Cell Biology Education
Vol. 1, 70–72, Fall 2002

Meeting Report: Genomics in the Undergraduate Curriculum—Rocket Science or Basic Science?

A. Malcolm Campbell

Biology Department, Davidson College, Davidson, North Carolina 28035

Submitted June 5, 2002; Revised June 18, 2002; Accepted June 20, 2002

At the 102nd annual meeting of the American Society for Microbiology (ASM) in Salt Lake City, Utah, members of the Genome Consortium for Active Teaching (GCAT; http://www.bio.davidson.edu/GCAT/) and faculty from around the world gathered to discuss educational genomics (http://www.bio.davidson.edu/people/macampbell/ASM/ASM.html). The focus of the gathering was a series of presentations by faculty who have successfully incorporated genomics and bioinformatics into their teaching of undergraduates. The presentations described genomics in both laboratory courses and student independent research projects.

The session began with an overview of GCAT and DNA microarray methodology (http://www.bio.davidson.edu/Courses/genomics/chip/chip.html). The first speaker was Myra Derbyshire from Mount Saint Mary's College, Emmitsburg, Maryland (http://www.msmary.edu/college/html/undergraduate/science/sciencefaculty.htm). Her presentation described 2 yr of student-based research using *Escherichia coli* and *Saccharomyces cerevisiae*. Thirty-three students conducted their research in two settings during a 2-yr period. Some of Derbyshire's students performed their research in a genetics course while other students became involved in her ongoing research program. The focus of Derbyshire's research is to understand the mechanism of transcriptional silencing and specifically the roles of yeast gene *SIR2* and its *E. coli* ortholog *cobB*. Students used bioinformatic tools to identify functionally related genes and created null mutants by using molecular and genetic techniques. The final project was to measure genome-wide gene activity of both species by using DNA microarrays distributed through GCAT and printed by Fred Blattner's lab at the University of Wisconsin–Madison (http://www.genome.wisc.edu/) and Lee Hood's group at the Institute for Systems Biology in Seattle, Washington (http://systemsbiology.org/research/core_fac/microarrays.html). During the intervening summer, Derbyshire worked with some students at the National Cancer Institute in Frederick, Maryland (http://web.ncifcrf.gov:8080/research/grcbl). She surveyed her genetics and research students' reactions to their experiences in the lab and received the following feedback:

DOI: 10.1187/cbe.02-06-0014
Corresponding author. E-mail address: macampbell@davidson.edu.

- "I am working on protein structure predictions algorithms . . . very neat stuff!" (former student pursuing a Ph.D. in bioinformatics)
- "Thank you again for the wonderful opportunity and experience you afforded me in genetics class." (former student who is enrolled in a cellular and molecular medicine graduate program)
- "Thank you for everything you have given and taught me. I carry it with me all the time." (former student currently pursuing a master's degree in bioscience and technology)

Like Derbyshire, the second speaker, Todd Eckdahl from Missouri Western State College, Saint Joseph, Missouri (http://griffon.mwsc.edu/~eckdahl/), summarized his work in two undergraduate laboratory courses in which both yeast and *E. coli* DNA microarrays were used. The students included majors in biochemistry and molecular biology, biology–health sciences, and biology secondary education. Eckdahl wanted students to understand the scope and larger context of genome sequences, functional genomics, and proteomics. He wanted students to become familiar with the data-rich science of functional genomics through exposure to the primary literature and first-hand experiences. Working with class sizes of as many as 20 students and 3-h weekly laboratory periods made the adaptation of experimental protocols challenging. Included at the beginning of the schedule was time for students to discuss ideas before they chose a class research project and designed experiments.

For their yeast work, Eckdahl's students chose to measure the consequence of the minor groove DNA-binding compound DAPI (4′,6-diamidino-2-phenylindole) on gene expression. Student projects using *E. coli* were designed to compare a wild-type strain with mutants in which one of two different genes for putative transcription factors was deleted. Eckdahl's presentation provided a substantial amount of experimental detail as he outlined the different components of DNA microarray experiments performed: cDNA versus oligo DNA microarrays, isolation and characterization of RNA, two methods of probe production, and a range of control spots on each DNA microarray. Emphasis was placed on the use of controls to troubleshoot procedures and assess data reliability. DNA microarray control spots included some that were duplicated or contained poly-A DNA, DNA from introns, DNA encoding tRNA, noncoding genomic DNA, or no DNA. Experimental controls included reversal of dyes for probe production and replication of RNA isolation. Like

Derbyshire, Eckdahl reported that data analysis proved to be the most difficult aspect for his students. Student representatives from each of his two courses and students who pursued independent projects using microarrays presented their findings at the Missouri Academy of Science, Tri-Beta district and national conventions, the American Chemical Society (ACS) national meeting, and the National Conferences on Undergraduate Research (NCUR).

The third speaker offered a different view of educational genomics. Jeff Newman from Lycoming College, Williamsport, Pennsylvania (http://srv2.lycoming.edu/~newman/), explained his multi-year efforts to bring molecular, genomic, proteomic, and bioinformatic methods to all levels of the biology curriculum. He started by explaining the use of DNA sequence analysis as a tool for beginning students to formulate hypotheses for subsequent testing in the laboratory and finished with his use of DNA microarrays. He discussed in detail the context for incorporating genomics into the classroom in several courses. Newman described the results from a 2-yr assessment of the impact of his curriculum innovations. He devised a clever strategy to encourage students to participate in the lengthy evaluations: a free and legal copy of a live concert recording burned onto a CD. Newman surveyed 40 students in the areas of content, skills, previous experiences, courses taken, and attitude. In his analysis, Newman demonstrated statistically significant gains in several DNA sequence analysis skills among students who had completed related activities in the laboratory. Content knowledge of genomics and bioinformatics was substantially higher for students having been exposed to the fields through the microbiology or upper-level courses that incorporated microarrays. These students also recognized the value of microbial genomics for understanding human gene/protein function, disease processes, microbial evolution, evolution, and applications such as drug development and microbe identification.

Laura Hoopes of Pomona College, Claremont, California (http://pages2.pomona.edu/~llh04747/), gave a fourth perspective on undergraduate genomics. She highlighted student projects in two upper-division courses, with a research project as part of each course, and a senior thesis submitted by Jessica C. Brown, a 2002 graduate. Focusing only on yeast, Hoopes and her students combined genetic and molecular methods with yeast two-hybrid and DNA microarrays. Hoopes and Brown utilized two types of software for DNA microarray data analysis: 1) Excel and 2) GeneSpring (Silicon Genetics, Redwood City, CA), which was provided free to GCAT members. Her presentation demonstrated how the two software solutions provided different ways to discern interesting trends. Hoopes also stressed the potential for discovery science as well as hypothesis testing with the same data sets. She provided an example of both when Brown tested predictions and made an unexpected discovery when a *pol2–sir3* double mutant had lower expression of a number of cell cycle control genes and was then found to have previously unexpected changes in progression through parts of the cell cycle. Citing the impact of this research, Hoopes noted that Brown received a National Science Foundation (NSF) graduate fellowship and is now attending Massachusetts Institute of Technology (MIT) to study molecular genetics. In addition, Hoopes has cited her preliminary data in two grant proposals and intends to continue her student-based genomics research to better understand DNA replication and aging.

The fifth and final talk was summary of GCAT's current status and its future prospects. A. Malcolm Campbell of Davidson College, Davidson, North Carolina (http://www.bio.davidson.edu/people/macampbell/macampbell.html), explained the status of DNA microarray requests for the 2002–2003 academic year. *Escherichia coli*, yeast, partial mouse, and partial human chips were confirmed. The status of *Arabidopsis* is uncertain because the lab that produced 2001–2002 *Arabidopsis* chips closed down. Campbell explained the need for reliable sources of affordable chips and identified an academic lab that is willing to co-sponsor an NSF proposal to fund the production of DNA microarrays. Campbell also outlined his plans to develop a "teaching chip" that will enable more faculty to bring DNA microarrays into their courses because this chip would be less expensive to produce and not require RNA isolation for probe production. Finally, Campbell discussed ongoing software development by Dr. Laurie Heyer in the Mathematics Department at Davidson College (http://www.bio.davidson.edu/Courses/CompBio/webpage/home.htm). Campbell and Heyer are collaborating with their student researchers to produce Java-based applications that would perform spot finding, gridding, ratio calculations, and clustering in an integrated package. This software will work on Macintosh computers (Classic and OSX), personal computers (PCs), and Linux computers and will be freely available through the GCAT web site.

Further discussions centered on a range of topics such as DNA microarrays with 16S ribosomal DNA spotted for researchers to identify the range of species present in environmental samples. Mike Snyder's TRIPLES (transposon-insertion phenotypes, localization, and expression in *Saccharomyces*) yeast resources (http://www.bio.davidson.edu/people/macampbell/ASCB/2000/mTn.html) have been used by a few faculty members to perform phenotype macroarray analysis and protein localization experiments. During the final question-and-answer session, there was very clear interest in a hands-on workshop for faculty to learn how to go from beginning to end of the DNA microarray procedure. This interest included a strong desire for training in data analysis. The fact that teachers want better training in this area was not surprising because labs at research institutions are clamoring for the same thing. Campbell urged audience members to collaborate on ways to organize and fund a workshop in the next year or two.

We all know that an important aspect of professional meetings is the personal interaction. Prior to this session, many GCAT members recognized one another by name but not by face. The GCAT listserv and direct e-mails have created a virtual community of colleagues most of whom have never met one another. In addition, the audience of about 200 people was filled with interested and eager teachers from several countries and types of institutions. The supportive nature of GCAT was evident in the room as people exchanged ideas and offered to help develop proteomic curricular materials and reagents and environmental DNA microarrays. Many attendees lingered for nearly an hour creating new contacts and gaining enthusiasm from a group of peers who are willing to help one another.

During a lunch meeting after the morning session, six GCAT members discussed teaching and research issues but quickly focused on the need for a hands-on workshop for

faculty during the summer of 2003. These GCAT members were willing to take leadership roles by securing a facility and housing and searching for sources of money to defray costs. The group converged on a two-part workshop. Part one would be a 2- or 3-d wet-lab session in which each faculty member would work with one student (rising junior or senior) from the member's home institution. The student–teacher pair of investigators would begin by making media to grow cells and finish with scanned chips. Included in these procedures would be quality control assessment of progression through important milestones. There would be a break on Saturday afternoon to allow some free time, and a Saturday night stay over would be permitted for participants in both halves of the workshop. Part two of the workshop would consist of a couple of days for data analysis. Participants in the second half could mine their own data and/or download data sets from public domain sites such as Expression Connection (http://genome-www4.stanford.edu/cgi-bin/SGD/expression/expressionconnection.pl).

By the end of the day, the answer to the question posed at the ASM education session was clear: GCAT members are not rocket scientists, genomics is becoming a critical component of biology, and it *should* be incorporated in the undergraduate curriculum.

Faculty members often work alone on curriculum improvements, which may partially explain the pervasive synergy and enthusiasm that accompanied the ASM educational genomics session. To build on the excitement from the ASM session, Liz Vallen (http://www.swarthmore.edu/NatSci/evallen1/index.html) and Malcolm Campbell will convene an informal gathering of undergraduate faculty members at the 2002 American Society for Cell Biology Annual Meeting in San Francisco (http://www.ascb.org/meetings/am2002/main02mtg.htm). From 6:00 pm to 8:00 pm Sunday night, December 15, anyone interested in meeting with undergraduate instructors is invited to meet *CBE* Editorial Board members and other faculty members. Although some may express an interest in bioinformatics and genomics, persons interested in any aspect of undergraduate education are encouraged to participate. With the growing momentum and cooperative leadership of many faculty, it appears that faculty are ready to shape the future of educational genomics.