lee Ledbetter, Anne Rosenwald, and Consuelo Alvarez for providing information on microarrays, MAGIC Tool, and protocols to help me design my laboratory exercise. Ben Tiede (Dickinson College class of 2005) helped refine the data analysis process. Tom Arnold and Rachel Sanders assisted with statistical analysis of assessment data. I thank Amy Cheng Vollmer for critical review of the manuscript. Special thanks go to the 68 Dickinson College students who took my microbiology course between 2003 and 2005 and performed the microarray studies described herein.

**REFERENCES**

A Discussion Group Program Enhances the Conceptual Reasoning Skills of Students Enrolled in a Large Lecture-Format Introductory Biology Course

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It has been well-established that discussion groups enhance student learning in large lecture courses. The goal of this study was to determine the impact of a discussion group program on the development of conceptual reasoning skills of students enrolled in a large lecture-format introductory biology course. In the discussion group, students worked on problems based on topics discussed in lecture. The program was evaluated using three assessment tools. First, student responses to pre- and posttests were analyzed. The test question asked the students to demonstrate the relationships between 10 different but related terms. Use of a concept map to link the terms indicated an advanced level of conceptual reasoning skills. There was a 13.8% increase in the use of concept maps from pre- to posttest. Second, the students took a Likert-type survey to determine the perceived impact of the program on their conceptual reasoning skills. Many of the students felt that the program helped them understand and use the main course concepts to logically solve problems. Finally, average exam grades increased as the semester progressed. The average final grade in the course was 75%. Students enrolled in the course the previous year (where the lecture component of the course did not assess or reflect student learning in the discussion group) had an average final grade of 69%. The results of this study demonstrate that the discussion group program improves the conceptual reasoning skills of students enrolled in a large lecture-format introductory biology course.

Many undergraduate colleges and universities throughout the United States typically offer large freshmen-level courses due to financial constraints and high enrollment (5, 15). For a typical freshman, the first undergraduate year is a time of transition from the extremely structured learning environment that is common in high school settings to an environment which requires them to take more personal responsibility for their own learning (2). Many freshmen have difficulty taking ownership of their learning in larger classes (1, 8). This may partly be due to the fact that many first-year courses repeat materials that are covered in the high school curriculum, leading to boredom and a lack of interest in learning (2). Additionally, it is not unusual for instructors responsible for teaching freshmen-level large lecture courses to use traditional teacher-centered methods as their primary lecture style. This teaching approach emphasizes the rote memorization of facts and often promotes passive student learning, again, leading to student apathy (2). Several reports suggest that introductory courses need to introduce students to new and innovative ideas using student-centered teaching approaches that will inspire students to become more active participants in their learning (2, 16, 23). In response to these teaching techniques, students should begin to develop higher-order cognitive skills, such as conceptual reasoning, that are required for progression through the undergraduate curriculum (2, 16, 23).

Active-learning techniques such as problem-based, discovery-based, or inquiry-based learning are difficult to employ in large lecture-format courses, due to the number of students enrolled in the course and time constraints. These techniques enable students to interact with newly acquired knowledge by requiring students with different learning styles to use varying methods in order to assimilate the newly acquired knowledge in a small social setting (6, 9, 22). Active-learning strategies include such activities as small group problem solving, answering questions in real-time using classroom response systems, discussion group programs, web-based assignments, and analysis of case studies. These methods have been proven to promote the development of conceptual reasoning skills (7, 13).

In the scientific disciplines, active-learning techniques have aided in the enhancement of scientific literacy, retention of information, creativity, communication skills, self-evaluation skills, and preparedness for scientific research studies (2, 11, 19). Many undergraduate educators now support reforming science education so that it is more like “scientific teaching”—a teaching method that actively engages students in the process of science and demonstrates to them the rigor of the scientific disciplines (11). Udovic and colleagues created the Workshop Biology Project to emulate scientific teaching in their introductory biology courses. They demonstrated that using such a technique improved student performance dramatically compared to students who were enrolled in a typical lecture-style introductory biology course (21). McInerney demonstrated that adding scientific teaching techniques (using team-based projects) to his undergraduate microbial physiology course significantly improved final exam scores compared to a traditional lecture-format (14). Finally, Lyle and colleagues (12) and Tien and colleagues (20) introduced a discussion group program in their organic chemistry courses.
that used scientific teaching techniques and saw enhanced student performance as compared to traditional lecture-style courses.

Biology 101, the introductory biology course for science majors at Pace University—New York City, is a large lecture-format freshmen-level course. Enrollment in the course typically exceeds 100 students per semester. Based upon the information presented above, it was apparent that teaching the course using a traditional teacher-centered lecture style would not be the most effective pedagogical method to use for the students enrolled in the course. Therefore, a discussion group program, using the Peer-Led Team Learning (PLTL) model developed by Gosser and Roth (10), was added to the course. For this program, students enrolled in the Biology 101 course were broken into groups of 10 and each group met for an additional 1 hour per week with a trained peer leader. During each 1-hour session, the peer leader guided the students through problem sets (modules) that were designed by the PLTL Biology Task Force (http://www.pltl.org). The modules were related to the topics discussed in lecture. The peer leaders were students that had successfully completed the first-year biology curriculum the previous academic year and received an A or B as a final grade in Biology 101. The peer leaders were trained in how to facilitate small group discussions highlighting the thinking process, as opposed to emphasizing the answers to the problem sets, and how to work with different learning styles. The goal of this program was to engage students in the “scientific teaching” method discussed above.

The Learning Pyramid developed by the National Training Laboratories for Applied Behavioral Sciences (http://www.ntl.org) demonstrates that students only retain 5% of the materials presented to them in a traditional lecture setting. Retention rates go up to 50% upon addition of a discussion group component to a course, and they go up even further to 90% if the students are asked to teach others the materials that they have recently been taught. The National Training Laboratories assert that discussion group programs benefit students in different ways depending upon their ability levels. Wenker students receive additional inquiry-based problems to supplement the materials covered in lecture. Average students are exposed to different view points to aid them in problem solving. Stronger students are allowed to teach, which in turn, aids in the retention of the materials discussed.

The PLTL discussion group model has been effectively used in an organic chemistry course (12, 20). The hypothesis for this study is that the PLTL discussion group program will improve introductory biology students’ conceptual reasoning skills. The development of conceptual reasoning skills is essential for undergraduate science majors to be successful in their given fields. These skills aid in the ability of individuals to understand concepts and see the connections between those concepts. This, in turn, enables individuals to logically and sequentially address problems and arguments. To determine if the Biology 101 discussion group program enhanced students’ conceptual reasoning skills, student performance and opinions were assessed during the fall 2005 semester. A comparison of pre- and posttest results strongly suggested that the students’ conceptual reasoning skills improved as the semester progressed. Student comments indicated that they benefited from the program. The enhancement of the students’ conceptual reasoning skills enabled them to perform better overall on examinations as compared to students enrolled in the Biology 101 course the previous year. All of the results from this study strongly indicate that the discussion group program did indeed enhance the conceptual reasoning skills of the students enrolled in the course.

MATERIALS AND METHODS

Implementation of the Biology 101 PLTL discussion group program. Students registering for Biology 101 were required to coregister for a Biology 101 PLTL discussion group section. To guarantee that discussion groups remained small, the Registrar’s Office limited enrollment to 10 students per section. Each section met once per week for 1 hour. Participation in the PLTL discussion group comprised 15% of the students’ final course grade.

Peer leaders to run the discussion group sections were chosen on the basis of their outstanding performance in Biology 101; they earned a final grade of A or B. Peer leaders attended a general information session in late April and were officially hired in August. They then participated in a 2-day orientation and training session co-led by myself and the Director of the Pace University Center for Academic Excellence and Tutorial Services, Dr. Claire Berardini. During training, the peer leaders learned and practiced small group facilitation with an emphasis on promoting thinking processes and incorporating different learning styles. They also trained on how to incorporate biology study skills into their group meetings. During fall term, the peer leaders met with me on a weekly basis to prepare each module (problem set), discuss their experience as leaders, identify problems, ask questions, and ensure ongoing supervision.

The modules for the Biology 101 PLTL discussion group program were modeled after modules that are currently in use at other institutions using PLTL (developed by the PLTL Biology Task Force, http://www.pltl.org). They reinforced materials covered in lecture including topics such as the scientific method, basic and biological chemistry, metabolism, cell biology, cell cycle, meiosis, Mendelian genetics, and DNA, RNA, and proteins. The modules included activities such as concept maps, open-ended questions, reading comprehension, and case studies. Each module was designed to foster conceptual reasoning skill development using small group participation.

Assessment of the impact of the PLTL discussion group program on the development of conceptual reasoning skills: evaluation of pre- and posttest answers. At the beginning of the fall 2005 semester, students in Biology 101 were asked to take a pretest to evaluate their conceptual reasoning skills prior to participating in the discussion group program. A posttest was given to the students at the end of the Biology 101 course to assess the impact of the discussion group program on their conceptual reasoning skills.
question on both the pre- and posttest was, “Demonstrate the relationship between the following terms in a way that you feel is most appropriate.” On the pretest, the terms were, “bright colors, pot of gold, fantasy, prism, sun, rainbow, Somewhere Over the Rainbow, rain clouds, leprechauns.” The terms on the posttest were, “stapler, pencil, pen, computer, printer, paper, desk, lamp, push pins, chair”. Nonbiological terms were chosen for the pre- and posttests because the students enrolled in the course had different levels of biology preparedness. I did not want the different levels of preparedness to affect their answers to the questions. It was assumed that the terms used for the pre- and posttests were familiar to all of the students. Although not traditionally done, different terms for the pre- and posttests were used because I did not want the students to recall and use their pretest answers on their posttests. Finally, upon asking the peer leaders to answer both the pre- and posttest questions, there was little difference in the types of responses between the two tests. This suggests that the terms on the tests did not influence the types of answers (data not shown).

A total of 115 students took the pretest and 85 students took the posttest. Among the pre- and posttests, I was able to obtain 61 matched pretest-posttest pairs. I was unable to match the remaining tests because the students either forgot the ID number that they used on the pretest when they took the posttest or they dropped or added the course after the pretest was given.

Assessment of the impact of the PLTL discussion group program on the development of conceptual reasoning skills: evaluation of student perceptions. In order to assess the perceived impact of the discussion group program on the development of the students’ conceptual reasoning skills, students were asked to fill out a web-based questionnaire with Likert-type questions. This questionnaire was a modified version of a Student Assessment of Learning Gains (SALG) survey designed by Dr. Victor Strozak of the PLTL Biology Task Force. Likert-type questions require that students respond to a statement by choosing whether they strongly agree, agree, disagree, strongly disagree, or are neutral with respect to the statement. Survey questions were designed to evaluate the perceived impact of: (i) the discussion group’s organization and materials on student learning; (ii) the content of the modules on the student’s ability to learn the different topics in the course; (iii) the program on student enthusiasm, confidence, and communication; and (iv) the program on the student’s abilities to understand concepts and solve problems in Biology 101 and other courses at the University. For every question on the survey, 50% or more of the students strongly agreed or agreed that the discussion group program helped them.

Students received two points of extra credit on their final exam for completing the survey. Ninety-seven students filled out the survey but not every student answered every question. In this manuscript, the responses to 4 of the 37 questions are presented. These four questions directly assessed the students’ opinions about the impact of the discussion group program on their conceptual reasoning skills.

Assessment of the impact of the PLTL discussion group program on the development of conceptual reasoning skills: evaluation of student performance. During the fall 2005 semester, students enrolled in the Biology 101 course took four pop quizzes, three lecture examinations, and one cumulative final examination. The quizzes had five questions each, and each question was similar to the questions that appeared in the discussion group modules. The students were permitted to work in groups to answer the questions on the quizzes. Each quiz was worth 0.6% of the final Biology 101 grade and did not significantly impact final student grades. The lecture exams had 50 questions each. Approximately 50% of the exam questions were designed to test knowledge retention, and 50% were designed to test the conceptual reasoning skills of the students. Finally, the lecture final examination had 100 questions and contained only knowledge retention questions that were similar to the ones used on the lecture examinations.

Fall 2005 grades were compared to the grades obtained by students in the fall 2004 Biology 101 course. Students in the fall 2004 course did participate in the discussion group program, but they did not receive quizzes in lecture with questions reflecting the modules and the lecture exams only contained knowledge retention questions. In essence, no connection was made between the modules and the tools used to assess student performance in fall 2004. Additionally, although lecture content was the same both semesters, I was more conscious of ensuring that students saw connections between the different topics covered by using examples from the discussion group modules in the fall 2005 class. The lecture final examinations were identical for the fall 2004 and fall 2005 Biology 101 courses. One hundred seventeen students were enrolled in the fall 2004 Biology 101 course, and 115 students were enrolled in the fall 2005 Biology 101 course. I was the lecture instructor for both courses.

Statistical analyses. The answers to all of the pre- and posttests that were matched pairs (n = 61) were marked as either correct or incorrect. The most complex answer and, therefore, the “correct” answer to the pre- and posttests was a concept map. A concept map is a graphical tool that links concepts in a hierarchical fashion with the most general concepts at the top of the map and the less general concepts linked to them in a hierarchy below (17). All other student answers were considered incorrect. Using a paired t test, I was able to assess the students’ conceptual reasoning skills based on their responses to the pre- and posttest question. The results are reported as the percentage of students that got the pre- and posttest questions correct. The P value from a paired t test analysis comparing the pre- and posttest scores was also determined. A P value of ≤0.05 was considered statistically significant.

For the SALG survey, the student responses to four representative questions are reported as the averages of the responses for each question (Table 1). Student grades on exams and quizzes are given as averages with the corresponding standard deviations (Table 2). Finally, unpaired t tests were used to compare the fall 2004 Biology 101 average
cumulative final examination scores and average final grades (n = 117) with those from fall 2005 Biology 101 (n = 115; Table 2). Again, a $P$ value of $< 0.05$ was considered statistically significant. Pace University Institutional Review Board approval for these studies was granted in August 2005.

**RESULTS**

**Evaluation of pretest-posttest results.** Students enrolled in the fall 2005 Biology 101 course were required to participate in the PLTL discussion group program. Those students also elected to participate in this study to assess the impact of the discussion group program on the development of their conceptual reasoning skills. On the first day of lecture, the students were asked to answer a pretest question in order to supply a set of baseline answers for this study. The pretest question asked the students to demonstrate the relationships between related, but nonbiological, terms in the best way that they could. On the last day of lecture, they were asked to answer the same question on a posttest with different related, but non-biological, terms. One hundred fifteen students took the pretest, and 85 students took the posttest.

The answers given on both tests were separated into four categories: (i) formation of a concept map to link the terms, (ii) use of all the terms in a paragraph, (iii) use of a one-to-three word phrase to describe what the terms reminded the student of (in this case, none of the words given were used by the student), and (iv) other assorted answers (e.g., relisting the terms, no response, or “I don’t know”). The percentages of students that answered the pre- and posttest questions using answers from one of these four categories are depicted in Fig. 1. In the first category (formation of a concept map), there was a 13.8% increase in the number of students that used this answer on the posttest versus the pretest. Representative examples of concept maps prepared by the students are depicted in Fig. 2. There was no significant difference in the number of students that answered the question by using the terms in a paragraph (22% and 20% on the pre- and posttest, an nonbiological, terms in the best way that they could. On the last day of lecture, they were asked to answer the same question on a posttest with different related, but nonbiological, terms. One hundred fifteen students took the pretest, and 85 students took the posttest.

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respectively) or by answering the question by using a one word phrase to describe what the terms reminded the student of (49% and 52% on the pre- and posttest, respectively). Finally, there was a 15% decrease in the number of students that gave some other answer to the question on the posttest versus the pretest. Taken together, these results suggest that there was a shift in the types of responses the students used to answer the questions between the pre- and posttest. This shift resulted in an increase in the number of students that used a concept map on the posttest and a corresponding decrease in the number of students that used some other response on the posttest.

Sixty-one of the pretest-posttest answers were matched to form pretest-posttest pairs. Matching the pretest-posttest pairs enabled a more detailed statistical analysis of the student answers. In reviewing answers from the matched pairs, 16.4% of the students used a concept map on the pretest, and 27.9% used a concept map on the posttest. This shows an 11.5% increase in the number of students that used the concept map on the posttest versus the pretest. A paired t-test analysis of these results demonstrated that the increase in concept map usage on the posttest versus the pretest was statistically significant ($P = 0.034$).

Upon comparing the pretest-posttest responses, it was determined that the concept map was the most complex answer to the question because there was an increase in the number of students that used a concept map on the posttest. Supporting this decision, the literature suggests that one of the most advanced answers to questions such as the one on our pre- and posttests is the development of a concept map linking the terms together. Experts commonly make connections using concept maps to organize information (4). Additionally, Rebich and Gautier (18) used concept map pre- and posttests to analyze changes in their students' conceptual reasoning skills. The results from their studies demonstrated that their students displayed evidence of significant learning and an increase in conceptual reasoning skills as determined by an increase in the complexity of the concept maps created on the posttests compared to the pretests.

Students choosing to link the terms using a paragraph demonstrated that they were indeed able to link the terms but their linkages were linear—with a distinct start point and end point. Concept mapping enables students to make connections between concepts in any order. Cohen (3) suggested that concept mapping requires more metacognitive reflection than paragraph writing. Metacognitive reflection results in enhanced conceptual reasoning. These data suggest that the shift detected in the number of students that answered the posttest question with a concept map may reflect an increase in the ability of the students to make connections between terms in ways that are not necessarily linear and are similar.
to how experts work (4).

During the first discussion group session (which followed the first lecture and administration of the pretest), students were introduced to concept maps. They were asked to fill in a preconstructed concept map using supplied basic chemistry terms. Along with introducing the concept map, the peer leaders instructed the students on how to prepare the maps on their own and suggested to the students that the construction of concept maps would help ensure that they understood the materials covered during the course. The students were never asked to construct concept maps on their own as an assignment or requirement for the course, and the peer leaders did not discuss their usefulness as study tools after the initial discussion group session. Because of the students’ limited encounter with concept mapping during the discussion group, the posttest answers were not influenced by concept map exposure.

**Evaluation of Student Assessment of Learning Gains (SALG) survey results.** At the end of the fall 2005 semester, students were asked to complete a Likert survey to describe their perceptions of whether or not the Biology 101 PLTL discussion group program enhanced the development of their conceptual reasoning skills. The results from the four most pertinent survey questions are depicted in Table 1. Of the 97 students that took the survey, 65% of them strongly agreed or agreed that the discussion group program helped them to understand the main concepts in Biology 101 and the relationships between those concepts. Sixty-four percent of the students strongly agreed or agreed that the program made them feel more comfortable with the complex ideas presented to them. Finally, 52% of the students strongly agreed or agreed that the discussion group program helped them to make gains in their ability to logically and sequentially think through problems or arguments addressed during Biology 101. The student responses to the survey questions indicate that, overall, the students found the discussion group program beneficial and that it helped them to improve their conceptual reasoning skills.

**Evaluation of student performance on quizzes, lecture exams, and cumulative final exams and comparison of average final course grades.** Throughout the fall 2005 semester, several methods were used to evaluate student performance in the Biology 101 course. The students were responsible for taking four pop lecture quizzes with questions based on materials from the discussion group modules, three lecture examinations, and one cumulative final examination.

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**FIG. 2.** Representative examples of student-prepared concept maps in response to the (A and B) pretest question and (C and D) posttest question.
All of the questions on the lecture and final examinations were multiple choice. On the lecture examinations, 50% of the questions were knowledge retention questions and 50% assessed the conceptual reasoning skills of the students. Although the questions on the lecture examinations varied from year to year, the questions on the final examination are identical every year. The final examination included only knowledge retention questions.

Students were permitted to work in groups to answer the questions on the pop lecture quizzes. This enabled them to discuss answers with their peers in an active fashion that highlighted different learning styles and thinking processes. The average quiz grades, as expected, were high and increased as the semester progressed (89%, 94%, 97%, and 100%, respectively). Student performance on lecture examinations and cumulative final examinations and final grades is depicted in Table 2. During the fall 2005 semester, student examination grades increased as the semester progressed (66%, 66%, and 71.2%, respectively). In contrast, during the fall 2004 semester, as the course progressed and the concepts covered became more difficult, examination grades decreased (85%, 72.5%, 74%, and 63%, respectively). The questions on the fall 2004 lecture examinations were all knowledge retention questions. On the cumulative lecture final examination, students in the fall 2005 course received an average grade of 74% while those in the fall 2004 course received an average grade of 66% ($P = 0.0003$). This shows an 8% increase in the average final examination grade for the fall 2005 semester compared to fall 2004. Finally, the average final grade in the fall 2004 course was 69%, while in the fall 2005 course it was 75% ($P = 0.004$). This represents a final grade increase of 6% for the fall 2005 semester compared to fall 2004. Taken together, these data demonstrate that the Biology 101 PLTL discussion group program did indeed impact the students’ performance on their quizzes, examinations, and overall (as evidenced by their final grades) in a positive fashion.

**DISCUSSION**

The goal of these studies was to demonstrate that the Biology 101 PLTL discussion group program would improve introductory biology students’ conceptual reasoning skills. The development of conceptual reasoning skills is essential for undergraduate science majors in order for them to be successful in their given fields (11). These skills aid in the ability of individuals to understand concepts and see the connections between those concepts. This in turn, enables individuals to logically and sequentially address problems and arguments in their discipline. The data obtained from these studies strongly suggest that the Biology 101 PLTL discussion group program does indeed enhance the conceptual reasoning skills of students enrolled in the course.

The pre- and posttest results demonstrated that the students improved in their ability to make connections between different concepts. These gains were shown by the 11.5% increase in the number of students that answered the question using a concept map on the posttest versus the pretest (Fig. 1). The shift detected in the number of students that answered the question with a concept map reflects an increase in the ability of the students to make connections between terms in ways that are similar to how experts work (4). According to the literature, expert knowledge is organized around important ideas or concepts. Experts have a thorough knowledge of their discipline and can use that knowledge to aid them with conceptual reasoning in response to questions such as the one posed on the pre- and posttests (4). Additionally, Rebich and Gautier (18) demonstrated that pre- and posttest concept maps enabled them to detect increases in students’ conceptual reasoning skills. They reasoned that the metacognitive reflection required for concept mapping enabled their students to better demonstrate the relationships between terms and enhanced their learning. The students that used a concept map to answer the pre- and posttest questions in Biology 101 responded in an expert-like fashion suggesting that the discussion group program enabled them to better develop their conceptual reasoning skills.

The student comments, as determined by the SALG Likert survey, clearly indicated that the students felt that they benefited from the discussion group program. The students felt very strongly that the program enabled them to better understand the concepts introduced in Biology 101. They also concurred that the discussion group program helped them to make connections between the different concepts in the course. This is supported by the increase in the number of students that used concept maps to answer the posttest question. The survey also indicated that the discussion group program made the students feel more comfortable with the materials covered in the course. As suggested by the Learning Pyramid (http://www.nltl.org), retention of course materials is enhanced by 50% upon the addition of a discussion group program to a course. It is logical to assume that one of the reasons for the increase in retention rates upon addition of a discussion group is that the materials covered in the lecture are repeated in the discussion group. Repetition of new and complex materials increases student comfort when they are asked questions about the materials. Finally, according to the survey, the students felt that the PLTL discussion group program helped them to make gains in their abilities to answer questions more logically and sequentially than prior to taking the course. This indicates that the students felt they had grasped the concepts presented to them in the course and were comfortable enough to use the knowledge they had obtained to logically reason answers to questions posed to them about the subject matter.

The enhancement of the students’ abilities to make connections between the different topics covered in the course enabled them to perform better overall as indicated by the increase in the fall 2005 Biology 101 student grades. The average grades that the students received on the pop lecture quizzes and lecture examinations increased as the fall 2005 semester progressed (Table 2). In contrast, during the fall 2004 semester, the average lecture examination grades decreased as the semester progressed (Table 2)—even though the types of questions (knowledge retention) on the fall 2004 lecture examinations were less challenging than the types of
questions (knowledge retention and conceptual reasoning) on the fall 2005 lecture examinations. Upon comparison of the average cumulative final examination and average final grades between the fall 2004 and fall 2005 semesters, it was determined that students in the fall 2005 semester did significantly better on an identical cumulative final examination and received significantly higher final grades (Table 2). Students in the fall 2004 course did participate in the discussion group program, but they did not receive quizzes in lecture with questions reflecting the modules and the lecture exams only contained knowledge retention questions. No connection was made between the modules and the tools used to assess student performance in fall 2004. Taken together, the performance of the fall 2005 students on their quizzes, examinations, and final grades indicates that the enhancement of the students’ conceptual reasoning skills due to the discussion group program did enable the students to achieve higher grades compared to those in the fall 2004 course.

The Biology 101 PLTL discussion group program was designed to engage the students in a small group setting. The modules developed for the program require active participation, highlight the process required to answer problem sets, and aim to develop strong critical thinking skills. The results from this study strongly indicate that the discussion group program implemented for the Biology 101 course at Pace University—New York City does enhance the conceptual reasoning skills and overall performance of the students enrolled in the course.

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Comparison of Online and Onsite Bioinformatics Instruction for a Fully Online Bioinformatics Master’s Program

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The completely online Master of Science in Bioinformatics program differs from the onsite program only in the mode of content delivery. Analysis of student satisfaction indicates no statistically significant difference between most online and onsite student responses, however, online and onsite students do differ significantly in their responses to a few questions on the course evaluation queries. Analysis of student exam performance using three assessments indicates that there was no significant difference in grades earned by students in online and onsite courses. These results suggest that our model for online bioinformatics education provides students with a rigorous course of study that is comparable to onsite course instruction and possibly provides a more rigorous course load and more opportunities for participation.

Bioinformatics combines the disciplines of computer science, bioscience, and information technology for the purpose of storing and retrieving biological data and for discovery of novel biological relationships or associations. The Master of Science in Bioinformatics degree, a joint offering of Johns Hopkins University, Krieger School of Arts and Sciences, and Whiting School of Engineering, provides students pursuing a career in bioinformatics with a specialized course of study that emphasizes advanced topics in computational biology. This eleven course program, available online and onsite, includes science courses such as Molecular Biology and Gene Organization and Expression, and computer science courses such as Foundations of Algorithms and Databases and bioinformatics courses such as BioPerl and Protein Bioinformatics (Fig. 1). The Department of Education recently reported that 84% of students are nontraditional learners (9) and thus will require a more flexible classroom. The completely online format of the program is designed to allow working professionals access to the program and an opportunity to pursue a graduate degree in bioinformatics while maintaining rigorous academic standards. Bioinformatics, at the cross-roads of bioscience and computer science, is particularly suited to the online format as much of the analysis is completed in the digital environment (11).

The online program was designed in 2005 to reproduce in as many aspects as possible the onsite courses. In preparation for online delivery, the program’s online courses are first taught three times onsite by the instructor before the course content is converted and taught in the online format. Thus, the instructor has determined the content necessary for a comprehensive course and the appropriate assessments of student competence before proceeding with online instruction. The course management system WebCT is used for online instruction with a model of content delivery containing at least four main components: streaming video or web conferencing software (Elluminate, Inc.), narrated PowerPoint, asynchronous threaded discussions, and access to multiple online resources. Each content delivery component allows the students and instructor to become connected and engaged in the class by visual, auditory, or text-driven interactions.

Streaming video introductions and summaries are effective means to deliver content and provide context. In addition, video allows the student to see the instructor present material as if it were an onsite course and to replay the video for analysis and review. Elluminate, a delivery system that has voice and video capabilities, permits both real time and archived delivery of instructor-generated material, so students can access introductions and summaries at a later time. Narrated PowerPoint is a method whereby the instructor can explain the content of a PowerPoint slide set as the student reviews the material. The student learns through both auditory and visual modalities to better reinforce the concepts of the lesson. Several authors (7, 10, 12) have reported that interaction with faculty and other students online is one of the most important components for a successful class. Our model provides connection through the threaded discussion, e-mail, and chat rooms. The threaded discussion is the primary vehicle for class and instructor interaction. This asynchronous discussion occurs several times during a week of instruction and allows the class and instructor to discuss the week’s topics in detail. Students are required to post three to four substantial contributions to the threaded discussion in each unit. Many instructors use the informal meeting places in the courses’ online chat rooms, referred to as “coffee houses” or “the water cooler,” to continue networking outside of the threaded discussion without the pressure of assessment, which is essential to establishing a sense of community in the distance education environment. Collaboration is an important learning tool and critical in the online environment (3). All of our courses include group projects to foster interactive learning.

Optimally, online education differs from traditional classroom education only in its delivery, not in the content...
or interactions among students and with faculty. The challenge for online education is to ensure that course content and student interactions online are comparable to the onsite environment. Master’s degree programs are second only to associates degree programs in online offerings (2). Few fully online graduate programs have been evaluated for student success and satisfaction and no fully online bioinformatics program has been analyzed. Kearsley reported on the Masters of Engineering in Professional Practice program, a fully online program at the University of Wisconsin (5). Analysis of student satisfaction indices revealed that students found the fully online experience academically rewarding and that it contributed to professional development. Analysis of the S-Star bioinformatics course, a fully online bioinformatics course established by the S-Star group, indicated that students were satisfied with their online experience and would take another online course (6). Stansfield, McClellan, and Connolly reported on two Master’s degree programs, Management of eBusiness and IT with Web Technology (8). Their analysis of student performance on exams in courses taught face-to-face and online showed that students in online sections did better than their counterparts in the face-to-face classes. Ali and Elfessi (2) undertook a study to examine graduate and undergraduate student attitudes and performance in an educational media and technology class. They reported no significant difference in attitude or performance whether the class was online or face-to-face. The data indicates that in most cases online education is at least comparable and may be better than face-to-face training.

Each online program uses different elements for delivery of content and interaction, which will affect the outcome of these studies. To evaluate the success of the Johns Hopkins University online program and its model for online education, we have compared student course evaluations and exam performance for courses in the online and onsite bioinformatics program. Analysis of one course, Gene Organization and Expression, taught online and onsite during the spring semester 2005 indicated that students’ performance on the midterm exam was not statistically different. Thirteen students in the online course and 23 students in the onsite course completed the exam. The average grade for the online course was 86% (range: 67 to 98.5%). The average grade for the onsite course was 88% (range: 67 to 99.5%). In this study we examined student satisfaction with bioinformatics courses online and onsite and analyzed student success in a course taught online and onsite.

**METHODS**

Student satisfaction was assessed online and onsite using a standard questionnaire administered at the end of the course. The evaluation instrument measures 17 areas that assess student responses to both the course structure and instructor performance. In this study, only six questions were evaluated. The evaluation instrument asks students to respond to statements with any of the following responses: strongly agree, agree, neutral, disagree, or strongly disagree (Fig. 2). Students complete the evaluation instrument on the last night of class onsite or when the last unit opens online. The data pertaining to course structure for three online (n = 79) and four onsite courses (n = 261) was collected, combined,
and analyzed. Biochemistry and Molecular Biology, prerequisite and core courses in our bioinformatics program were analyzed. To determine if there was a significant difference, student responses were subjected to a chi-square analysis. We assigned the responses to two categories, “agree” which included “strongly agree” and “agree,” and “other,” which included “neutral,” “disagree,” and “strongly disagree” responses. A two-by-two chi-square analysis was performed for each of the following statements: “The course was taught at a level I expected,” “I learned a great deal from the course,” “Assignments were an effective way to learn the material,” “Instructor encouraged participation,” “The work load was rigorous,” and “I would recommend this course.” Student responses to these six questions were evaluated because they would provide information on interactivity, content delivery, and overall satisfaction. The same survey instrument was used in the onsite and online classes to eliminate any bias that might be introduced using separate surveys.

Student performance was analyzed by comparing the assessment grades for a quiz, midterm exam, and final exam for students enrolled in Gene Organization and Expression (spring 2006) either online or onsite from the same instruc-
tor with exactly the same content and assessment tools. This course is representative of the type of courses offered in the bioinformatics program as the content delivery mode of this online course is similar, incorporating the elements of asynchronous discussion, group work, and both timed and take-home assessments. In addition, as the same instructor taught both online and onsite sections at the same time, we were able to eliminate variability due to different instructors or to the semester the course was offered. The students self-selected whether they took the course online or onsite. The quiz assessment was a timed quiz; the midterm and final exams were “take-home” essay exams. The course grades were analyzed by two-way $t$ test using Origin75 software (Origin Corp).

RESULTS
We compared student satisfaction with online and onsite instruction using the standardized survey instrument in Fig. 2. Holcom, King, and Brown reported that the student population they surveyed believed that the traditional course evaluation used by the University was appropriate for Web-based courses (4). As seen in Fig. 3, students were at least as satisfied with the online courses as their counterparts were with onsite courses. In general, students were highly satisfied with their academic experience whether they took the course online or onsite. Over 75% of students reported that the course was taught at the expected level, they learned a great deal, assignments were an effective way to learn the material, the instructor encouraged participation, the work load was rigorous, and they would recommend this course. Further investigation of the data by chi-square analysis indicated that there was no significant difference in the responses given by online and onsite students to “The course was taught at a level I expected,” “I learned a great deal from the course,” and “I would recommend this course.” However, there was a significant difference for the student responses to the questions, “Instructor encouraged participation” ($P < 0.001$) and “The workload was rigorous” ($P < 0.05$). More online students tended to agree with the statement “assignments were an effective way to learn the material” than onsite students, but the difference was not significant.

We investigated whether online and onsite students achieve

![Graph](image-url)

**FIG. 3.** Comparison of online and onsite student responses. The data represent the percentage of students who agreed with the statements, “The course was taught at a level I expected,” “I learned a great deal from the course,” “Assignments were an effective way to learn the material,” “Instructor encouraged participation,” “The work load was rigorous,” and “I would recommend this course.”
or learn at the same level by analyzing exam data from the course Gene Organization and Expression taught onsite and online. The course was taught by the same instructor with the same content in the same semester (spring 2006). The data from assessments—quiz 1, midterm examination, and final exam—were compared by a two-tailed $t$ test. Quiz 1 was a timed test; the midterm and final were take-home exams for both online and onsite courses. Analysis of the data (Table 1) showed that for all three assessments, there was no significant difference between the grades received by the onsite and online students.

**DISCUSSION**

The completely online Master of Science in Bioinformatics program differs from the onsite program only in the delivery of content. Several mechanisms are required to assure comparable quality between onsite and online courses, such as the courses are taught by the instructor onsite three times prior to online development, the use of standard assessments for courses online and onsite, and collection of student satisfaction data. The online courses are designed for interaction between faculty and students through the threaded discussion and include streaming video and narrated PowerPoint so that students may learn through both visual and auditory modalities.

Analysis of the results indicated a statistically significant difference for the metrics “the course load was rigorous” and “the instructor encouraged participation.” While our hypothesis was that there is no difference in student satisfaction with online or onsite courses, we found online students were more likely to find the course rigorous and to report that the instructor encouraged participation. The data indicate that the online environment is challenging and highly interactive. In addition, online students tended to respond more positively as compared to onsite students to the statement, “assignments are an effective way to learn the course material.” Collection of additional data may elucidate whether this result has true significance. Analysis of student performance in the online and onsite sections of Gene Organization and Expression, a representative bioinformatics class, using three assessments indicated that there was no significant difference in grades earned by students in online and onsite courses. This result agrees with preliminary data collected in spring 2005 from the same course for the midterm exam. These results suggest that our model for online bioinformatics education provides students with a rigorous course of study that is comparable to onsite course instruction, and that online course assignments may be more beneficial to student learning; however, a longitudinal study assessing long-term recall and employer satisfaction with graduates of the program would be informative. One can surmise from this result that students are engaged with the course material in novel ways using technology to enhance the learning process. To better understand the factors which affect this outcome, we plan to track and analyze student work across course management functions and in other classes to better assess how students engage with course content in the online environment.

This project was reviewed by the Johns Hopkins University Homewood Institutional Review Board.

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Learning Geomicrobiology as a Team Using Microbial Mats, a Multidisciplinary Approach

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Microbial mats are one of the best suited laminar organo-sedimentary ecosystems for students from different educational backgrounds to visualize the direct relationship between microbes and minerals. We have used tropical hypersaline microbial mats from Puerto Rico as educational tools to promote active learning of geomicrobiology introductory concepts for undergraduate students organized in multidisciplinary teams with biological and geological backgrounds. Besides field trips and independent research projects focused on microbial mats, four intensive workshops and one capstone activity were designed to expose students to the different geomicrobiology subdisciplines (microbiology, molecular biology, geology, and geochemistry). The teaching-learning process was assessed using pre- and posttests, group discussions, activities including Gallery Walks and exquisite cadaver’s, case studies, and focal interviews. While the posttest showed a significant difference in conceptual understanding, the Gallery Walk and the capstone activities demonstrated an increase in the depth, coherence, and thoughtfulness in answering questions, including a clear integration of the different subdisciplines during their presentations. Finally, the main themes described by the students as important outcomes of their participation in the Research at Undergraduate Institutions: Microbial Observatory (RUI-MO) program were: (i) the opportunity to study and learn new and different science disciplines, (ii) the microbial mats were excellent tools to learn from and integrate different science disciplines, and (iii) working in multidisciplinary teams gave them the opportunity to learn from their peers’ discipline backgrounds. To our knowledge this is the first educational initiative that uses tropical hypersaline microbial mats to teach geomicrobiology in a multidisciplinary fashion.

Geomicrobiology focuses on the role of microorganisms in the geological transformations that take place at the interface of Earth’s biosphere and lithosphere in space and time (5). Specific transformations in which microorganisms serve as mediators of geological processes include: alteration of geochemical microenvironments through redox reactions (e.g., using \( O_2 \) and producing \( H_2S \)), precipitation and dissolution of minerals (e.g., the \( CaCO_3 \) deposits), and solubilization and dispersion of insoluble metals (e.g., \( Fe(III) \)-oxide reduction) (7, 12). Microbes also produce biomass and exopolymeric substances (EPS) that help stabilize sediments (12). Production of EPS is particularly important in the cyanobacteria-dominated biofilms that we commonly refer to as “microbial mats.” These organosedimentary structures are not only considered analogs of the oldest (2) but also the most productive ecosystems on Earth (9).

Microbial mats are indeed the quintessential systems for important geomicrobiological studies (2, 9, 12). As these studies are based on interactions of microorganisms and their geochemical environment through the Earth’s history, investigations in geomicrobiology span vast temporal and spatial scales. It is indispensable that students introduced to this emerging field first understand the specific physicochemical conditions of the ecosystem (such as light and nutrient availability, temperature, \( pH \) and oxygen content, and sediment composition). Only when students fully understand the range of these environmental conditions, can they identify the role of the microbial component and its potential to alter, precipitate, dissolve, and accrete the different minerals. Studies in geomicrobiology are interdisciplinary in nature and students need to learn how to work as part of a multidisciplinary team. Indeed that is the main educational goal of our work, to use mats as tools to promote active and effective learning of basic concepts in geomicrobiology within a multidisciplinary team. If our students are able to visualize the link between the geochemical and biological components of a microbial mat, then they will be able to use the mats as a tool to conduct a successful multidisciplinary study with peers from other disciplines. This strategy of team work using a multidisciplinary approach has been recommended by the National Research Council (NRC) as one of the main priorities in the new educational reforms at the undergraduate level (11).

To promote the interaction of our students, we assembled a series of multidisciplinary teams that were requested to perform a series of activities. These activities ranged from traditional (i.e., participation in workshops and oral presentations) to nontraditional such as field approaches to one specific site in Puerto Rico named Cabo Rojo. This location contains various types of interesting microorganisms as well as microbial mats (3, 4). Students

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comprising the multidisciplinary teams were requested to investigate these ecosystems by conducting extensive microbiological, geochemical, and geological analysis of them using the main strengths of each member of the team.

**Description of the program.** One of the main goals of the Cabo Rojo Salterns (CRS) NSF-sponsored Research at Undergraduate Institutions (RUI): Microbial Observatory (MO) program is the training of undergraduate students in geomicrobiology (http://www1.uprh.edu/salterns/). For four consecutive years we have used the microbial mats from these salterns as a “living” laboratory. Undergraduate students from the biology and geology programs of the University of Puerto Rico (UPR) and Turabo University (TU) have interacted here to understand basic concepts of geomicrobiology. One of the main strengths of the program is the collaboration with the geosciences and marine sciences programs of the University of Connecticut through which our students interact with faculty and graduate students during two field trips each year. The rest of the academic year, our undergraduate students perform a series of individual research projects in their main universities until they receive their degree. Most students enter into a graduate program and pursue a master or doctoral degree in different fields of the biological sciences.

**METHODOLOGY**

Fourteen students from the Biology departments of the UPR-Humacao, Mayagüez, Bayamón, as well as from TU, and the Geology department of the UPR-Mayagüez were trained in the field of geomicrobiology during academic year 2005-2006 under the CRS-RUI-MO program. Four multidisciplinary teams were formed, and it was imperative that each team included students from at least three different fields. The training consisted of four intensive workshops and one capstone activity designed to expose students to the different subdisciplines that span the geomicrobiology science field: microbiology, molecular biology, geology, and geochemistry. All these activities used the Cabo Rojo saltern tropical hypersaline (CRth) microbial mats as a central educational and research tool (Fig. 1 summarizes the activities and aims of the program).

**Geomicrobiology multidisciplinary workshops.**

**Workshop 1. Cultivation of microbial communities from the mats using general microbiology culture techniques.** During the first field trip the students received a 30-minute talk about general microbial physiology concepts and the influence of physicochemical parameters such as light, oxygen, and salinity on the growth of the different populations in the CRth-microbial mats (3). The main geomicrobiology subdiscipline question of this workshop was: “which specific microbial communities can be isolated from the CRth-microbial mats based on the environment where they are located?” After the talk, multidisciplinary teams were assigned to sample specific CRth-microbial mats and determine environmental physicochemical factors such as temperature, light, pH, as well as dissolve oxygen and nutrient contents. The teams were also responsible for dissecting and culturing CRth-microbial mat samples in petri plates using culture media with different salinities and pH. Some plates were incubated at different temperatures or put into an anaerobic jar (13). As the different organisms take time to grow, results from this workshop were presented at workshop 2.

**Workshop 2. Using molecular techniques for the identification of microbial groups in the CRth-microbial mats.** Our second workshop consisted of two intensive days where the students were first introduced to the organisms able to grow under such conditions and then received a short talk about DNA extraction methods, electrophoresis, restriction enzyme analysis, cloning, and PCR. In addition to introducing the general concepts of genetic engineering, the talks focused on how to apply those technologies and techniques in order to identify the nonculturable CRth-microbial communities. The main geomicrobiology subdiscipline question of this workshop was: “can we determine and/or detect specific microbial groups present in the different layers of the CRth-microbial mats using molecular techniques?” The students were organized into four multidisciplinary teams and received sections of the top (green) and bottom (black) layers from the CRth-microbial mats with a set of primers specific to cyanobacteria (8), archaea (7) and bacterial 16S rDNA (1). Each team was responsible for extracting DNA from the mats and determining the presence of members from the different groups in the distinct mat layers.

**Workshop 3. Mineral characterization in the organo-sedimentary layers of the CRth-microbial mats: their sources and genesis.** Teams of students were exposed to some of the minerals present in the mats, and how microorganisms play an important role in mineral formation (4, 5, 12). The main geomicrobiology subdiscipline question of this workshop was: “Are minerals present in the CRth-microbial mats the result of specific biological activities, binding and trapping of the mats, or other geological processes?” The workshop started with a 1-hour talk, then the students were able to manipulate different types of rocks and minerals commonly found in the CRth-microbial mats.

**Workshop 4. What is it that we need to know and how do we measure it? In situ geochemical assessment of geomicrobiological processes in the CRth-microbial mats.** In this workshop the teams were introduced to a holistic approach typical for an in situ geomicrobiological investigation. The concepts of coupled microbial populations, metabolic rates, and mineral products were introduced, and as a snapshot of the system, students learned to measure how the oxygen and sulfide profiles change across the different CRth-microbial mats (3, 12). The main geomicrobiological subdiscipline question of this workshop was: “Can oxygen and sulfide depth profiles help us assess the microbial communities and their activities in each layer of the CRth-microbial mats?” After learning how to operate the microelectrodes and conduct in situ analyses, each multidisciplinary team measured the geochemical gradients (including physicochemical conditions, pH, salinity, and light), constructed depth profiles of oxygen and sulfide for the various mats, and plotted and analyzed the data (14).
Geomicrobiology capstone activity—case studies: how to perform a geomicrobiological investigation in other microbial mats, putting it all together. After being introduced to many concepts basic to a geomicrobiology study ranging from molecular microbiology to geology, multidisciplinary teams were asked to do a specific case study. They had to formulate a project description for the following field sites: (i) microbial mats in the Dry Valleys, Antarctica, (ii) microbial mats in the Iron Mountain Mine, California, and, (iii) biofilms in the deep biosphere, ca. 400 m below the sediment surface, off the coast of Peru.

Each group of students was provided with an information sheet that included some useful facts about each study site including pictures, specific instructions, and main goals of the activity. In addition, colored markers and poster boards were given to each group to prepare their oral presentation. The main goal of the activity was for the groups to produce hypothesis-driven predictions about the relevant geochemical factors present in the environment and the microbial communities that could be present due to those factors. The students needed to describe strategies for successful enrichments of these microorganisms and how to analyze specific biogeochemical signatures expected to be present in the ecosystem. Students were assisted by the CRS-RUI-MO research investigators.

Assessment at the Microbial Observatory. Several assessment strategies were used to determine the student learning process during participation in the Microbial Observatory projects. All assessment measures were performed by both investigators associated with this project and the educational coordinator of the program. Assessment for the first and second workshops was conducted through a pre- and posttest, exquisite cadavers, and group discussions in which the students shared their knowledge about the organisms per
layer and their associated physiologies. A modified Gallery Walk was employed in the third workshop and in the fourth we used group discussions. A case study was used as the final approach to coherently measure integration of the knowledge acquired by students. In addition a focus group interview helped to explore the perception of the students regarding their learning process through the program.

Pre-and posttest. The tests were given to assess student’s knowledge and understanding about molecular ecology, particularly the molecular techniques needed for the identification of the most relevant microbial groups in the mats. The pre- and posttests were identical and consisted of 21 questions which included multiple-choice, matching, true-or-false, and short answer questions for a total of 29 points. For the true-or-false questions, students had to identify the word or phrase that made the false statements false. A paired t test was performed to compare student’s knowledge before (pretest) and after the workshop experience (posttest) and to determine any significant differences. The results are shown with box and whisker plots.

Exquisite cadaver. Exquisite cadaver, an educational tool, is a game in which students summarize their ideas about one specific topic. In our case, the general theme was microbial mats, and the students were organized in four multidisciplinary teams. Initially we requested that one student from each team write a sentence on whatever came to mind about one specific topic (e.g., Cabo Rojo mats). Once the student finished writing, he folded the paper and wrote the last word of his statement on a new space. The next student used this word to start a new sentence. After all the students on the team finished writing their sentences, the whole document was edited in order to make a paragraph. The final document is named the exquisite cadaver and shared with the others at the end of the activity. The exquisite cadaver is a collective of several sentences that are all linked by one main idea. The activity was derived from surrealistic painters and the technique they use to put different ideas into one specific work of art. Our students used this activity before and after workshop 2.

Individual versus group Gallery Walk. Gallery Walk is a discussion technique that promotes active engagement while students work in teams to synthesize information written from a variety of perspectives (6, http://serc.carleton.edu/introgeo/gallerywalk/index.html). We modified this technique by first asking our students four questions after workshop 3. Then, the multidisciplinary teams rotated around the conference room to answer the same questions, which were posted on pieces of paper located at different stations (6). Each group had 3 minutes to answer each question and after rotating through the different stations the students returned to their original station to write a summary. The activity ended with an informal oral report in which each group synthesized comments to the particular question assigned. All questions were framed according to Bloom’s hierarchy into knowledge, comprehension, and application (10). Answers given by students were compared with those given by the mentors according to their depth, coherence, and completeness.

Group discussion after generating the profiles. Once depth profiles for oxygen and sulfide from the CRth-microbial mats were generated, each multidisciplinary team gave an oral presentation to discuss their findings. Microbial Observatory mentors evaluated how the students related the knowledge obtained from the profiles that they generated with the microbial communities and their physiologies in the mats.

Geomicrobiology capstone activity: case studies. Two different strategies were used for the assessment of student learning through the case studies, after the oral presentations and construction of the posters. The first one measured the team performance based on a rubric (Table 1). The second was based on open-ended questions answered by the MO mentors and used to analyze and evaluate their perception of team integration of the workshops into geomicrobiology, and performance during the capstone activity.

Focus group. Upon completion of all MO workshops and activities, a focus group interview was held to collect and explore shared understanding from students about their views and learning process during participation in the program. One of the main objectives of the focus group was to determine the students’ perceptions upon completion of the different geomicrobiology multidisciplinary workshops. Five students participated in the focus group interview. All interviewees completed an informed consent form before beginning the interview. This consent form was approved by the University Development Office, Institutional Investigation Area, UPR-Humacao. The interview was organized and conducted by the educational coordinator of the Microbial Observatory.

RESULTS

Assessments of the Microbial Observatory workshops. Pre- and posttest and group discussion. There was a significant difference in conceptual understanding about the microbial community of the mats and the techniques to study them after student’s participation in the first workshops. Results from the pre- and posttest conducted during workshop 2- (paired student’s t test (9) = -6.48, p < .001) indicated a difference mean value of -11.3 and an increase in median values (of correct answers) from the 15th to the 25th percentile (Fig. 2).

Our exquisite cadaver activity also revealed an increase in students’ knowledge. Before the second workshop students were more oriented to microorganisms and the geologic content of the mats. The documents after the workshop were more oriented toward the molecular aspects of the mats (data not shown).

After completion of the workshop, the discussion of the interdisciplinary teams was evaluated using a rubric (not shown) with a scale from 1 (poor) to 3 (good) based on three criteria: (i) technique proficiency, (ii) relevance to the CRth-microbial mats, and (iii) overall presentation clarity. After their presentations, the average scores for the teams were 2.5, 2.5, 3.0 and 2.25. The global presentation average score was 2.6.

Individual versus team Gallery Walk. Each investigator compared the answers provided by the students once they went through the gallery individually and as a team. The
TABLE 1. Scoring rubric developed by the Microbial Observatories mentors to evaluate the performance of the students after their poster presentations of the case studies

<table>
<thead>
<tr>
<th>Components</th>
<th>Scoring criteria</th>
</tr>
</thead>
<tbody>
<tr>
<td>Knowledge</td>
<td>3: The concepts and principles used for the experimental design are appropriate to the study. The student’s response reflects thorough understanding.</td>
</tr>
<tr>
<td></td>
<td>2: The concepts and principles used for the experimental design are appropriate to the study with no significant errors.</td>
</tr>
<tr>
<td></td>
<td>1: The student explains the experimental design but misapplies some concepts or principles, or omits some facts that are important for understanding the study.</td>
</tr>
<tr>
<td>Scientific method</td>
<td>3: Use scientific method to pose the project’s hypothesis. The experimental design addresses all important questions raised by the prediction.</td>
</tr>
<tr>
<td></td>
<td>2: Use scientific method to pose the project’s hypothesis. The experimental design addresses the most important questions raised by the prediction.</td>
</tr>
<tr>
<td></td>
<td>1: Partially use scientific method to pose the project’s hypothesis. The experimental design addresses some important aspects of the prediction, but omits others.</td>
</tr>
<tr>
<td>Integration of different subdisciplines</td>
<td>3: The experimental approach to understand the field site is truly multidisciplinary.</td>
</tr>
<tr>
<td></td>
<td>2: The experimental approach to understand the field site crosses the disciplinary boundaries to some extent.</td>
</tr>
<tr>
<td></td>
<td>1: The experimental approach to understand the field site does not show a multidisciplinary character at all.</td>
</tr>
<tr>
<td>Creativity in the experimental design</td>
<td>3: The students present the information in a way that reflects creativity in the experimental design.</td>
</tr>
<tr>
<td></td>
<td>2: The students present the information accurately but with minimal creativity.</td>
</tr>
<tr>
<td></td>
<td>1: The students present the information with little or no originality.</td>
</tr>
<tr>
<td>Clarity of the presentation</td>
<td>3: Presentation is clear and to the point. Ideas and opinions are well prepared.</td>
</tr>
<tr>
<td></td>
<td>2: Presentation is somewhat clear. Some ideas and opinions need to be refined.</td>
</tr>
<tr>
<td></td>
<td>1: Presentation is not well organized. Thoughts and opinions are unclear.</td>
</tr>
</tbody>
</table>

CRS-RUI-MO research investigators detected an increase in the depth, coherence, and completeness of the answers given by the teams over those given by individuals. Such improvements were a direct result of the active discussions of the students on the team. Contrary to their individual assignments, students participating in the Gallery Walk were able to defend, exchange, and rethink their final answers. Improvement in the final answers provided was independent of the level of abstraction used (i.e., knowledge, comprehension or application). For example, for a knowledge-level question individual students were unable to discuss specific concepts, they just copied information from the written presentation. During the team Gallery Walk students not only mentioned specific concepts but were capable of discussing them. Similar results were reported in the comprehension-level question where students listed more reasons for their analysis; their answers were more coherent and thoughtful as teams. Also, when students were asked to apply the knowledge they had acquired, only during the team Gallery Walk were the relevant techniques required for mineralogy analyses and the detection of biogenesis in mat samples mentioned.

**Measuring and constructing geochemical depth profiles.** All teams measured and constructed vertical depth profiles for oxygen and sulfide from the CRth-microbial mats (3, 14). In order to accomplish this, the students were first taught the underlying electrochemical principles of microsensor construction and operation, then learned how microbiology affects geochemistry and that key biogeochemical characteristics of sediments can be determined by depth profiles of oxygen and sulfide (12, 14). All of the teams performed an abbreviated system calibration, measured the geochemical profiles, learned the major factors (microbiological compo-
sition, light, salinity, and temperature) that determine the oxygen and sulfide profiles, and converted the raw data into actual values. During the exercise, students were able to assess the key factors, including microbial and physicochemical characteristics of the mats. At the end of this workshop, the students could explain all of the observations, and also had a clear understanding of the significance of the geochemical snapshot in the context of the microbial mat functioning.

**Geomicrobiology capstone activity: case studies.** The oral presentations given by the students at the end of the capstone activity were summarized in three main posters. Each presentation consisted of a hypothesis, predictions, and tests needed to conduct a full geomicrobiology study in each location (Fig. 3). The individual team’s rubric global average scores (Table 1) after evaluation of the posters from each team ranged from 1.9 (63%) to 2.66 (89%). The results obtained globally by category indicated that the highest scores were given to the integration of the different subdisciplines (89%) and the lowest to the knowledge (74%).

Based on the second assessment strategy, the overall perception of the MO mentors was that the multidisciplinary teams worked well, as evidenced by the quality of their poster presentations. Each team member contributed information and insights from his area of specialization while at the same time understanding enough of the basics from the fields outside of theirs.

**Focus group.** During the focus group, students shared their experiences as participants of the CRS-RUI-MO program. From the six brief open-ended interview questions, three emerging themes were related to learning a multidisciplinary discipline, geomicrobiology, as they work in multidisciplinary teams: (i) the CRS-RUI-MO program gave the opportunity to study and learn new and different science disciplines, (ii) the microbial mats were excellent tools to learn from and integrate different science disciplines, and (iii) working in multidisciplinary teams provided an opportunity to learn from their peers.

**DISCUSSION**

We have presented evidence that microbial mats are excellent educational tools that can be used by multidisciplinary teams of students from biology and geology backgrounds to learn more of the geomicrobiology field. A series of teaching and learning strategies were assembled using these mats as the central piece. Initially we took advantage of the incredible microbial diversity within these productive ecosystems to teach the students how to grow organisms from the mats by placing them under different growth conditions. Once the students understood how to culture some of the communities from the mats, we taught them how they are able to determine the identity of cultivatable and noncultivatable organisms by generating genomic libraries using group-specific primers.
### Study case 2: Microbial Mats in the Iron Mountain Mine, California

<table>
<thead>
<tr>
<th>Observations of the study site</th>
<th>Hypothesis</th>
</tr>
</thead>
<tbody>
<tr>
<td>• Metal minerals: Iron, silver, gold copper, zinc, pyrite</td>
<td>Due to the great quantity of metal minerals the soil and water are very acidic. We suspect that pyrite may be the mineral involved in cellular respiration of these microbes.</td>
</tr>
<tr>
<td>• Underground mine, no sunlight and extreme temperatures</td>
<td>FeS = Fe^{2+} + SO^{2-}</td>
</tr>
<tr>
<td>• Fracture of the (mine) mountain due to mining activity, exposing minerals to surface water, rain water and oxygen</td>
<td>S^{2-} + 2O_2^{-} SO_4^{2-}</td>
</tr>
<tr>
<td>• Microbes live hundreds of feet underground (no sunlight, scarce nutrients)</td>
<td>H_2 SO_4 (this product is responsible for the acidic pH of the soil)</td>
</tr>
<tr>
<td>• Microbes don’t survive outside the mine</td>
<td>The product of cellular respiration could be responsible for mine erosion.</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Predictions</th>
<th>Tests</th>
</tr>
</thead>
<tbody>
<tr>
<td>• If this environment is acidic, we expect to find acidophilic microorganism</td>
<td>• Measure physicochemical parameters:</td>
</tr>
<tr>
<td>• If pyrite and Fe^+ are involved in cellular respiration this explains why this environment is acidic</td>
<td>- Temperature and pH</td>
</tr>
<tr>
<td>• If the product of cellular respiration contribute to erode the mine, then pyrite (Fe_2SO_4) is essential for these microbes</td>
<td>- Dissolve oxygen (mass spectrometer)</td>
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</tbody>
</table>

#### Predictions
- If this environment is acidic, we expect to find acidophilic microorganism
- If pyrite and Fe^+ are involved in cellular respiration this explains why this environment is acidic
- If the product of cellular respiration contribute to erode the mine, then pyrite (Fe_2SO_4) is essential for these microbes

#### Tests
- Measure physicochemical parameters:
  - Temperature and pH
  - Dissolve oxygen (mass spectrometer)
  - Dissolve sulfate
- FAME (MIDI)
- Molecular analysis:
  - DNA extractions
  - PCR
  - Co-enzyme analysis
- Electronic microscopy
- X-ray diffraction
- Electron microprobe

FIG. 3. Schematic of the poster presentation for case study 2 in which a multidisciplinary team described the communities and biogeochemical signatures expected from the microbial mats present in the Iron Mountain Mine, California. As assigned on the information sheet, the team divided their presentation into observations at the site, hypothesis, predictions, and tests to be conducted to prove the hypothesis.

The importance of the mats as platforms for several geological transformations was addressed in the third workshop. The students were exposed to the main techniques used by geologists to determine the biogenicity of specific minerals in sediments, such as the ones surrounding the Cabo Rojo salterns, and their implications not only in the formation of the early Earth but also in the possibility of extraterrestrial life. These enticing topics served to captivate the students who at the end of the talk manipulated some of the most abundant minerals on the planet. However, one of our most interactive learning techniques was the generation of oxygen profiles by the students. Each student was in charge of taking in situ measurements of the oxygen content within the mats at different depths. Once they assembled all the data needed, students generated their own profiles and gave an oral presentation describing their findings. A final capstone activity challenged the students to assemble all of their acquired knowledge and provide hypothesis-driven proposals for how the metabolisms associated with the microorganisms in the location and how to analyze them in order to gain more knowledge about the environment. Students had to apply what they already knew about the Cabo Rojo ecosystem and the microbial mats, which environmental conditions, organisms, climate, seasons, day/night, etc., play a role to understand the field sites assigned to work on and then formulate their project description. The students were motivated by the different investigators to mentally revisit previously performed experiments and the workshop taken at the observatory, and based on the knowledge acquired through the CRth-microbial mats, use them as dissecting tools to critically analyze and understand the given environmental system. The effectiveness of this activity was also evident and sustained by the fact that the teams communicated ideas related to the different subdisciplines that comprise geomicrobiology (molecular science, microbiology, geology, etc.) in terms that both their peers and research investigators understood.

According to our qualitative and quantitative data, the students were able to understand the CRth-microbial mat...
system and integrate the knowledge from the different sub-discipline perspectives. The improvement observed in the posttest and team discussion scores, and the generation of coherent answers at the Gallery Walk proves their acquisition of knowledge and skills development during the workshops. Also, the students were able to verbalize during the focus group interview how important the mats were as an integrative ecological system and as an educational tool. Some of the main facts described by the students after these pedagogical activities included the relevance of the CRH-microbial mats as a tool to understand microbial diversity and the importance of team work.

Promotion of discussion among students from different disciplines was indeed a main goal of our study. To specifically determine how group discussions were linked to a meaningful learning of the multidisciplinary teams, we compared the answers provided by individual students and groups during a Gallery Walk activity. As previously reported, this technique promoted discussion among the students who were then able to provide more complete and coherent answers. To our knowledge this is the first time the technique was applied to discuss topics related to the geomicrobiology field.

The ultimate goal of our program was to expose our students to novel educational challenges as future professional alternatives by exploring emerging disciplines such as geomicrobiology. Although such statistics are beyond the goals of this publication, we currently have five former students of our program that are pursuing a graduate degree in geomicrobiology. In addition we have offered the first undergraduate course in topics of geomicrobiology within Puerto Rico. Both indicators of the success of the CRS-RUI-MO program have in common a single location: the Cabo Rojo tropical hypersaline microbial mats.

ACKNOWLEDGMENTS

We would like to thank the Educational Coordinator of the MO program Beatriz Hernandez, M.S. and other MO mentors including Dr. Sharon Cantrell and Jose Perez from Turabo University and Dr. Wilson Ramirez from the Geology Department for their help during the field trips and the assessment of various educational activities. We also thank Prof. Carlos Olivo for his valuable comments during the manuscript preparation, the Minority Access to Research Careers (MARC) and Advance Institutional Transformation (AIT) programs for the UPR-Mayagüez for partial funding and coordination of some of our activities. This work was supported by a Research at Undergraduate Institutions: Microbial Observatory grant MCB-0455620 from the National Science Foundation.

REFERENCES


Annual Biomedical Research Conference for Minority Students

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KEYNOTE SPEAKERS
Opening Session - Delorese Ambrose, Ed.D. (Ambrose Consulting)
Luncheon Keynote - Tavis Smiley, B.A. (Radio and TV Commentator/Writer)

PLENARY SCIENTIFIC SESSION SPEAKERS
James Hildreth, Ph.D. (Meharry Medical School)
Elba Serrano, Ph.D. (New Mexico State University)
Robert Shaler, Ph.D. (Pennsylvania State University)
S. Allen Counter, D.M.Sc., Ph.D. (Harvard University)

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