COMPUTATIONAL AND GENOMIC ANALYSIS OF MYCOBACTERIOPHAGE: A LONGITUDINAL STUDY OF TECHNOLOGY ENGINEERED BIOLOGY COURSES THAT IMPLEMENTED AN INQUIRY BASED LABORATORY PRACTICE DESIGNED TO ENHANCE, ENCOURAGE, AND EMPOWER STUDENT LEARNING

By

GAIL P. HOLLOWELL * JAMES E. OSLER ** APRIL L. HESTER ***

* *Associate Professor, Department of Biology, North Carolina Central University (NCCU), North Carolina.*
** *Faculty Member, School of Education, North Carolina Central University (NCCU), North Carolina.*
*** *Educator, Guilford County Schools.*

ABSTRACT

This paper provides an applied research rational for a longitudinal investigation that involved teaching a "Technology Engineered Science Education Course" via an Interactive Laboratory Based Genomics Curriculum. The Technology Engineering [TE] methodology was first introduced at the SAPES: South Atlantic Philosophy of Education Society) 51st Conference. The TE philosophy was further expanded on in the book "The Aftermath of Hurricane Katrina: Educating Traumatized Children Pre KG through College" in a chapter titled, "Technology Engineering Educational Solutions for the Hurricane Katrina Region". TE as a practice was later expounded upon in greater detail in an i-manager Journal on School Educational Technology article entitled, "Technology Engineering Science Instruction in the Information Age: Integrating Instructional Technology in K12 Education", (Vol. 4, No. 1, pp.12-17). This study is a continuation of all of the aforementioned research. The research investigation introduced interactive advanced genomic teaching measures for scientific education via a series of "$TE_{Genomic}$ *Biology courses". The courses involved interactive laboratory teaching methodologies that actively encouraged authentic research-based student learning. The paper also historically explores similar previous research as a foundational precursor to the year long longitudinal applied research inquiry. The research investigation took place over three years and involved three technology engineered genomics courses designed for introductory science majors, the courses respectively were: BIOL 1101 (General Biology I); BIOL 2030 (Genomics Research Initiative I); and BIOL 2030 (Genomics Research Initiative II). The research outcomes yielded positive outcomes by participants over time, thereby indicating that the* $TE_{Genomic}$ *Biology courses were a positive and dynamically interactive way of teaching advanced science education topics.*

Keywords: Analysis, Genomic Analysis, Genomics Education Partnership (GEP), Inquiry Based Laboratories, Instruction, Laboratory, Metacognition, Mycobacteriiophage,Phage Hunters Integrating Research and Education (PHIRE), Phage Hunters Advancing Genomics and Evolutionary Science (PHAGES), Science Education, [Science, Technology, Engineering and Mathematics] (STEM), and Technology Engineering.

INTRODUCTION

The implementation of the 3 Year PHAGES (Phage Hunters Advancing Genomics and Evolutionary Science) Genomics Course

$TE_{Genomic}$ *Biology Courses Longitudinal Study Objectives:*

The Implementation of Inquiry-Based Laboratories at Selected Universities

This research investigation focused on five institutions including North Carolina Central University (NCCU) that each has some type of inquiry based laboratory on their campuses and in their respective collegiate science education curricula. These Universities include Cabrini College, Davidson College, James Madison University, University of Maryland Baltimore County, and North Carolina Central University. This diverse group of schools includes small, medium and large institutions. These campuses are also private, public, majority institutions, and a single Historically Black College and University (HBCU). For NCCU as the basis for the $\text{TE}_{Genomic}$ Biology Courses (Technology $\text{Engineered}_{Genomic}$ Biology Courses), they will be compared to the other programs and emphasize our findings since joining the HHMI-SEA (Howard Hughes Medical Institute-Science Education Alliance) in 2010.

The Howard Hughes Medical Institute (HHMI) Science Education Alliance (SEA) and other organizations such as the Department of Energy's, Genomic Education Partnership (GEP) share a common theme of giving opportunity to students to experience genuine research, either combined with the lecture classroom and laboratory setting or separate as a computer laboratory. The HHMI-SEA currently has over 70 institutions participating in its alliance. This alliance uses a platform introduced by Dr. Graham Hatfull, Chairman of Department of Biological Sciences; Co-Director, Pittsburgh Bacteriophage Institute; and HHMI scientist who studies bacteriophages and their importance to phage therapy. Genome researchers use bacteriophages, because it is a simple model system and students who conduct research with bacteriophages learn how to use a variety of basic laboratory research techniques. Thus, HHMI has now made this type of scientific research available to thousands of first year college students around the country.

Several schools are now using inquiry based laboratories as a way to introduce first year college students to research. It is more cost-effective and reaches more students than the more common approach of individual mentoring that occurs when only selected few undergraduate students get the opportunity to work in an investigator's laboratory for two to three years. Howard Hughes Medical Institute is affiliated with three such programs that offer inquiry based laboratories to undergraduate students and high school students across the nation (GEP, PHIRE, and PHAGES). GEP, PHIRE, and PHAGES are different research programs that share similar interests in supplying high school and college student with genuine research opportunities; either laboratory-based, computer-based, or both. Not only do these programs increase science interest and literacy, but are also preparing undergraduate students (and potential high school students) for graduate education, as well as, careers in the science and biomedical field. According to Lopatto (2008), most Undergraduates begin their research with mentoring by faculty member, Graduate student, or postdoc. during a summer spent in the lab, nevertheless; excluding many students who do not have the summer free or lack funds. Thus, incorporating student research into the regular academic-year curriculum makes such experiences more broadly available (Lopatto et.al, 2008).

Technology Engineering ™ ©

"Technology Engineering" is the combination of Learner–Based Tools, Educational Games, Educational Systems, Relevance, and Collaborative Learning Strategies to create an interactive and dynamic cognitive economy (Osler, 2008). Technology Engineering leads to Product–Based Inquiry (Osler, 2006). An example of "Technology Engineering" as a methodology is the combination of innovative technology tools such as Instructor–Authored Interactive Meta metric Learning Modules with effective teaching strategies and dynamic distance education tools such as Course Management and Learning Management Systems (Osler, 2010). Technology Engineering is an innovative form of interactive technology used as a method of teaching science and math content and curriculum through collaboration with teachers in the classroom (Osler, Hollowell, and Palmer, 2008). Technology Engineering is used in this longitudinal study in the Genomics software used to analyze the student research outcomes.

The History of Teaching Laboratory Science Education

The history of laboratory exercises to learn science extends back as far as the 19th century. Laboratory exercises were used to engage students in the scientific experiences with objects and concepts. In 1910, the dynamics of science learning changed drastically, in particular, the role of laboratory exercises on science learning. During this time, John Dewey, the leader of the progressive education movement became an advocate for the investigative approach for science laboratory exercises. As the movement continued, the debate about the best way to teach laboratory exercises to promote student learning arose.

Since that time, laboratory exercises to learn science have been illustrated by information read in a textbook or presented by the course instructor. This approach to learn science remained the same until the 1960's where new approaches to teaching laboratory exercises were adopted. One such approach focused on the process of science and developing higher cognitive skills in the students. In the 1960's and 1970's, several science educators articulated that the uniqueness of laboratory exercises provided students with the ability to participate in an inquiry based or investigative process. David Ausubel, an American psychologist who made significant contributions to cognitive science and science education believed that, inquiry–based laboratory exercises would give the students a better appreciation of science methods, promote problem–solving, and improve their analytical skills (Hofstein and Lunetta, 1982).

Three decades ago, Hofstein and Lunetta (1982) proposed that laboratory exercises were a great asset to learn science. They reviewed several studies that compared how the instruction was provided during these laboratory sessions (i.e., as a 'laboratory group', a 'demonstration group'; and a 'discussion group') and it was determined that there were no significant differences between student learning in those students who performed traditional laboratory experiments versus those students who viewed filmed laboratory experiments. The only area that showed a measurable advantage over the other modes of instruction was the mode of instruction that enhances the development of laboratory skills (Hofstein and Lunetta, 1982). It was determined that exercises which involved the development of laboratory skills allowed students to be creative and combine ideas and techniques in an innovative way. Inquiry based or investigative laboratory exercises provided students with the best opportunity to not only increase their comprehension, but also to develop their creative thinking and problem–solving skills as well. Traditional laboratory exercises often lead to a narrow conception of science and is often unrelated to the capabilities and interest of the students (Hofstein and Lunetta, 1982). In contrast, when students are performing inquiry based laboratories, they can appreciate the thought process of a scientist when they are engaged in actual hands–on exercise (Hofstein and Lunetta, 1982). Inquiry based laboratory exercises also enhances the students' ability to recognize problems and apply the scientific method, and develop a conceptual understanding and improve their intellectual ability (Hofstein and Lunetta, 1982). More recently, the benefits of the laboratory exercises used to learn science were re–evaluated when science educators stated their concerns about how the outcomes of these laboratory exercises were not as obvious (Hofstein and Lunetta, 2003). In the thirty years since their review, Hofstein and Lunetta stated that the science education community has expanded its knowledge on students' understanding of science concepts and the nature of science. There has been an increase of advanced technology tools for teaching, learning, and research in the school laboratory that has led to a paradigm shift in how social science researchers evaluate science classroom and laboratory practices (Hofstein and Lunetta, 2003). As a result, there has been an increase in research on learning aptitudes and metacognition.

Metacognition supports the notion that inquiry based laboratory instruction increases observational, manipulation, and cognitive skills that reflect the true understanding of scientific concepts. For the purposes, metacognition is a students' reflection on their own thought process about what is required to learn science. It is believed that it is this application of one's' thought process that increases the students' comprehension of the subject material. Science educators believe that implementing science as inquiry within laboratory courses involves strategies to increase instructional effectiveness and the outcomes of assessment strategies within the curriculum standards (Suits, 2004).

Traditional Laboratories and Laboratory Methodologies Used for Science Education

For several years, students have performed laboratory experiments with a set of pre-determined known outcomes. These types of experiments are henceforth referred to as traditional laboratory experiments that have been the most common approach within laboratory courses in science for decades. However, this approach highlights laboratory techniques while decreasing the development of investigative skills (Suits, 2004). These traditional laboratory experiments provide students with pre–determined outcomes that are often verified by a step–by–step approach, fill in the blank data sheet, and conclusion questions that only require calculations or knowledge of facts. The traditional approach within laboratory courses often utilizes minimal amounts of equipment, time, space, and personnel. On the other hand, the inquiry–based approaches within laboratory courses have been shown to enhance discovery, investigative skills, written and oral communication skills, as well as enhancing the students' comprehension of the underlying biological principles and scientific concepts.

More recently, reforming Undergraduate Science Education has become the focal point of government agencies, private foundations, and general education system which includes Post Secondary Education. Over the past decade, reforms of biology education has been motivated by the perception that students in the United States have lost their competitive edge in the areas of Science, Technology, Engineering and Mathematics (STEM)(Boyle 2010, NRC 2003, PKAL 2006). These reforms have focused on changing the conventional importance on lecture and memorization to focusing more on the student. For example, pedagogy that utilizes small groups, case studies, as well as open–ended laboratories that contains enormous amounts on critical thinking and problem–solving (Boyle, 2010). According to Hatfull, Pedulla, Jacobs-Sera, Cichon, Foley, Ford, and Hendrix (2006), Bacteriophage Educational platform requires only modest prior comprehension of biological facts and concepts. This type of platform simplifies the access to first and second year college students to gain experience with scientific research as well as providing opportunities to students who do not necessarily excel in more traditional classroom settings (Hatfull, Pedulla, Jacobs-Sera, Cichon, Foley, Ford, and Hendrix,2006). The platform also offers numerous opportunities for student to learn concepts in Microbiology, Ecology, Genetics, Computational Biology and evolution within an inquiry–driven environment and is fully inclusive of a diverse variety of learning styles (Hatfull, Pedulla, Jacobs-Sera, Cichon, Foley, Ford, and Hendrix, 2006). In addition, the significant bioinformatics component of the program appeals to students with computer science and engineering backgrounds, and in doing so, it creates a diverse research group that offers advantages both to the participants and the research agenda (Hatfull, Pedulla, Jacobs-Sera, Cichon, Foley, Ford, and Hendrix, 2006). According to researchers Hanauer, Jacobs-Sera, Pedulla, Cresawn, Hendrix, and Hatfull (2006), many studies have been performed on bacteriophages because of their massive numbers and diversity, but their genetic diversity is still under exploration. The genetic diversity of bacteriophages is so large that there is a very low probability of isolating identical isolates to previously characterized bacteriophage listed in the Mycobacteriophage database.

Inquiry Based Science Education Laboratories

There are several inquiry–based laboratories implemented at various institutions within the United States, but this research study will only focus on three inquiry–based laboratories: 1) Genomics Education Partnership (GEP); 2) Phage Hunters Integrating Research and Education (PHIRE); and 3) Phage Hunters Advancing Genomics and Evolutionary Science (PHAGES). Genomics is not only essential for students to understand biology, but also provides unprecedented opportunities for undergraduate research (Shaffer, Alvarez, Bailey, Barnard, Bhalla, Chandrasekaran, and Buhler, 2010). The goal of the GEP is to provide research opportunities while collaborating between a growing number of colleges and universities around the country and the Department of Biology and Genome Center of Washington University in St. Louis. According to researcher Shaffer and colleagues Alvarez, Bailey, Barnard, Bhalla, Chandrasekaran, and Buhler (2010), a major challenge for our nation, is the issue overcoming minority under representation (i.e. retention) in the sciences at multiple career levels. Researchers found that students, including at–risk and first–generation minority students, benefit from undergraduate research experiences. Furthermore, undergraduate research influences career pathways for members of under represented populations by increasing the retention rate of minority undergraduates and increasing their rate of participation in graduate education. However, colleges and universities are not always able to provide independent research experiences for majority of their students because of the cost of equipment, supplies and laboratory space, and the fact that the need for trained mentors is usually beyond the budget of many institutions (Shaffer, Alvarez, Bailey, Barnard, Bhalla, Chandrasekaran, and Buhler (2010). This is even more difficult for larger schools that contain a high student–to–faculty ratio and a decreased pool of Graduate students and Postdoctoral researchers who could serve as mentors. According to Shaffer, Alvarez, Bailey, Barnard, Bhalla, Chandrasekaran, and Buhler (2010), the GEP helped to incorporate genomics based undergraduate research into the biology curriculum in colleges and universities across the country. The GEP has grown into a partnership of diverse schools, including Primarily Undergraduate Institutions (PUIs) and research Universities (Shaffer, Alvarez, Bailey, Barnard, Bhalla, Chandrasekaran, and Buhler,2010). Through the GEP project, faculty gain training and resources enable them to introduce students to genome science research through the utilization of computers and internet access. The GEP project also provide students with opportunities to make discoveries, learn research methodology, observe the interdisciplinary nature of biological science, appreciate the importance of collaboration, and understand the connection between their classroom activities and the real world (Shaffer, Alvarez, Bailey, Barnard, Bhalla, Chandrasekaran, and Buhler, 2010). It has been designed to allow flexibility for faculty to offer research in this field as either an independent experience or as a classroom activity, either as a stand–alone course or as part of the laboratory in a broader course in molecular biology–genetics–genomics, which in essence allows flexibility to be integrated into different curricula servicing diverse students at very different institutions (Shaffer, Alvarez, Bailey, Barnard, Bhalla, Chandrasekaran, and Buhler, 2010).

According to Hanauer (2006), working in research laboratory to generate new scientific information can give high school students an experience in real scientific investigation. At the University of Pittsburgh, the PHIRE program was founded on the idea that bacteriophage discovery and comparative genomics allows students at multiple levels of development to engage in true scientific inquiry (Hanauer et.al, 2006). In PHIRE, undergraduate and high school students isolate novel bacteriophages from the local soil environment, purify the genomic DNA for sequencing, and compare the sequence to known bacteriophage genomes (Hanauer et.al, 2006).

The knowledge and practical skills needed to isolate bacteriophage from the environment is minimal, which allows middle school students fully to participate. From 2003 to 2006, 57 high schools totaling 3534 students participated in the PHIRE bacteriophage–isolation program, which led to the isolation of 94 novel bacteriophages, of which three were completely sequenced (Hanauer, 2006).

The PHAGES project is supported by the HHMI Science Education Alliance. This project is a research–based laboratory course for undergraduate students who have had little or no independent research experience. The PHAGES course is offered at many schools across the United States as a collaboration between HHMI and Graham Hatfull's research group at the University of Pittsburgh. The 2013–2014 academic year will be the sixth year of the SEA–PHAGES course. Since 2008, over 73 schools and over 4,800 undergraduates have participated, 97 student– annotated phage sequences have been deposited in GenBank, and 7 peer–reviewed papers have been published on mycobacterial phage genomes and science education. Three of those publications had student authors.

According to Hatfull (2006), the PHAGE hunters program developed at the University of Pittsburgh in which students discovered and genomically characterized their own bacteriophages, provides particularly a strong combination of attributes that maximizes the Educational benefits within a research environment. There are two important features of this Educational platform: the strong emphasis on scientific discovery and project ownership (Hatfull et.al, 2006). Within this program there are three discovery elements: isolating a bacteriophage from the environment with its own unique qualities, discovery of new genes, and the discovery of homologs. Hatfull (2006) indicated that the high diversity of the bacteriophage population, the preponderance of novel genes, and the mosaic architecture of the genomes provide a high promise of discovery for each participating student. The opportunity for students to discover novel genes and viruses is important since it is stimulating and highly motivating, providing a strong encouragement for students to become engaged in scientific research and to maintain their involvement even through the more challenging aspect of their projects (Hatfull et.al , 2006). Hatfull (2006) also believed that the PHAGE isolation and genomics is a powerful Educational platform that provides research opportunities for students from diverse educational backgrounds. The high diversity of bacteriophage populations offers the excitement that each student can isolate a unique virus and use genomic approaches to understand the relationship of the newly discovered bacteriophage to the broader biological world (Hatfull, 2006).

Implementation of Inquiry Based Laboratories at Selected Universities

General Education Program (GEP) (Retrieved from http://gep.wustl.edu) is a collaboration among faculty at many different institutions working together to engage undergraduates in a genomics research project analyzing the dot chromosomes of Drosophila. This research is funded by the Department of Biology and Genome Center at Washington University and HHMI, engages students in improving the sequence and annotating the dot chromosomes of Drosophila species. While there are similarities to the phage work, there are substantial challenges in annotating a eukaryotic genome that do not occur in the phage analysis. Consequently, this project is most often utilized in upper–level lab courses. Several schools are now using both projects in their curriculum, and finding benefits of this continuum. The overall organizational model is very similar to SEA. According to Shaffer, Alvarez, Bailey, Barnard, Bhalla, Chandrasekaran, and Buhler (2010) by using computers and Internet access, the students are given opportunities to make discoveries, learn research methods, observe the interdisciplinary nature of biological science, appreciate the importance of collaboration, and understand the connection between their classroom activities and the real world. The goal of this program is not only to increase the research opportunities for Undergraduates, but also to increase the retention rate of minorities in the sciences, as well as, increasing the rate of participation in graduate education by incorporating Genomic based research into the undergraduate biology curriculum. The GEP found that curriculums in Genomics can train students to think like scientist.

PHIRE was a program that started at University of Pittsburgh in 2003, which was offered to high school students on multiple development levels to participate in true scientific inquiry. These high school students isolated a novel bacteriophage, extracted genomic DNA, sequenced and analyzed the genome of a bacteriophage. This program was founded on the concept of bacteriophage discovery by Dr. Graham Hatfull at the University of Pittsburgh.

The PHAGES course mirrors the ongoing research of Dr. Graham Hatfull at the University of Pittsburgh, which involves isolating, purifying and characterizing a novel bacteriophage. After the characterization process, the extracted genomic DNA is sent to a sequencing center, sequenced, and is uploaded to an electronic file. The electronic file is transferred to the Institution, to be annotated. The genomic DNA from the schools that participated in the PHAGES program was outsourced to a SEA affiliated DNA sequencing center; moreover, most SEA affiliated schools are primarily undergraduate teaching institutions. For example, North Carolina Central University shipped their genomic DNA to Virginia Commonwealth.

According to researchers Caruso, Sandoz, and Kelsey, (2009) the PHAGES course is appropriate not just for students who are already interested in science, but for non–science students as well. The PHAGES course is an opportunity to positively influence students who had little to no experience in science, however providing non–science and non–STEM students' an opportunity to carry out authentic research that would allow them to experience the excitement and rewards in scientific inquiry and exploration (Caruso, Sandoz, and Kelsey, 2009). It is possible to conclude that similar problem–based courses in other STEM disciplines could be just as successful and appreciated in non–science disciplines (Caruso, Sandoz, and Kelsey, 2009). For example, Cabrini College implemented two different surveys to measure the impact of the Genomics course on the students. One survey focused on the students' consideration of pursuing graduate education which indicated that the students gained a great research experience that increased the interest in considering graduate school or medical school. The other survey focused on their peer–mentoring experiences in the Genomics course which indicated that peer–mentoring increased the understanding of the research, a sense of responsibility and increased communication skills.

Other Institutions that Implement Genomics Courses

Cabrini College

Cabrini College is a private Catholic Liberal Arts College outside of Philadelphia. Cabrini's current enrollment is over 3500 undergraduate and graduate students, with a majority of white, non–Hispanic population. There is a growing body of research that has established the benefits of authentic research experiences by undergraduates in the sciences (Harrison, Dunbar, Ratmansky, Boyd, and Lopatto, 2011). At Cabrini College, the PHAGES Genomics course was offered in 2008 and was opened to both science and non–science majors that were enrolled in the college's honors program; however, the student with similar academic backgrounds to the honors students expressed interest in taking the course and enrolled as well. Sixteen students were enrolled in the course: 13 freshman biology majors, (9 of whom were from the honors program, the remaining 3 students were non–science major sophomores that were in the honors program and elected to enroll in the course to satisfy their science general education requirement). The 4 students who were not in the honors program were enrolled at Cabrini College as biology majors and showed a strong interest in the PHAGES Genomics course during an Open House visit. As freshman, the PHAGES Genomics course replaced the Introductory Biology laboratory course that the students were required to undergo. During the Fall semester, the PHAGES Genomics lab met twice a week for a total of 4.5 hours of laboratory class work; but during the spring semester, the students met once a week for 3 hours for laboratory instruction. Since the fall semester is more labor–intensive for the PHAGES Genomics course, Cabrini College felt, students needed more time to isolate and characterize their bacteriophage, however, since spring semester was less intense and did not have a deadline to meet, a lecture portion was incorporated into the curriculum (Harrison, Dunbar, Ratmansky, Boyd, and Lopatto, 2011).

Davidson College

Davidson College is an Independent Liberal Arts College located in Davidson, with a current enrollment of approximately 1,700 undergraduate students. Davidson College is an institution of higher learning established in 1837 by Presbyterians of North Carolina. The primary purpose of Davidson College is to assist students in developing humane instincts and disciplined creative minds for lives of leadership and service.

Davidson College offered a Genomics course to upper classmen that started in 2001, which was computer and internet driven only. The course was designed to incorporate public–domain databases, research tools, and peer–reviewed journal articles. The online resources provided the students with exciting entry into the new fields of genomics, proteomics, and bio-informatics (Campbell, 2003). This course was offered to upper classmen and the enrollment ranged from 11–14 students per semester.

The students who were enrolled in the Genomics course were evaluated by their ability to utilize online information as well as achieve the Educational goals of the course. The students' evaluations assessed their learning in comprehension, application, analysis, synthesis and asked the students' opinion of the course. Some of the evaluations were open–book, take home, and required extensive use of the internet; the students were given several days to complete the evaluation. According to Campbell (2003), the evaluation/assessments left the instructors satisfied with the outcome. The evaluation/assessment illustrated that the students retained and acquired a great understanding of the information that was taught in the course. The assessments allowed the instructor to recognize if the students had improved their knowledge within the field and if there were any changes in the students' attitudes towards research in Genomics (Campbell, 2003).

James Madison University

In 1908, James Madison University (JMU) is a comprehensive University that is a part of the statewide system of the Commonwealth of Virginia. JMU is a majority, coeducational research university located in Harrisburg, Virginia; with a current enrollment of approximately 19,000 students who participated in one of the 108 degree programs on the Bachelor's, Masters, Educational Specialist and Doctoral levels.

JMU has offered two levels of Genomics courses in their biology curriculum. The first level (freshmen only) Genomics course was entirely experiential, as well as, taught concepts, processes and vocabulary; the upper level Genomics course developed in 2005, was based on literature and the ability to read and analyze literature on exams. The upper level genomics course was a 4 credit hour course within the biology curriculum that is offered as an elective and can be used for either biology or biotechnology majors. For students, in order to be eligible to enroll into this upper level Genomics course, the student has to complete a 2–year core sequence first. According to the feedback from faculty and students who were involved in the Genomics courses they expressed that both courses were successful in exposing the students to a hands–on experience in the world of Genomics (Temple, Cresawn, and Monroe, 2010). According to researcher Temple and his colleagues Cresawn and Monroe(2010), at James Madison University, they believe that incorporating hand–on, inquiry based activities provide a superior learning environment for science major students.

University of Maryland Baltimore County

The University of Maryland Baltimore County (UMBC) is a public research university that specializes in natural science and engineering located in Baltimore. Known for its Meyerhoff Scholars Program, it has a current enrollment of 13,000 students. The initial gift of $500,000 that created Meyerhoff Program in 1988 allowed 19 young men from Baltimore City who were interested in studying Science, Engineering, or Mathematics to study at the University of Maryland Baltimore County (University of Maryland, 2005). The genomics course at UMBC is offered to freshmen and sophomores and is open to science majors, non–science majors, and non–STEM majors.

The Site of the Genomics Courses Longitudinal Study: Inquiry Based Technology Engineered Science Education Courses Conducted Over 3 Years at North Carolina Central University

North Carolina Central University (NCCU) has been a constituent member of the University of North Carolina System since 1972. Chartered in 1909 as the nation's first public liberal arts institution for African Americans, NCCU is now classified as a Comprehensive Level 1 Institution with an approximate enrollment of 8,500. All STEM programs offer both BS and MS degrees. In the fall of 2012, NCCU welcomed its first class of PhD students in Biosciences.

Since the Fall of 2010, NCCU has offered a Genomics special topics laboratory course. The Genomics laboratory course has met twice a week for two hours in the fall semesters. In year one, a cohort of students have participated in the FUTURES (Fostering Undergraduates Through University Research and Education in the Sciences) program, as well as, attendees of Josephine Dobbs Clement Early College High School were enrolled in to the Genomics course, totaling 22 students. The remaining students were freshman biology majors, one transfer student from East Carolina University and one non–traditional biology major student. In year two, 19 students enrolled into the Genomics course; four students were participants of the FUTURES program and the remaining students comprised of one second degree student and 14 freshman biology majors. In year three, a total of 49 students were enrolled in two sections of the genomics course. In all three years, students who participated in the NCCU's Genomic course collected soil samples from Durham, North Carolina and their respective hometowns in North Carolina, South Carolina, Virginia, and Maryland in an attempt to isolate and identify novel bacteriophages.

In spring semesters, students were enrolled in the 'in silico' portion of the Genomics course where they annotated either a bacteriophage genome, either one of their classmates or a donated genome from one of the partner institutions. In year 1, NCCU students analyzed and annotated an adopted bacteriophage genome named 'Eric B' which was subsequently uploaded to 'GenBank', the online database of genetic sequences maintained by the National Center for Biotechnology Information of the National Institution of Health (NIH). In Year 2, NCCU students analyzed and annotated an adopted bacteriophage genome named 'NuevoMundo'. Currently, NCCU students are analyzing and annotating an adopted bacteriophage genome named 'Obama12'.

During the year–long Genomics course offered at NCCU, the 'in silico' activities involve the use of bio-informatics tools to enable genomic finishing, annotation, and gene comparison to increase the insight of the diversity of bacteriophages in the environment as well as the distinct and unique characteristics of bacteriophages. Algorithms that were used in the 'in silico' portion of the course were: Apollo, GeneMark, GeneMark TB, GBrowse, Glimmer, and Phamerator. These algorithms were used to define potential genes, assign putative function to the genes, and determined the order in which they appear in the genome. In the Analyze section of the 'in silico' component, the quality of the sequence was assessed by elucidating the genomic properties, and the preliminary genome structure and organization were characterized. The elements, such as coding potential, start and stop codons, and shine dalgarno predictions are important in transcription, translation,and non–protein–encoding genes are genomic features that were used to identify and define the genes.

In the 'Discover section', it was necessary to identify the arrangement of the putative genes across the entire genome. Determining the potential function of the putative gene product and comparing the structure and organization of a particular genome to other bacteriophage genomes, as well as, determining and confirming the bacteriophages' cluster membership tasks in the Discover portion. Once the genome sequence was completed, the next step was to identify the coding regions by using bio-informatics software that can determine coding regions within the sequence of the bacteriophage genome. In order to accomplish this task, 6 different bio-informatics tools (GBrowse, GeneMark, GeneMark TB, Glimmer, Apollo, and Phamerator) were developed by researchers within the HHMI–Science Education Alliance (SEA) and University of Pittsburgh to help define the structure and function of the gene.

The Genomics course was offered twice a week for two hours, and weighed 25% of the 1101 General Biology Course final grade. However, the laboratory work was independent of the lecture course work. The students who were enrolled into the Genomics course were required to work in a peer mentoring environment, wear laboratory coats, maintain laboratory notebooks with two notebook checks per semester, and answer a scientific question monthly for a grade. The monthly questions were retrieved from the HHMI_SEA–Wiki (a website that is used by the HHMI staff as well as the graduate students and the students enrolled in the Genomics course) or the Mycobacteriophage database website (www.phagesdb.org). Within the first two weeks of the course, the students were introduced to sterile technique to increase awareness of ways to prevent contamination; which was demonstrated by the class instructors, as well as the Graduate Teaching Assistant (GTA). Students enrolled in the course did not have laboratory exams; however, the student did have laboratory skills assessments and case studies to read and respond to. The GTAs were available during class time and for four hours before class time, twice a week to assist students who needed extra help.

Longitudinal Study Methodology and Results of the Inquiry Based Technology Engineered Science Education Courses at NCCU by Years 1 through 3

TE$_{Genomic}$ Biology Courses:Implementation of the PHAGES Genomics Course – Year 1

This course is designed for introductory science majors. In the Fall Semester, students had to co–register for BIOL 1101 (General Biology I) and BIOL 2030 (Genomics Research Initiative I). BIOL 1101 is a 4 credit hour course with 3 lecture hours and 2 laboratory hours per week. BIOL 2030 is a 1 credit hour course with 2 laboratory hours per week. In the Spring Semester, students registered for BIOL 2030 (Genomics Research Initiative II). BIOL 2030 is a 3 credit hour course with 3 computer laboratory hours per week. The selection criteria were:

1. Freshman or sophomore science major;
2. First–time registrant for General Biology I; and
3. Earned a minimum SAT score of 1000 (for first–time freshmen) *or* have maintained an overall grade point average of 3.0 (for continuing NCCU students).

$TE_{Genomic}$ Biology Courses Responses: Year 1 Longitudinal Research Outcomes

Year 1 concluded with all the students being able to participate in the NCCU–College of Science and Technology Annual Research Day Symposium through group poster presentations on the research that was performed. Interestingly, one student was selected from the class to travel to HHMI Janelia Farms Research Campus to give a PowerPoint presentation at the Annual HHMI SEA symposium. Based on multiple discussions with students who were enrolled in the Genomics course, each expressed that they gained a genuine research experience in their freshman year of college.

$TE_{Genomic}$ Biology Courses Results: Scientifically Based Technology Engineered Course Mycobacteriophage Gene Sequencing Longitudinal Research Results: Year 1

In Fall 2010, NCCU was unable to send a DNA sample to be sequenced due to the low genomic DNA yield; however, the 'Mycobacteriophage Eric B' was adopted by NCCU in January 2011 from HHMI. Mycobacteriophage EricB was founded by Kevin Bradley at HHMI Research Campus, Janelia Farms in Ashburn Virginia in 2008. The sequencing of EricB's genome was completed on January 29, 2011 at Virginia Commonwealth University (VCU). EricB has 51,702 base pairs, 61.5% of GC (Guanine-Cytosine) content and its morphology is characterized as Siphoviridae. EricB has 97 genes, three transfer RNAs, and the entire genome is searchable in GenBank and the National Center for Biotechnology Information (NCBI) website.

Longitudinal Study Attrition

During the Spring semester of Year 1, the number of students decreased by ~30% (or 8 students), which may be a result of students' perception of the 'in silico' computer laboratory component. In general, they perceived it to be less interactive as the in the laboratory bench experience as described in Table 1.

Table 1 provides the detailed information on student participant perceptions in terms of Pros and Cons regarding Year 1 of the HHMI–SEA Phage Genomics [$TE_{Genomic}$ Biology Courses] longitudinal study. Table 1 Findings consisted of the following: 1) Freshman science majors learned primary lab skills (experiments were not always completed, minimal results regarding DNA, and DNA specialized skills did not occur); and 2) Freshman science majors were exposed to 6 genome computer-based annotation programs (that were found to be complex and time consuming).

$TE_{Genomic}$ Biology Courses: Continuation of the PHAGES Genomics Course–Year 2

Year 2 concluded as all students were able to participate in the NCCU–College of Science and Technology Annual Research Day Symposium through group poster presentations on the research that were performed within the year, along with two students being selected from the class to travel to HHMI Janelia Farms Research Campus to give a poster presentation at the Annual HHMI SEA symposium. Again, the students who were enrolled in the Genomics course expressed that they gained a genuine research experience in their freshman year of college. The selection criteria were as follows:

1. Freshman or sophomore science major;

Year 1 Outcomes	Pros	Cons
In situ Fall 2010 (n=24)	- Freshman science majors how to pipette, make serial dilutions, plate cultures, and maintain a laboratory notebook.	- Students did not always finish the -experiments in the allotted class time period The amount of DNA that was extracted was very low. Did not experience DNA restriction digestion or electro micrograph imaging.
In silico Spring 2011 (n=16)	- Freshman science majors exposed to 6 computer-based annotation programs (Apollo, GenBank, GeneMark TB, GeneMark, Glimmer, Phamerator).	- The annotation software which consisted of the 6 different computer programs was time consuming and not user friendly.

Table 1. Students' perspective of the HHMI–SEA Phage Genomics in Year 1

2. First–time registrant for General Biology I; and
3. Earned a minimum SAT score of 1000 (for first–time freshmen) *or* have maintained an overall grade point average of 3.0 (for continuing NCCU students).

$TE_{Genomic}$ Biology Courses Responses: Year 2 Longitudinal Research Outcomes

This year long research project was split into two major parts, an 'In Situ' portion followed by an *In Silico* portion. In the 'In Situ' portion, the bacteriophage was isolated by collecting soil samples and purified by plaque screening. The authors then performed a spot test, a phage titer assay, and conducted the final purification with phage lysate which then allowed the phage to be sequenced. Once the sequencing was completed, the 'In Silico' process begins. In this process, computer based algorithms are used to define potential genes and their function and position for annotation. These algorithms are conducted using the following DNA software programs – DNA Master, GeneMark, Genemark TB and Glimmer. DNA Master is a sequence editor and analysis package that combines, analyzes, and displays data from a variety of DNA analysis programs, including GeneMark, Glimmer, Aragorn, and BLAST. GeneMark calculates the probability that the given DNA sequence codes for an ORF in 1 of 6 possible frames. GeneMark TB is used to indicate the coding potential. Coding potential is the likelihood that a given portion of the genome codes for a protein. The algorithms of this program are based on the defined genes of the Mycobacterium tuberculosis genome. Glimmer is a DNA software program used to predict protein coding genes. Glimmer also identifies alternate start codons. The algorithms in this program differ from those used in GeneMark and GeneMark TB. While the DNA programs are responsible for computing the algorithms and the potential gene location, authors used biological principles to associate genes and their functions. Annotation allowed authors to discover genes that were unique to our newly discovered bacteriophage and similar to other bacteriophage genomes. The bacteriophage that was used for annotation was NuevoMundo, which was acquired by a student from the University of North Texas. This bacteriophage is 155, 945 base pairs long and contain 239 genes.

$TE_{Genomic}$ Biology Courses Results: Scientifically Based Technology Engineered Course Mycobacteriophage Longitudinal Research Results: Year 2

During the Spring semester for Year 2, the number of students decreased by 7 (~30%). This may have been due to the students' notion of the 'in silico' computer laboratory component not sounding as interactive as the in situ component during the first semester.

Table 2 provides the detailed information regarding the discovery and characteristics of Bacteriophage NuevoMundo. Table 2 Findings primarily consisted of information on Bacteriophage NuevoMundo which had the following characteristics: (1). Founded by researcher Izamar Flores Castillo; (2). Location of discovery was University of North Texas in 2011; (3). As a Bacteriophage this particular plaque is fairly small, about 5mm circular, and is clear; (4). It has 155,943 base pairs; (5). Its Guanine/Cytosine Contentis 64.7%; (6). Its character of genome end is circularly permutated; (7). Its 3 inch Overhang Length is 10 base pairs; Its 3 inch Overhang Sequence is CGGTCGGTTA; (8). Its Cluster is C; (9). Its Subcluster is C1; and (10). Its Morphotype is Myoviridae.

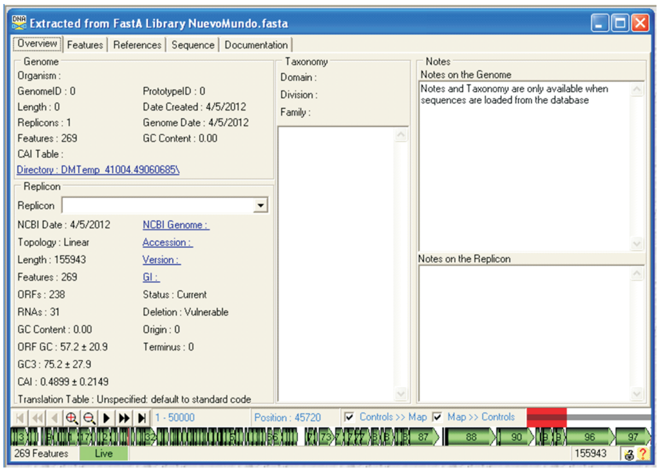
A sequential series of following Figures illustrate the Longitudinal Study Technology Engineered Genomics Outcomes.

Figure 1 Summary

Figure 1 displays a screenshot of an example of the DNA

Phage Name	NuevoMundo
Found by:	Izamar Flores Castillo
Found in/year:	University of North Texas, 2011
Plaque Notes:	This plaque is fairly small, about 5mm circular; Plaque is clear
Program:	Phage Hunters Advancing Genomics and Evolutionary Science (PHAGES) Program
Length of Genome:	155,943 base pairs
Guanine/Cytosine Content:	64.7%
Character of genome end:	Circularly Permutated
3' Overhang Length	10 base pairs
3' Overhang Sequence	CGGTCGGTTA
Cluster	C
Subcluster	C1
Morphotype	Myoviridae

Table 2. Bacteriophage NuevoMundo detailed information from www.phagesdb.org



Organism :
GenomeID : 0
PrototypeID : 0
Length : 0
Date Created : 4/5/2012
Replicons : 1
Genome Date : 4/5/2012
Features : 269
GC Content : 0.00
CAI Table :
Directory : DMTemp_41004.49060685\

Domain :
Division :
Family :

Notes on the Genome
Notes and Taxonomy are only available when sequences are loaded from the database
Notes on the Replicon

Replicon
NCBI Date : 4/5/2012
NCBI Genome :
Topology : Linear
Accession :
Length : 155943
Version :
Features : 269
GI :
ORFs : 238
Status : Current
RNAs : 31
Deletion : Vulnerable
GC Content : 0.00
Origin : 0
ORF GC : 57.2 ± 20.9
Terminus : 0
GC3 : 75.2 ± 27.9
CAI : 0.4899 ± 0.2149
Translation Table : Unspecified: default to standard code

1 - 50000
Position : 45720
269 Features
155943

Figure 1. A Screenshot of an example of DNA Master

Master software interface that shows an Extracted Fasta file of NuevoMundo. DNA Master is a genome annotation and exploration software tool designed and written by Dr. Jeffrey Lawrence, of the University of Pittsburgh. The application of DNA Master in the science education laboratory environment is an ideal example of Technology Engineering. This screenshot shows the statistics of the selected bacteriophage and the entire genome displayed in green at the bottom of the screen. The DNA Master interactive interface is a prime example of Technology Engineering of software designed to allow the student to engage in hands-on experience with genomic data in the laboratory environment. DNA Master is a comprehensive DNA sequence editor and analysis package that combines, analyzes, and displays data from a variety of DNA analysis programs, including GeneMark, Glimmer, Aragorn, and BLAST. It organizes and collates all of these data into various tables and forms and saves it a single file with a '.dnam5' software file extension (Hatfull, Jacobs-Sera, Welkin, Russell, andCresawn,2013).

Figure 2 Summary

Figure 2 displays a screenshot of an example of the complete genome map from the Technology Engineering science education laboratory/classroom application of DNA Master software. This component of the DNA Master features is clearly shown in Figure 1 as one of the features within the tabs at the top of the menu items. This screenshot is a detailed and in-depth illustration of the statistics of the selected bacteriophage and the entire genome displayed in green at the bottom of the screen (also displayed at the bottom of the DNA Master software interface in Figure 1).

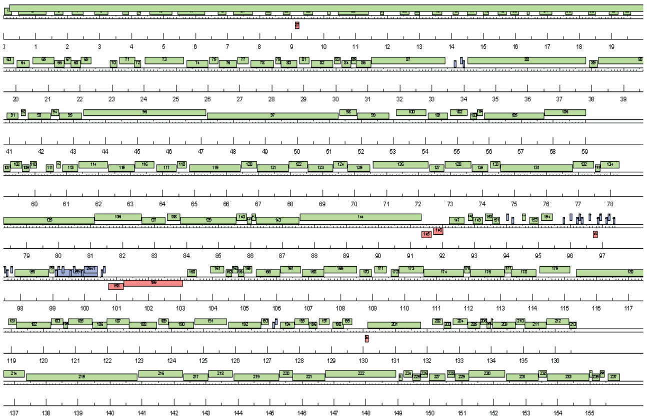


Figure 2. Genome Map of NuevoMundo from DNA Master

Figure 3 Summary

Figure 3 displays a Phamerator map illustrating in great detail the homology (similarity in sequence of a protein or nucleic acid between organisms of the same or different species) among the different bacteriophages (a virus that infects and replicates within a bacterium) within a subcluster (a subset of a number of things of the same kind, growing or held together). It is important to note that for the most part the vast majority of bacteriophage genomes have mosaic architectures and are replete with small open reading frames of unknown function, presenting challenges in their annotation, comparative analysis, and representation. Phamerator is a bio-informatic tool that assorts protein-coding genes into phamilies of related sequences using pair wise comparisons to generate a database of gene relationships. This database is used to

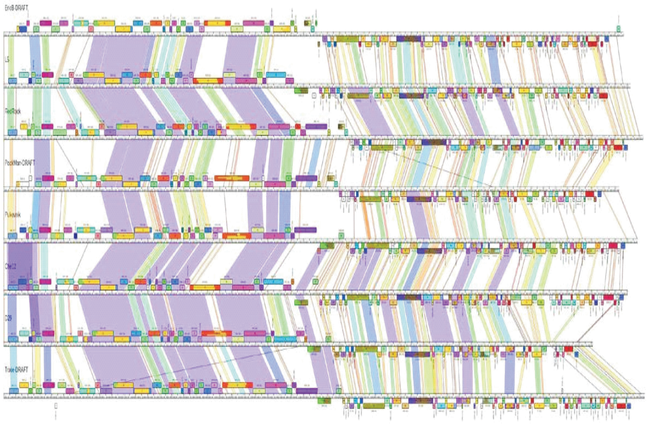


Figure 3. Phamerator Map

generate genome maps of multiple phages that incorporate nucleotide and amino acid sequence relationships, as well as genes containing conserved domains. Phamerator also generates phamily circle representations of gene phamilies, facilitating analysis of the different evolutionary histories of individual genes that migrate through phage populations by horizontal genetic exchange (Cresawn, Bogel, Day, Jacobs-Sera, Hendrix, and Hatfull, 2011).

Figure 4 Summary

Figure 4 displays a screenshot of an example of a sequential BLAST file of Bacteriophage NuevoMundo in color key according to the alignment of scores. This particular genomic sequence referenced 93 Dorothy as a "Complete Sequence" with the following features: 58866 bp including 10 bp 3- over S = 387, E = 1e-104. Scores are arranged in a specific numerical sequential color code with a minimum of less than 40 and a maximum of greater than or equal to 200.

Figure 5 Summary

Figure 5 displays a screenshot of an example of a sequential BLAST file of Bacteriophage NuevoMundo from DNA Master. BLAST is an acronym for "Basic Local Alignment Search Tool". The "Basic Local Alignment Search Tool" is a sequence comparison algorithm optimized for speed used to search sequence databases for optimal local alignments to a query (Altschul, Gish, Miller, Myers, and Lipman, 1990). The queries are represented by the sequential links associated with the Score (bits) E Values determined by integer values for Bacteriophage NuevoMundo.

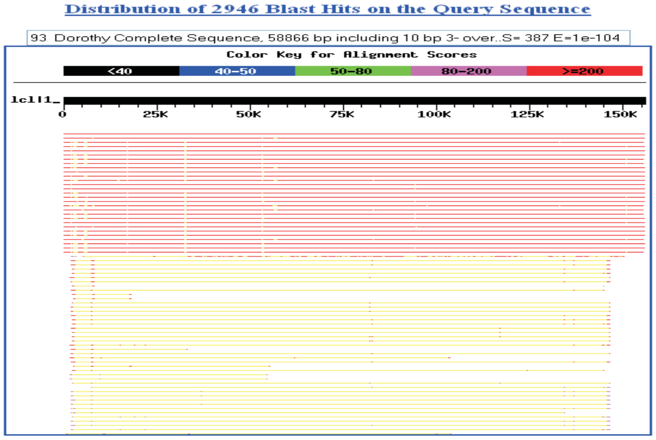
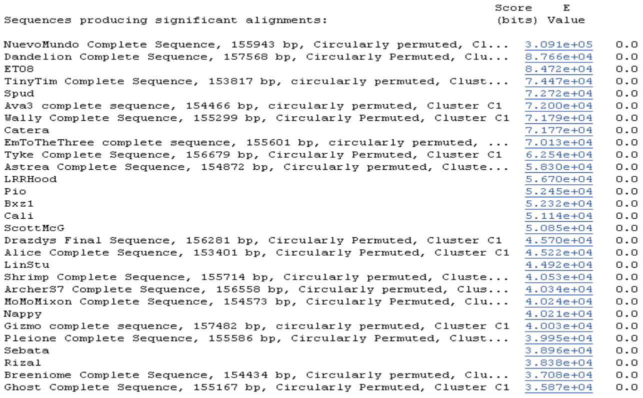


Figure 4. BLAST file of Bacteriophage NuevoMundo



```
                                                                Score    E
Sequences producing significant alignments:                    (bits)  Value

NuevoMundo Complete Sequence, 155943 bp, Circularly permuted, Cl...  3.091e+05   0.0
Dandelion Complete Sequence, 157568 bp, Circularly Permuted, Clu...  8.766e+04   0.0
ET08                                                                 8.472e+04   0.0
TinyTim Complete Sequence, 153817 bp, circularly permuted, Clust...  7.447e+04   0.0
Spud                                                                 7.272e+04   0.0
Ava3 complete sequence, 154466 bp, circularly permuted, Cluster C1   7.200e+04   0.0
Wally Complete Sequence, 155299 bp, Circularly Permuted, Cluster C1  7.179e+04   0.0
Catera                                                               7.177e+04   0.0
EmToTheThree complete sequence, 155601 bp, circularly permuted, ...  7.013e+04   0.0
Tyke Complete Sequence, 156679 bp, Circularly Permuted, Cluster C1   6.254e+04   0.0
Astrea Complete Sequence, 154872 bp, Circularly permuted, Cluste...  5.830e+04   0.0
LRRHood                                                              5.670e+04   0.0
Pio                                                                  5.245e+04   0.0
Bxz1                                                                 5.232e+04   0.0
Cali                                                                 5.114e+04   0.0
ScottMcG                                                             5.085e+04   0.0
Drazdys Final Sequence, 156281 bp, Circularly Permuted, Cluster C1   4.570e+04   0.0
Alice Complete Sequence, 153401 bp, Circularly Permuted, Cluster C1  4.522e+04   0.0
LinStu                                                               4.492e+04   0.0
Shrimp Complete Sequence, 155714 bp, Circularly permuted, Cluste...  4.053e+04   0.0
ArcherS7 Complete Sequence, 156558 bp, Circularly permuted, Clus...  4.034e+04   0.0
MoMoMixon Complete Sequence, 154573 bp, Circularly Permuted, Clu...  4.024e+04   0.0
Nappy                                                                4.021e+04   0.0
Gizmo complete sequence, 157482 bp, circularly permuted, Cluster C1  4.003e+04   0.0
Pleione Complete Sequence, 155586 bp, Circularly Permuted, Clust...  3.995e+04   0.0
Sebata                                                               3.896e+04   0.0
Rizal                                                                3.838e+04   0.0
Breeniome Complete Sequence, 154434 bp, Circularly permuted, Clu...  3.708e+04   0.0
Ghost Complete Sequence, 155167 bp, Circularly Permuted, Cluster C1  3.587e+04   0.0
```

Figure 5. Report of BLAST file of Bacteriophage NuevoMundo

Table 3 provides the detailed information on student participant perceptions in terms of Pros and Cons regarding Year 2 of the HHMI–SEA Phage Genomics [$TE_{Genomic}$ Biology Courses] longitudinal study. Table 3 Findings consisted of the following: Freshman science majors learned all lab skills, laboratory experiments were all completed, 4 excellent results regarding DNA, and DNA specialized skills did occur (however, there was contamination of specimens and students wanted to continue with portions of the experimental process) Freshman science majors were exposed to DNA Master

Year 2 Outcomes	Pros	Cons
In situ Fall 2011 (n=19)	Freshman science majors learned how to pipette, make serial dilutions, plate cultures, and maintain a laboratory notebook. Students completed the enrichment protocol. Students finished all experiments in the allotted class time period. Isolated DNA from 4 different bacteriophages. Performed DNA restriction digestion.	Contamination No micro graph images of the bacteriophages that were isolated Students wanted to continue the in situ portion during the spring semester, rather than the in silico portion.
In silico Spring 2012 (n=12)	Freshman science majors were exposed to DNA Master. A suite of 6 computer based annotation programs (Apollo, GenBank, GeneMark TB, GeneMark, Glimmer, Phamerator).	Students felt like the course was trying to combine two different fields of study into one course. Students expressed more likeness to either the in situ portion or the in silico portion, but did not like the combination of both.

Table 3. Students perspective on the course pro's and con's for HHMI–SEA Phage Genomics implementation at NCCU in Year 2 of the longitudinal study

software and the suite of 6 genome computer-based annotation programs (unfortunately, students felt that too much was packed into one course and they preferred to continue with portions of the experimental process as well).

Continuation of the PHAGES Genomics Course–Year 3

NCCU is currently in Year 3 of the Phage Genomics class supported by HHMI–SEA. NCCU has also received funding from HHMI Precollege and Undergraduate Science Education Programs to expand the genomics research experience for all of the General Biology laboratories. The selection criteria can be seen below:

1. Freshman or sophomore science major
2. First–time registrant for General Biology I
3. Open Enrollment (i.e., no SAT or GPA requirement)

Year 3 (Final Year) Longitudinal Research Outcomes

The novel bacteriophage in isolated in Year 3 was from a soil sample collected from Tyler Slade, sophomore Biology major from Yanceyville, North Carolina. Tyler collected the soil sample and the soil sample was processed by the enrichment protocol, followed by plating, spot tests, ten–fold serial dilutions, high–titer lysate, and ten plate phage infections. The plating of the enriched sample was done numerous times to ensure that all plaques yielded were consistently present. Spot tests were performed on the plaques to ensure the quality and reliability of the sample. Purification of the sample was done by a series of ten–fold serial dilutions, followed by harvesting of the sample by a high–titer lysate. Phage Genomic DNA was isolated and a restriction digest was performed with six different restriction enzymes. The genomic DNA was sequenced at Virginia Commonwealth University using the Sanger Method. The background information for Obama12 has been entered into a National Mycobacteriophage Database (http://phagesdb.org). Obama12 belongs to subcluster A4 has 87 genes (51,797 bp) and is currently being annotated.

Scientifically Based Technology Engineered Course Mycobacteriophage Longitudinal Research Results: Year 3 (Final Year)

According to the National Research Council (2003), students need to appreciate that science is a process and not a set of memorized facts. Traditional laboratories focus more on the memorization of facts to answer questions correctly on a fill–in–the blank worksheet, and requires minimal thought about the "hows" and "whys" of the experimental design and anticipated outcomes, rather than understanding the concepts. The report from the NRC also believes that science experiments should enable a student to think independently while at the same time exposing them to scientific protocols and research methods. The examples of inquiry based laboratories presented from the select schools in the prior section indicate students' ability to work in a group setting to discuss and resolve problems, project ownership, student enthusiasm, and the ability for students to make a contribution to the scientific research and the scientific literature. Because of the resource–intensive nature of basic research, too few students are given this type of opportunity, thus inquiry based laboratories as a part of the science curriculum impact a larger number of students.

HHMI supports the idea that undergraduate students should be exposed to an authentic research experience as early as possible. PHAGES introduces Undergraduate students to an authentic research experience via a bacteriophage genomics course. This course builds on themes and techniques across biology that are supported by fundamental concepts. This type of research experience connects students, teaching assistants, and faculty via experiments that enable them to share results, resources, and expertise.

One of the major goals of this initiative is to assess the educational value and learning potential of the SEA–National Genomics Research Initiative (NGRI) as implemented in standard education settings at colleges and universities. Our institution applied to the SEA to improve first year retention rates from General Biology I to General Biology II; to help the students better to apply concepts; and provide students with an early exposure to research. It was anticipated that this experience would motivate students to strive for better class participation and strive for better lecture and laboratory grades. By participating in this NGRI project, students were "doing science" with an enhanced ability to investigate a real–world problem, interpret the data and make conclusions about their results. The results of this research are extremely meaningful because the data generated by the students will be used by other researchers to answer medical, ecological, and evolutionary scientific questions, thus underscoring the collaborative nature of science as a result of the SEA.

In General Biology I, with the genomics–based laboratory course, the first few weeks of the fall semester are used to orient the students with basic science skills. This includes familiarizing the students with scientific equipment, using aseptic techniques, maintaining bacterial cultures, and performing serial dilutions. This course was team–taught by two biology instructors and two biology graduate students. Instructors were present to show the students proper techniques and answer any questions that the students may have had, while the graduate students were available in case additional assistance was needed during class. After the first year of this course implementation, there was an 80 % pass rate or better from the fall semester genomics course to the spring semester genomics course.

After the first semester of this course implementation, authors observed several things that worked to the benefit; for example, even though the laboratory component does not reinforce the lecture material, here was an increased student retention (80% pass rate or better) from General Biology I to General Biology II. Upon reflection, authors would also make changes within the Genomics laboratory course, such as allowing the students to work at their own pace rather than trying to keep the entire class working at the same pace. In addition, laboratory notebooks should be checked early and on a more frequent basis throughout the semester.

A short term goal has shown that participation in this PHAGES genomics research course has motivated students to participate more in class and strive to obtain better lecture and laboratory grades. A long term goal would be that by improving the students' overall educational experience, they would seek out summer research programs after their freshmen and sophomore year and subsequently pursue graduate degrees and careers in the science field.

At NCCU, the PHAGES Genomics course was offered under a special topics course, Biology 2030, which was for students enrolled in General Biology I (BIOL 1101) starting in 2010. The course met twice a week for a total of four hours and weighed 25% of the 1101 General Biology lecture course. Although the Genomics course weighs 25% of the General Biology lecture course, it also counted towards another 1 hour laboratory grade (one class with two separate grades). Genomics research courses such as; Biology 2030 has such important attributes for the undergraduate students who participated in it. Lists of attributes are as follows: technical simplicity in bacteriophage isolation, minimum background is required to be a bacteriophage hunter, and multiple achievement milestones within the enrichment protocol (Hatfull et.al, 2006). The students participated in a real research opportunity that was publishable, interesting to others, and had the ability to have ownership on project completed (Hatfull et.al, 2006).

According to the National Research Council (NRC,2003), students need to appreciate that science is a process and not a set of facts to be memorized. The NRC has suggested that students should be provided with opportunities within the undergraduate biology curriculum to engage in scientific research. Numerous studies have demonstrated the benefits of undergraduate research, including personal and professional gains such as increased confidence, ability to think like a scientist, and gains in communication and organizational skills. Moreover, it has been demonstrated that undergraduate research experiences enhance the retention rates in pursuit of the undergraduate degree (Hippel, Lerner, Gregerman, Nagda, and Jonides, 1998) and the interest of students in research careers in STEM disciplines (Lopatto et.al, 2008). As a result of these reports, Course–based Undergraduate Research Experiences (CUREs), have been developed to engage more undergraduate students in research, at both institutions such as ours, which are not research intensive and at research intensive Universities that cannot accommodate large numbers of undergraduates in internship–style research (Desai, Gatson, Stiles, Stewart, Laine, and Quick, 2008; Wood, 2003). Thus, CUREs make biology education look more like biology research.

Since 2010, NCCU has participated in the PHAGES program, supported by the HHMI– SEA, which permitted NCCU to introduce an authentic research experience, using Dr. Graham Hatfull's bacteriophage genomics model to one laboratory section of our General Biology I course for majors. For all other sections, NCCU continued with the traditional "cookbook" style laboratories, in which critical thinking is not as strongly emphasized and students frequently have misconceptions of what research science entails and what a career in the sciences is like. By the end of the Fall semesters (2010 and 2011), the students gained vital laboratory skills such as; micropipetting, making serial dilutions, plating bacterial culture and maintaining laboratory notebooks. In Spring 2011, the students used computer based bioinformatics tools such as GBrowse, GeneMark, GeneMark TB, Glimmer, Apollo, and Phamerator to analyze and annotate an adopted sequence from HHMI. Challenges encountered during year 1 were that the students did not complete the experiments in the allotted class time of 2 hours due to classroom scheduling conflict and the DNA yield did not comply with the 10 μl of purified DNA needed to be sequenced due to the decreased amount of DNA that was isolated. In Spring 2012, year 2 of the PHAGES implementation at NCCU, students used DNA Master, a newly created bioinformatics tool to complete the genome annotation process. Challenges encountered in year 2 were that the students' results were compromised due to contamination within the preparation solutions.

In 2012, formative assessment of the General Biology I students at NCCU which included both students enrolled in the traditional laboratory (1 section) and students enrolled in the PHAGES course (2 sections) reflected on the need for a more interactive environment in the lecture as well as the laboratory. Overall student feedback reflected positively on hands–on interactive experiences. They included valuable experiences, student expectations, areas of improvement as shown in Table 4 .

Overall Summative Student Feedback Regarding the [$TE_{Genomic}$ Biology Courses]	
Participating Student Responses in terms of Valuable Experiences	1.The hands on laboratory experience; 2.Learn Smart on–line modules/activities; and Uniqueness of the laboratory experience compared to other laboratory at NCCU.
Participating Student Responses in terms of Student Expectations	1.More than 60% of participants felt that the course challenged them to think critically; 2.More than 47% of participants agreed that taking this course has motivated them to pursue a career in the sciences; and More than 45% of participants agreed that this course has motivated them to attend graduate/professional school.
Participating Student Responses in terms of Areas of Improvement	1.Request for a more interactive environment during lecture (less lecture, more worksheets, more homework, etc.); and One professor/section vs. team taught.

Table 4. Student feedback from Year 3 reflected positively on hands–on interactive experiences

Table 4 provides the detailed information on student participant perceptions in terms of summative final feedback regarding the final year 3 of the HHMI–SEA Phage Genomics [$TE_{Genomic}$ Biology Courses] longitudinal study. Table 4 findings consisted of cumulative representation of student feedback regarding participation in the $TE_{Genomic}$ Biology Courses longitudinal study. The responses were as follows: 1) Valuable Experiences consisted of hands on laboratory experience, Learn Smart on–line modules/activities, and Uniqueness of the laboratory experience; 2) Student Expectations consisted of 60% of participants who felt that the course challenged them to think critically, 47% of participants agreed that taking this course has motivated them to pursue a career in the sciences, and 45% of participants agreed that this course has motivated them to attend graduate/professional school; and 3) Students stated that areas of improvement should consist of a more interactive environment during the course lectures (which should also include the following improvements –a.) Less time spent on instructor to student course lectures, b.) More course topical worksheets, and c.) More homework should be offered regarding specific course content). Student participants also stated as an improvement that one professor per course section is preferable to being team taught.

Summary

This paper details a longitudinal investigation into teaching genomics via a Technology Engineered Science Education course. A model for teaching examines inquiry based laboratory courses at several types of academic universities across the United States to further examine the benefits and limitations of a non–traditional approach. The teaching of science has evolved from laboratory courses that sought to confirm and illustrate teacher and textbook derived information to incorporating the process of science and emphasizing the development of higher cognitive skills. There is a fundamental belief among science educators that laboratory instruction increases observational skills, manipulation skills, and cognitive skills that reflect the understanding of scientific concepts. Despite the numerous changes science pedagogy has experienced, the process of learning science in the laboratory has been scrutinized due to increased understanding of metacognition and learning aptitudes. Over the past two decades, science educators have proposed the need to rethink the role and practice of biology-based laboratory exercises within the course. There remains a continual discussion among science educators as to whether inquiry based laboratory courses should be solely utilized in Academic-based settings and whether there remains a need for Traditional-based laboratory courses.

Findings

Genomics is a course where memorization is a difficult skill to use due to the nature of the massive amounts of data involved in the DNA sequences and gene structures that are native to the field. In order to measure the student understanding and success in the NCCU $TE_{Genomic}$ Biology Courses, examinations were given that entailed questions of comprehension, analysis, synthesis, application, and evaluation along with Technology Engineered supportive materials. For example, students at times received an article on *Nature* or *Science* that paralleled their in course laboratory experiences. The readings actively discussed different databases that were used in the $TE_{Genomic}$ Biology Courses and the students were then tested on their comprehension of the article with relevant questions that needed in-depth answers regarding course content. Through the technology re-engineering of the genomic science education courses the instructional delivery methodologies were re-adapted to take advantage of technology, resources, and multiple student learning styles. Thus, all of the course examinations were re-designed to increase student learning in genomics. Exams were open–book, take–home, and made active use of internet websites and online resources. Due to the intensity and length of the exams, the usual time allotted for test completion was between 8 to 24 hours and required an intense dedicated effort. In some cases, students were given several days to complete the exams (due to length and the amount of allotted genomic work).

In terms of student learning outcomes, the vast majority of institutions that were using re-engineered genomics courses reported positive feedback and outcomes from students. For example, the course instructors at Davidson College were highly pleased with the outcome of student participation on the re-engineered course exams; because the instructors could better understand how the students formulated their thought processes. As a result interaction between students and their teachers maximized leading to better understanding of the course content and thereby led to peak student performance. In order for participating instructors to better assess the accomplishments in the $TE_{Genomic}$ Biology Courses, participating students were assessed on their ability to synthesize and utilize course content online genomic databases and relevant information. This was in direct alignment with the educational goals of the course, and in turn, the experience of positively influenced student's perceptions of how they might positively contribute to biology (as stated in the research by Campbell, 2003). Thus, similar to the NCCU $TE_{Genomic}$ Biology Courses patterns of inquiry and internet–based teaching strategies, the re-engineered Genomics course at Davidson College positively affected the students' overall attitudes and perception of Genomics (and science in general) due to the nature of the hands–on Technology Engineered teaching methodologies, interactive inquiry techniques, and active use of internet–resources native to the course. As a result, participating students were both encouraged and excited to learn more about genomics. They also increased their confidence in terms of their active approach to, ability to experiment with, and engagement in learning about and within the pedagogical and professional framework of the sciences. Additional research findings and outcomes included: 1) Best practices in science education concerning evaluations that can be used in order to continuously improve science laboratories to positively impact student learning in terms of outcomes; 2) Encouragement of measurable student growth in terms of student–centered self–evaluation of their learning; 3) Student inspiration into future explorations into the sciences as postgraduate career choices; and 4) Data–driven assessment of $TE_{Genomic}$ Biology Course entrance and exit.

Recommendation

The research investigators recommend that further research be conducted into $TE_{Genomic}$ Biology Course methodology to determine how the positive outcomes of the research can be replicated within and external of the discipline. As more courses of these types are implemented now and in the near future, both science education and science learning will be greatly enhanced. This will further promote active, engaging, and dynamic science-based laboratory courses.

Conclusion

Traditional Introductory Biology courses usually entail lecture and laboratory exercises that verify the information given in lecture. This specific course setup stresses the learning content of scientific processes; however, this approach is unsuccessful in involving students in authentic scientific work that embraces inquiry. According to (Harrison, Dunbar, Ratmansky, Boyd, and Lopatto, 2011), the traditional verification approach with laboratory courses is the reason that students eliminate majoring in science or even considering higher education or career in the sciences. Cabrini College illustrated that a year–long laboratory course that was hypothesis–driven increased the student's enthusiasm about science as well as a significant increase in the desire to pursue graduate–level science studies.

At Cabrini College, study outcomes that focused on the consideration of Graduate Education indicated that the students showed increased interest in attending graduate school, as well as, some students showed increased interest in considering attending medical school. The study that focused on peer–mentoring indicated an increase in understanding the research, increased sense of responsibility, and improvement in oral communication skills. According to (Harrison, Dunbar, Ratmansky, Boyd, and Lopatto (2011), the students also reported gains in specific skills such as, research design, hypothesis formation, data collection, data analysis, and computing and information literacy, as well as, personal gains such as, greater independence of work and thought, tolerance of obstacles, readiness for new challenges, growing–confidence, and a sense of accomplishment.

At JMU, the PHAGES course has run for 4 semesters with the enrollment ranging from 9 to 18 students per semester. According to Temple, Cresawn, and Monroe, (2010) genomics has become a subdivision of biology since genome sequencing started in the early 1990's, the underlying skills and content of genomics should be added to complete a biology curriculum; either as an add–on to bioinformatics or genetics or the course could stand alone. Over the same time period, science education research has shown that the incorporation of the hands–on, inquiry based activities provides a superior learning environment for science students (Temple, Cresawn, and Monroe, 2010). The two levels of the Genomics courses that were offered at JMU were successful, even in the first semester, based on the student and faculty feedback. The main goal of the Genomics courses was to introduce the students to the world of genomics through hands–on experiences. The student enthusiasm was illustrated through the retention rate (82%) of the freshman genomics course, between the first two semesters the course was offered, compared to the retention rate (55%) of the traditional biology laboratory course, of those two semesters. The students who participated in the genomics course remained biology majors over the years, unlike the students who were enrolled in the traditional laboratory course. James Madison University obtained a unique method on how to maximize the students' interest and effectiveness in the genomics laboratory course; by integrating social network tools into the course curriculum which gives the students a sense of familiarity and comfort in something the students already know.

References

[1]. **Altschul, S. F., Gish, W., Miller, W., Myers, E. W., & Lipman, D. J. (1990).** Basic local alignment search tool. *Journal of Molecular Biology*, Vol. 215(3), pp. 403-410.

[2]. **Boyle, M. D. (2010).** "Shovel–ready" Sequences as a stimulus for the next generation of life scientists. *Journal of Microbiology & Biology Education*, pp. 38–41.

[3]. **Campbell, A. M. (2003).** Public access for teaching genomics, proteomics, and bioinformatics. *Cell Biology Education*, Vol. 2(2), pp. 98-111.

[4]. **Caruso, S. M., Sandoz, J., & Kelsey, J. (2009).** Non-STEM undergraduates become enthusiastic phage-hunters. *CBE-Life Sciences Education*, Vol. *8*(4), pp. 278-282.

[5]. **National Research Council (2003).** *Biology 2010:Transforming undergraduate education for future research biologists*. Washington D.C.: The National Academies Press.

[6]. **Cresawn, S. G., Bogel, M., Day, N., Jacobs-Sera, D., Hendrix, R. W., & Hatfull, G. F. (2011).** Phamerator: a bioinformatic tool for comparative bacteriophage genomics. *BMC bio-informatics*, Vol.12(1), pp.395.

[7]. **Desai, K. V., Gatson, S. N., Stiles, T. W., Stewart, R. H., Laine, G. A., & Quick, C. M. (2008).** Integrating research and education at research-extensive universities with research-intensive communities. *Advances In Physiology Education*, Vol. *32*(2), pp. 136-141.

[8]. **Hanauer, D. I., Jacobs-Sera, D., Pedulla, M. L., Cresawn, S. G., Hendrix, R. W., & Hatfull, G. F. (2006).** *Teaching Scientific Inquiry*. Vol. *314*(5807), pp. 1880, Education Forum.

[9]. **Harrison, M., Dunbar, D., Ratmansky, L., Boyd, K., & Lopatto, D. (2011).** Classroom-based science research at the introductory level: changes in career choices and attitude. *CBE-Life Sciences Education*, Vol. *10*(3), pp. 279-286.

[10]. **Hatfull, G. F., Jacobs-Sera, D., Welkin, H. P.,Russell, D. A., &Cresawn, S. G. (2013).** *Annotation and bioinformatic analysis of bacteriophage genomes: A user guide to DNA Master.* DNA Master software by Dr. Jeffrey Lawrence, of the University of Pittsburgh.

[11]. **Hatfull, G. F., Pedulla, M. L., Jacobs-Sera, D., Cichon, P. M., Foley, A., Ford, M. E., & Hendrix, R. W. (2006).** Exploring the mycobacteriophage metaproteome: phage genomics as an educational platform. *PLoS genetics*,Vol. *2*(6), pp. e92.

[12]. **Hippel, W. V., Lerner, J. S., Gregerman, S. R., Nagda, B. A., & Jonides, J. (1998).** Undergraduate student-faculty research partnerships affect student retention. *The Review of Higher Education*, Vol. 22(1), pp. 55-72.

[13]. **Hofstein, A. and Lunetta, V. (2003).** The Laboratory in science education: Foundations for the twenty–first century. *Wiley Periodicals*, pp. 28–54.

[14]. **Hofstein, A. and Lunetta, V. (1982).** The Role of the laboratory in science teaching: Neglected aspects of research. *Review of Educational Research.* pp. 201–217.

[15]. **Lopatto, D., Alvarez, C., Barnard, D., Chandrasekaran, C., Chung, H. M., Du, C., & Elgin, S. C. R. (2008).** Under Graduate Research: Genomics Education Partnership. *Science (New York, NY)*, Vol. *322*(5902), pp. 684.

[16]. **Osler, J. E. (2010).** *Visualus™ ©: visioneering volumetrically: The mathematics of the innovative problem–solving model of inventive instructional design.* Durham, NC: Publishing Division, OSI.

[17]. **Osler, J. E., Hollowell, G. P., & Palmer, C. E. (2008).** Technology Engineering Science Instruction in the Information Age: Integrating Instructional Technology in K–12 Education. *i-manager's Journal on School Educational Technology*. 4(1) June-Aug, 2008 Print ISSN 0973-2217, E-ISSN 2230-7133, pp.12-17.

[18]. **Osler, J. E. (2008).** *Technology engineering educational solutions for the hurricane katrina Region. The aftermath of hurricane katrina: educating traumatized children prek through college.* University Press of America. Dorothy Singleton.

[19]. **Osler, J. E. (2006).** Technology engineering: A paradigm shift to promote academic freedom in the information age. *The South Atlantic Philosophy of Education Society 51st Annual Yearbook.*

[20]. **PKAL (Project Kaleidoscope) (2006).** Transforming America's scientific and technological infrastructure. *PKAL Report on Reports II: Recommendations for Urgent Action*. Washington D.C.: Project Kaleidoscope.

[21]. Shaffer, C. D., Alvarez, C., Bailey, C., Barnard, D., Bhalla, S., Chandrasekaran, C.,& Buhler, J. (2010). The Genomics Education Partnership: successful integration of research into laboratory classes at a diverse group of undergraduate institutions. *CBE-Life Sciences Education*, Vol. *9*(1), pp. 55-69.

[22]. Suits, J. (2004). Assessing investigative skill development in inquiry based and traditional college science laboratory course. *School Science and Mathematics*, pp. 248–257.

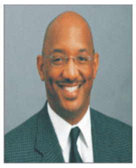
[23]. Temple, L., Cresawn, S. G., & Monroe, J. D. (2010). Genomics and bioinformatics in undergraduate curricula: contexts for hybrid laboratory/lecture courses for entering and advanced science students. *Biochemistry and Molecular Biology Education*, Vol. *38*(1), pp. 23-28.

[24]. University of Maryland, Baltimore County (2005). *UMBC: The Meyerhoff Scholars Program*. Retrieved October 5, 2012, from The Meyerhoff Scholars Program: http://www.umbc.edu/meyerhoff

[25]. Wood, W.B. (2003). Inquiry based undergraduate teaching in the life sciences at large research universities: A perspective on the Boyer Commission report. *Cell Biology Education*, pp. 112–116.

ABOUT THE AUTHORS

Dr. Gail Hollowell is an Associate Professor in the Department of Biology at North Carolina Central University (NCCU) in Durham, North Carolina. She is also the co-Program Director for NCCU's Howard Hughes Medical Institute Undergraduate Science Education grant which is designed to engage more minority students in science research opportunities. She has received her B.S. in Biology from NCCU and both her M.S. and Ph.D. in Microbiology and Molecular Biology respectively from Howard University in Washington. Her research interests are Infusing research modules in the Undergraduate Science Curriculum, Impact of technology in the Science classroom, Studying what motivates students to learn science.



James E. Osler is currently working as a Faculty member in the North Carolina Central University (NCCU) at School of Education where he is also the Program Coordinator of the Online Graduate Program in Educational Technology. He has authored multiple research articles, and published a series of books and e–books on Inventive Instructional Design, innovative research methods, and novel statistical analytics. Osler's additional interests include, ministry, fundamental Christian Education, building the mathematical foundations of inventive investigative inquiry, invention metrics, teaching, consulting and service–based initiatives. Presently he is involved in the research areas of developing novel mathematically grounded statistical metrics for in–depth analysis and Quantifying Instructional Design through qualitative and quantitative informatics.

April L. Hester is currently working as an Educator in Guilford County Schools. She teaches High School Science in Greensboro, North Carolina. She is specialized in educating lower economic demographics and students with lower reading and writing skills. She also has teaching experience with students on the pre-college level, lecturing on topics such as building relationships, time management, budgeting, study techniques, professionalism, public speaking and 5-year plans with short-term and long-term goals. As a professional Science Educator, she has in-depth laboratory experience with skill sets that entail aseptic technique, DNA isolation, bacterial growth, centrifugation, micropipetting, gel electrophoresis, isolation and purification of bacteriophages as well as an introductory skill level of bioinformatics.