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Connecting Underrepresented Scientists to the Biology Core Curriculum, Volume 1

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The background of the entire page is a collage of laboratory glassware. At the top, a pair of safety goggles is visible. Below them, several beakers and test tubes are arranged in rows. The liquids inside are various colors: yellow, red, and green. The central text is contained within a white rectangular box with a black border.

Connecting Underrepresented Scientists
to the Biology Core Curriculum

Volume 1

Edited by

Aaron E. Schirmer and Lisa C. Wallis

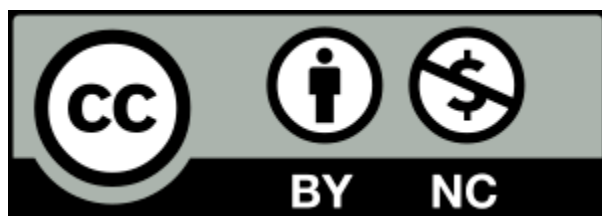
Connecting Underrepresented Scientists to the Biology Core Curriculum

Edited by
Aaron E. Schirmer and Lisa C. Wallis

Volume 1

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Introduction

The inspirations for this book came from the nexus of my own professional diversity, equity, and inclusion (DEI) journey, ongoing curriculum development, and a personal desire for better DEI resources for my students and myself. As a professional and STEM educator I have seen the impact that DEI work can have on a campus and in a classroom. The STEM fields have significant room for improvement with regard to diversity, equity, and inclusion, and I am working to learn more and use my position to effect change in the STEM classrooms of Northeastern Illinois University (NEIU). NEIU is a federally designated Hispanic Serving Institution (HSI) and has been ranked by *U.S. News and World Report* as the most diverse university in the U.S. Midwest. NEIU serves more than 7,000 undergraduate and graduate (masters level) students, the majority of whom fall into one or more of the groups that are underrepresented in STEM (*e.g.* minority, first generation college, or low income). Because of the population NEIU serves, it is a perfect place to maximize the impact of DEI work and create a future workforce of diverse, equity minded, scientists.

In my own classroom I have been working to center diversity and amplify the voices of underrepresented scientists. I believe that diversity in thoughts, opinions, and backgrounds enhances learning environments and improves academic outcomes. I also believe diversity is crucial to solving the many problems that are plaguing our environment, communities, and world. We need broad input, collaboration, and experience if we hope to tackle (and overcome) these extremely pressing issues. Future scientists will need to be familiar with the issues surrounding equity and inclusion and be able to embrace diversity if they wish to

be successful. Through exposure to these issues in my classroom, I hope to prepare students for success and support them in developing crucial life-long learning skills.

While I am working to center and amplify underrepresented voices in STEM, I am often frustrated by the lack of high quality resources and the time it takes to find them. For example, finding strong examples using internet searches or word of mouth is time consuming and difficult to organize when you are teaching multiple courses within a semester and different courses across semesters. Multiple examples are also necessary to find ones that the majority of students will find engaging once they are incorporated into the curriculum. If the examples do not have an impact for the students, then they can never achieve their intended purpose of creating awareness of DEI issues and diversifying STEM fields.

I believe what is needed are resources where these types of examples are compiled and the work of the underrepresented scientists is connected directly to the biology curriculum in ways that students find interesting and engaging. To begin creating such a resource, I developed an assignment where undergraduate and graduate students identified underrepresented scientists and researched their personal story and their contributions to science. The students then gave examples of these scientists' work and outlined how they felt it could be connected directly to core areas (Cell/Molecular Biology, Genetics, Ecology, Physiology, and Evolution) of the biology curriculum. This assignment culminated in a final paper that contained 4 sections (Scientist Story, Contribution to Science, Connection to the Biology Curriculum, and References) based on the students' research. In the Spring of 2023, I instituted this assignment in my Senior Seminar (BIO 390) and Biological Literature (BIO 405) courses for upper-level undergraduates and graduate students, respectively. Twenty-five students completed this assignment, and from this group I chose ten representative examples to compile into this book.

These ten scientists were selected by the individual students because they connected to them or their work in a meaningful way and wanted to share that connection with other students and faculty. Often the selected scientists have similar backgrounds, genders, and stories to their own, and the students can see themselves reflected in these scientists and their work. I hope that other students reading this book can be inspired by the work of these outstanding scientists and can also find examples where they see themselves reflected in this amazing science. I also hope that this book will be helpful to faculty who are engaged in their own DEI work. I hope this book will make meaningful examples easier to find and that the student's writing can identify simple (and engaging) ways to include these scientists' work in their personal curriculum. By centering and amplifying these works we can begin to close the DEI gap in STEM, improve the educational outcomes for all of our students, and hopefully create a better and brighter future.

- Aaron Schirmer

Editors and Acknowledgments

Aaron Schirmer is a Bernard J. Brommel Distinguished Professor in the Department of Biology at Northeastern Illinois University (NEIU). His research focuses on the impact of environmental perturbations, such as photopollution and social jet lag, on the circadian system and the development of new technologies for studying circadian clocks *in vivo* and *in vitro*. Aaron teaches a range of courses for non-majors, majors, and graduate students (e.g. Introduction to Biology, General Biology, Genetics, and Chronobiology) where he integrates his research interests and expertise into his courses. Aaron has also been working to celebrate diversity and elevate the work of underrepresented scientists in his classrooms and laboratory. He believes this assignment and book are a small step in this process and he hopes it will help others do the same. Aaron was drawn to NEIU by the diverse student body and the potential to have strong synergy between his teaching and research programs. He has been at NEIU since 2009.

Aaron would like to acknowledge all of his fantastic colleagues in the Department of Biology and across the University. They have all been instrumental in his DEI journey and he has learned so much from their examples. He tremendously appreciates their guidance which has helped him become a better and more conscientious educator! He would also like to acknowledge Dr. Shireen Roshanravan and the Office of Equity, Diversity, and Inclusion. Her programming around DEI in the classroom and her work to improve our campus culture have been extremely helpful. He has found all of the workshops enlightening and they contributed greatly to the inspiration for this book. Lastly, he would like to acknowledge his co-editor Lisa Wallis. He appreciates her help, guidance, and willingness to go on this journey with him.

As the NEIU eResources & Systems Librarian and Professor, **Lisa Wallis** is interested in analyzing users' information-seeking behaviors in order to simplify and streamline their access to information. A recent publication in *Information Technology and Libraries* examined the changes in library online resource usage during the COVID-19 pandemic. Lisa is also the NEIU Libraries' liaison to Biology, Chemistry, Earth Science, Mathematics, Physics, Health Sciences and Physical Education, and Public Health and a 2nd Bachelor's student in Biology at NEIU. She has been at the University since 2007.

Lisa is grateful to her NEIU Libraries colleagues for their campus-wide leadership roles in the Open Access movement to ensure students have access to free or affordable curricular materials. She would like to acknowledge the work of the NEIU Affordable Course Materials committee for its education and outreach around review, selection, and development of Open Educational Resources, with special thanks to committee co-chairs Robin Harris and Dr. Elizabeth Rodriguez. Finally, she extends a special thank you to Aaron Schirmer for extending the invitation to collaborate on this project.

A Note on References

Science journals and other scholarly publications use a variety of citation formats, with some titles developing standards unique to their publications alone. The different formats vary in ways such as author naming conventions, capitalization, or typeface styles. In order to maintain consistency and support reader ease, we have elected to prepare all the reference lists using the Name-Year system of *Scientific Style and Format*, 8th edition, published by the Council of Science Editors (CSE) in 2014. For more information, please visit <https://www.scientificstyleandformat.org/Home.html>.

- Lisa Wallis

Table of Contents

Introduction	3
Editors and Acknowledgments	6
A Note on References	8
Table of Contents	9
June Dalziel Almeida	10
Cell/Molecular Biology by Dallia Husameddin	
Xiaomin Bao	16
Cell/Molecular Biology by Brittany Zaruszk	
Elizabeth Bergey	23
Ecology by Sara Crow	
Aisha Burton	28
Genetics by Dahlia Lou	
Colleen Cavanaugh	34
Cell/Molecular Biology (Microbiology) by Sadia Khanam	
Kizzmekia Corbett	41
Molecular Biology by Nahid (Nina) Irani	
Esther Lederberg	48
Cell Biology by Ivan Morales	
Sandra Lopez-Vergès	53
Anatomy and Physiology by Carla M. Amaya	
Maria de Lourdes Cabezas Tapia	61
Cell/Molecular Biology by Eduardo Vaca	
Elba Serrano	67
Genetics by Sumaiya Ahmed	
Contributors	72

June Dalziel Almeida

Cell/Molecular Biology

by Dallia Husameddin

Scientist Story

June Dalziel Almeida (née Hart) was a Scottish virologist who discovered the first coronavirus to cause disease in humans (Gellene 2020). She is also the first person to witness the rubella virus (also called German measles) under an electron microscope, and is known to have developed several scientific techniques related to the detection and diagnosis of viruses and bacterial disease (Almeida 2008). Her accomplishments make for a curious read, as she did not receive a formal college education but was still able to succeed and make advancements in her career and field. Almeida was sixteen when she was forced to abandon her school's curriculum despite her excellent marks, and she instead pursued work in post-World War II Scotland to support her kin (Rothberg 2021). She began her career as a lab technician at a hospital in Glasgow, a feat that she would dedicate to her brother who died from diphtheria (June...[accessed 2023]). His death from the bacterial infection curated in her a keen interest in the biological sciences, one that would motivate her research, developments with viral infections, and other related experiences (June...[accessed 2023]). Almeida's narrative is distinct in that she did not allow certain setbacks (e.g. her tender age, sex, and poor background) to discount her interest, and pursuit in science. She took on menial work and used them as opportunities to develop and hone her skills. It was through this approach that she would later be entrusted with more difficult assignments and become an established scientist whose most notable contributions remain relevant and in use in present times. Her successes serve to demonstrate what those from limited

circumstances can achieve when their minds are nurtured in the right environment and are allowed to mature in more ideal conditions.

Contribution to Science

It was in Glasgow, Scotland as a hospital lab technician that Almeida learned how to use a microscope to detect disease in tissues, and in Ontario, Canada at a Cancer Institute that she learned how to operate an electron microscope and take detailed images of various organisms to determine their structure and function (Combs 2020). This instrument was a recent invention in her time and allowed for high-resolution images of cells and viruses. It however made the distinction of the product difficult (Combs 2020). Almeida developed a simple but effective technique to remedy this. She introduced antibodies that were extracted from infected patients into virus preparations that consisted of antigens. Antibodies are attracted to antigens, and surround the virus when introduced to the preparation (Combs 2020). This allowed her to differentiate the product as a virus rather than a cell and to indicate its location, which in turn revealed its structure and other general components. Clinicians are now able to diagnose viral infections in patients as a result of this technique (Combs 2020). Her technique also established and brought attention to the relationship between the structure and function of an organism (Brown 2020).

Her expertise in these developments would result in extensive discoveries for the scientific world as scientists are now able to observe the structures found in various viruses and diseases in high resolution. Virologist Albert Kapikian discovered norovirus, a virus that attacks the gastrointestinal tract, through the techniques that she developed. It was also through these methods that Almeida discovered the first coronavirus in humans, an infectious disease whose variant would cause a worldwide pandemic almost six decades later. She would come into

this role when briefed with a flu-like virus called B814. The director of the Common Cold Unit of the British Medical Research Council, Dr. David Tyrrell, had reached out and sent her samples when he had heard of her skills and expertise and was unable to cultivate and diagnose it himself (Combs 2020). She added a phosphotungstic acid into the sample, which stains the cells with color and heightens its contrast, and collected a clear image of the disease with an electron microscope (Gellene 2020). Almeida, Tyrrell, and the other scientists on their teams chose to call it “coronavirus” due to its appearance. The proteins that surround the membrane surface resemble a crown or wreath, and crown in Latin is *corona* (Brown 2020).

Almeida was considered one of the best scientists of her generation. Her colleagues, both domestic and abroad, lauded her work and ambition, and often sought out her expertise to collect images and diagnose viruses and disease. She was awarded a master’s and a doctorate in science for her research on antibodies, and her microscopic images continue to appear in textbooks and articles (Slade 2021). Her grand reputation did not succeed her however, and she and her work were overlooked until the spread of the human coronavirus in 2019, which prompted further research into the base she had developed almost six decades earlier. She has since received some recognition for her breakthroughs in the medical field, but her name remains buried behind those who have succeeded her, as developments in medicine and vaccines have been extensive since her retirement, and populations around the world have long acknowledged the Covid-19 pandemic and its side effects as their new normal.

Connection to the Biology Curriculum

June Dalziel Almeida’s work concerned the microscopic images of various organisms that she collected with an electron microscope. Electron microscopes

use accelerated electrons as a light source (Combs 2020). Electrons have a shorter wavelength than visible light, which allows for clearer and more resolute images (Combs 2020). Her images were used to research the particles and structures of viral infections, and to discover the relationships between viruses and other forms of disease. She shared her techniques with other virologists, who were then also able to diagnose infected patients based on the antibodies that these antigens attached themselves to, and to compare viruses based on their structural appearance and separate them into their own families or sects.

Biological sciences are at the heart of her research, and molecular and cell sciences are at the heart of her discoveries. Biological science entertains the cellular foundation of all life, the basis of all connections, and draws its conclusions from centuries of observations. Almeida's identification of the human coronavirus in particular was expanded and pursued further a mere six decades later, and scientists now have the information to detect and counter it as a result of her work. The general population also has access to diagnostic tools (*e.g.* PCR and antigen tests, extensive developments from online sources) that allow them to evaluate this information on their own. That is, in a sense, the purpose of science: the curation of knowledge, and the transcension of barriers. These details work to provide accurate and reliable information about the natural world, and to overcome the limitations that once burdened the scientific world.

Molecular and cell sciences entertain the structural and componential basis of cells and the activities that result from them. Almeida's work relates to the identification of viral infections, and the functions that can be assumed from these structures. Current ideas and descriptions of the coronavirus are based on her microscopic images. Her patience and persistence allowed scientists to observe variants of the first coronavirus with the technique she developed: the

incorporation of a phosphotungstic acid to a sample to heighten the contrast of the image. These images work to showcase their structures, which in turn allows scientists to have a clear sense of their function based on their shape and size. Almeida's attention to detail six decades earlier created a foundation for further development. Her contributions to the scientific world are immeasurable as her techniques have revolutionized newfound instruments from her time and have been shared and passed down for generations.

Students who specialize in natural sciences are provided with various opportunities to enhance their worldview through the connections made between their materials (textbooks, teachers) and their lab sessions (research, raw data collection). Lab sessions work to curate a certain appreciation for experimentation, for the collection of raw data and its communication to the outside world. Almeida's work in particular is rooted in trial and error. She took on menial work with optical and electron microscopes to enhance both her skills and the instruments themselves. Her curious and dedicated nature motivated the techniques that students now use to witness tissue and disease under a microscope, and relate their structure to their processes. Modern scientists also continue to use her techniques to diagnose and treat viruses and disease, to observe the interactions that occur between antibodies and antigens, and to understand the effects that viral and bacterial infections, such as the ones she had discovered, have on global public health. Almeida does not often receive recognition for her breakthroughs in science, but her name is echoed through the work that she founded and that others continue to build on. She is succeeded through her daughter Joyce, whose final comment about her mother compliments her legacy and outreach, "True to form, she could not leave electron microscopy forever" (Gellene 2020).

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Xiaomin Bao

Cell/Molecular Biology

by Brittany Zaruszk

Scientist Story

Xiaomin Bao is currently an assistant professor at Northwestern University in the Department of Molecular Biosciences and Department of Dermatology. Bao and her lab's focus are on gene regulation of adult stem cell maintenance and human tissue regeneration. Previously, Bao was a graduate student at Iowa State University and was a Postdoctoral Fellow at Stanford University School of Medicine. She has received several awards such as the NIH/NIAMS K99/R00 Pathway to Independence Award from 2014 to 2021, the Northwestern University Basic Insight Award in 2019, and the ESDR/SID Young Investigator Collegiality Award in 2019 (Bao Lab 2016).

I chose Xiaomin Bao because I was interested in her research on epidermal differentiation and somatic tissue. I wanted to learn more about the mechanisms and components that are involved in this type of differentiation. I was first introduced to this topic from a writing project I completed in a course for my bachelor's degree. After looking through different articles about differentiation, I decided to specifically look into epidermal differentiation. While continuing my search, I discovered Bao's article on the BRG1/BRM-associated factor (BAF) chromatin remodeling complex and its involvement in epidermal differentiation (Bao et al. 2015). At the time I did not use this article in my project, but I believed that for this book it would be good to discuss Bao's findings and highlight some of the other work that she has done. As a woman working in STEM, Bao has brought attention to important research involving epidermal differentiation, somatic tissue,

as well as other areas in her lab like tissue regeneration and stem cell maintenance. I believe this entry will provide further recognition for her work and introduce her research to other students who are also interested in learning about epidermal differentiation and learning more about other aspects of her research.

Contribution to Science

An aspect of Xiaomin Bao's work includes her research on somatic tissue. Somatic tissue is tissue that is made up of cells that are not either sperm or egg cells (Somatic...2023). Specifically, Bao's research focuses on differentiation of somatic tissue and self-renewing somatic tissue. Somatic tissue differentiation is necessary for cells to have specialized functions, and failure to differentiate can lead to various human diseases like the autoimmune disease psoriasis (Bao et al. 2015). The BRG1/BRM-associated factor (BAF) chromatin remodeling complex is a necessary part of the differentiation process for somatic tissue. It is needed for the differentiation of somatic tissues like the epidermis, which makes up the outer layer of skin and is composed of a catalytic subunit and 10 regulatory subunits (Bao et al. 2015). In her study, Bao and her colleagues examined epidermal differentiation with the BAF complex using Assay for Transposase Accessible Chromatin (ATAC)-sequencing. ATAC-sequencing involves direct probing of open chromatin regions in epidermal cells. Open chromatin regions are regions in the human genome that can interact with DNA regulatory elements, and accessibility to these regions is important for the gene expression of tissue cells (Wang et al. 2021). By sequencing regions of open chromatin through ATAC-sequencing, researchers can have a better understanding of how chromatin packaging and other factors affect gene expression. Bao and her colleagues discovered that both subunits, BRG1 and BRM, of the BAF chromatin remodeling complex are needed to maintain open chromatin sites during epidermal differentiation (Bao et al. 2015). Additionally, BAF

and p63, a transcription factor, work together in controlling the keratinocyte-specific open chromatin landscape which aids in epidermal differentiation. Keratinocytes are a type of skin cell that produces keratin and makes up the structure of the epidermis (Eckert and Rorke 1989).

Along with somatic tissue differentiation, Bao also conducted research on self-renewing somatic tissue. Self-renewing somatic tissue is maintained by a continuous cycle of progenitors and by the restricted activation of differentiation. Progenitors are descendants of stem cells and are cells that can differentiate into more specific cell types, but only have the capacity to do so a limited number of times (Mathia et al. 2018). Furthermore, premature differentiation can lead to tissue failure and loss of progenitors (Bao et al. 2017). Bao and her colleagues discovered the role of PRMT1, an arginine methyltransferase, in progenitor maintenance. PRMT1's role includes its involvement in sustaining proliferation genes, surpassing differentiation genes, and its necessary involvement in epidermal tissue development and homeostasis. Using tandem affinity purification, a technique for studying protein-protein interactions, Bao and her colleagues discovered that CSNK1a1, serine/threonine kinase, is involved with PRMT1 to maintain progenitor self-renewal (Bao et al. 2017). Specifically, CSNK1a1 directly interacts with PRMT1 by phosphorylating it to control its genomic targeting to sustain the expression of proliferation genes. Additionally, they discovered that the interaction of PRMT1 and CSNK1a1 worked to suppress the expression of GRHL3, a transcription factor and an activator for terminal differentiation that can drive premature differentiation, through chromatin immunoprecipitation sequencing. Chromatin immunoprecipitation sequencing involves antibodies and is used to enrich specific DNA-binding proteins along with their DNA targets (Park 2009). Overall, from this study Bao and her colleagues found that PRMT1 and CSNK1a1

work together to sustain the expression of proliferation genes and repress pro-differentiation genes (Bao et al. 2017).

Connection to the Biology Curriculum

Bao's research in somatic tissue differentiation and self-renewal somatic tissue are connected to the cell/molecular biology curriculum. Cell biology involves the study of cell structure, function, and behavior of cells. In her research, Bao focused on somatic cells which are the cells in the human body that are not germline that make up either sperm or egg cells (Somatic...2023). Somatic cells make up tissues and organs like skin. Specifically, Bao focused her research on somatic tissue and epidermal differentiation which is an essential process that works to enhance a cell's fate for specialized function. Bao's research into somatic tissue differentiation and its necessary components highlight how differentiation of somatic tissue is essential because failure for proper differentiation can lead to disease. From these findings, more research into this can be conducted such as on the physiological properties of somatic cells and their association with various diseases. While an important aspect of cell and molecular biology is learning about cell differentiation, another aspect is learning about how cells proliferate because cell proliferation is the process of multiplying the number of cells and cell differentiation is the process of forming different cell types which form tissues and organs (Ruijtenberg and van den Heuvel 2015). Through Bao's findings the reader can learn about the pathways and regulatory mechanisms that are involved in cellular differentiation specifically for somatic cells and the components that make up the process for cells to differentiate. Furthermore, the reader can learn more about the pathways and mechanisms associated with cellular proliferation such as the importance of different components needed for the self-renewal of somatic tissue cells.

Overall, Bao's findings can be used to expand people's knowledge and understanding of cellular differentiation and cellular proliferation that are associated with the topic of cellular and molecular biology. Bao's findings can be used to highlight the necessary components needed for cellular differentiation such as if both of the catalytic subunits in the BAF chromatin remodeling complex for epidermal cell differentiation are not present, then cellular differentiation of the somatic cells making up the epidermis will not differentiate properly or at all (Bao et al. 2015). Bao's findings from her research also highlight cellular proliferation by discovering additional roles of PRMT1, which is an arginine methyltransferase, and its ability to sustain proliferation genes that promote cellular differentiation (Bao et al. 2017). Along with these findings, Bao's research has opened up the doorway for more research to be conducted looking at other parts of cellular differentiation and cellular proliferation such as understanding other components involved and interactions among the various components to discover what happens when parts do not work properly.

This is interesting to me as a student because it shows that all components of things like the BAF, a multi-subunit chromatin remodeling complex, are necessary for proper functioning. As a student, I find that it is interesting to learn about these components and potentially see similarities to other fields because they highlight how all components of various molecular complexes may also be necessary for the whole system to function. It is important to be aware that in the different branches of science, such as the study of cells in the human body, various components have to work together for proper functioning. If one of these components is not working properly then the outcome could have a disastrous impact such as improper cell division. Additionally, reading about this research is interesting because it can have an impact on a person's way of thinking such as

having an expansionist view of the world versus a reductionist view of thinking such as an understanding of how parts work together and in isolation. For students, I believe it is interesting to learn about research that they may not otherwise have known about or researched for themselves. Reading and learning about novel research allows you to think critically and analyze it in depth such as understanding why the researchers chose to run the experiments that they did. While I only highlighted two of the many articles that Xiaomin Bao was a co-corresponding author on and published, I hope that other students find this just as interesting as I did and are inspired or encouraged to look more into this research topic and Xiaomin Bao's research.

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Elizabeth Bergey

Ecology

by Sara Crow

Scientist Story

Dr. Bergey has a broad area of interest in the ecology and conservation of land snails, freshwater invertebrates, and algae. She currently works at University of Oklahoma (OU) as a biology professor and conducts research with undergraduates and graduate students with an emphasis on urban snail ecology, the effects of disturbance on freshwater macroinvertebrates and algae, and invertebrate surveys. Dr. Bergey received a double B.S. in zoology and botany from OU in 1977, when women were not common in the scientific community. She later completed her masters from Colorado State University (1981) and then her PhD from University of California (1992). During her education she focused on benthic invertebrates and benthic algae.

Now as a professor, she still looks at invertebrates and algae but has grown to have a larger focus on land snails. Dr. Bergey encourages her students and researchers to find their own paths and supports them along the way. Her broad range of interests and work makes her a perfect candidate for this book and a great example for General Ecology. Dr. Bergey has a wealth of knowledge that makes every conversation with her unique, educational, and fascinating regardless of the topic; it was something that drew me to her at the North American Diatom Symposium.

Contribution to Science

Dr. Bergey has a wide range of work on algae, land snails, and crayfish. Her work has helped further our knowledge on those organisms. Dr. Bergey and colleague Lalit K. Pandey examined whether algae could be used as an indicator of metal toxicity and recovery in periphyton (Pandey and Bergey 2018). They found that diatom algae was a good indicator of stress caused by the metals in the water and even indicated recovery of the system when the metals were removed. Dr. Bergey also looked at diatom algae found on the shells of common snapping turtles with her former student researcher Shelly Wu. They found six diatom species across samples from five different states, two of those diatoms were previously undescribed and only known from the turtles from their study (Wu and Bergey 2017). They also showed that using museum specimens can be an effective method to study the distribution of epizoic organisms.

Dr. Bergey's work on land snails is just as broad as her work with algae. Some of her work with land snails was to understand the dispersal of nonnative species in urban areas when the snails' normal modes of dispersal are ineffective (Bergey et al. 2014). In that study Dr. Bergey and her team found that plant nurseries helped with the dispersal of the nonnative species of land snails, as only one snail had to be moved in order for a new population to form via asexual reproduction. Other work Dr. Bergey has done with snails is to look at prescribed fires in natural areas to see if they affect native land snails (Ray and Bergey 2015). In that study they found that while snails grew more in burned leaf habitats, the snails had a high post-fire mortality rate, and they recommend avoiding doing a prescribed burn in exceptionally dry conditions to minimize loss of native snail species.

Dr. Bergey's work with invertebrates has included looking at the multiple drivers of decline in crayfish (Richman et al. 2015). The group's findings showed that

increasing temperatures, land conversion from a natural state to agricultural use, and increased logging of mature forests leading to increased frequencies of forest fires are a few of many factors affecting the different crayfish populations. While the threats acting independently of one another may pose little danger to a species, threats acting together can significantly increase the rates of decline of the crayfish. Another crayfish project that Dr. Bergey worked on, looked at the implications of habitat fragmentation in stream crayfish (Jones and Bergey 2007). They found that the crayfish *Orconectes saxatilis* with a restricted range in the upper Kiamichi River watershed in Oklahoma preferred riffles, contrary to previous recorded data. The rivers that feed the upper Kiamichi River are intermittent and lead to dry periods where the *O. saxatilis* goes into a dormant state in dry riffles. The predominant use of riffles by *O. saxatilis* contribute to its small range and put this species at risk.

Dr. Bergey's wide range of work on algae, land snails, and crayfish not only has helped further our knowledge on those organisms, it has helped our understanding how the environment is being affected by various factors. By incorporating some of her work into the curriculum we can better understand how it's just not one thing that affects the environment but multiple things.

Connection to the Biology Curriculum

Dr. Bergey's research connects her to ecology courses in the biology curriculum used at Northeastern Illinois University. Her work covers a wide range of topics within ecology that can easily be integrated into ecology coursework. Dr. Burgey's work on how invasive land snail species can spread can add to the lectures that discuss invasive species. Our current examples tend to use invasive species such as zebra mussels and Asian carp, both being aquatic organisms. By using snails we can discuss dispersal via other animals, garden plants, and species that are hermaphroditic.

Another example we can use in our ecology classes is the pros and cons of prescribed fires on natural areas and their effect on snails and other invertebrates. We tend to focus on the plants and the control of nonnative species. This will add another element to our lectures when we can discuss how doing controlled burns at different points of the year can both positively and negatively affect the habitat and its inhabitants.

Dr. Bergey's work on algae can be incorporated into several lectures ranging from the effects of pollutants to population studies. These are items we could even do as class lab experiments in place of the buckthorn lab (a lab where students look at the invasive plant's allelopathic effects on the ecosystem). We can test the proficiency of biological indicators with the diatom algae by exposing them to different pollutants and environments. The students would be able to pick a condition and compare results with other groups with different conditions or pollutants. These are just a few examples of how we can tie in Dr. Bergey's work into the ecology curriculum.

It's important to incorporate new ideas into our lectures and labs as it brings a fresh light into what science is all about. Sometimes having a lab without a clear outcome was more of a learning experience than one with a set outcome. Working with diatom algae we will be able to get a wider range of results depending on the algae and the controls we choose that will get the students thinking about the big picture topics covered in General Ecology.

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Aisha Burton

Genetics

by Dahlia Lou

Scientist Story

Dr. Aisha Burton is a Chicago native who earned her bachelor's degree at the University of Illinois at Chicago (UIC) (ASM 2021). Her interest in science started at a young age by working in her parents' garden, visiting the Sandridge Nature Center and going to science camp during the summer (Spindler 2021). It was an AP chemistry class during high school that cemented to her that she wanted a degree in science. She was a chemistry major at UIC with a biology minor. It was during a microbiology elective course where she fell in love with microbiology (ASM 2021). This love led her to giving up a spot in the pharmacy college to pursue microbiological research. She applied for various graduate programs but was not admitted to any, however she did not give up and applied and got accepted to a post-baccalaureate program at the University of Missouri studying *Desulfovibrio vulgaris* Hildenborough as well as bacteriophages (ASM 2021).

After her post-baccalaureate program, she went on to get her PhD at Indiana University (IU). The first lab she worked in was not the correct fit for her, because she felt that her mentor was not providing adequate mentorship (ASM 2021). So, she made the tough decision of switching labs. This ended up being the best thing for her and allowed her to meet her mentor for her post-doctoral fellowship. In this fellowship she is studying the regulatory roles of small proteins on two-component systems in *E. coli* at the National Institutes of Health (NIH) (Spindler 2021). She is also an introductory biology adjunct instructor at Montgomery College. She has been listed as a Rising Star in Cell Mentor's list of 1,000 Inspiring Black Scientists in

America and wants to build her own research program studying protein-protein interactions on medically relevant bacteria (ASM 2021).

I chose Dr. Burton to be the subject of my paper because she is a microbiologist that looks like me. As a black woman in STEM, it is important to me to be able to see other black women achieving the same things I hope to one day achieve. I also chose her because she works a lot with the Black in Microbiology movement to increase the awareness of the lack of diversity and inclusivity in the microbial sciences.

Contribution to Science

Dr. Aisha Burton earned her PhD in 2019, performing molecular genetics and biochemical assays to characterize SigN, a plasmid-encoded sigma factor in the soil bacterium, *Bacillus subtilis*. Sigma factors are important because they are involved in the start of transcription in bacteria and help to regulate gene expression (Paget, 2015). SigN is a sigma factor that helps express genes on a plasmid that causes cell death after it has experienced DNA damage (Burton et al. 2019).

Sigma factors are one of five proteins that make up the RNA polymerase (RNAP) molecule that bacteria use (Rye et al. 2013). However, they are not part of the RNAP core enzyme. There are several different sigma factors that can assemble with the core RNAP enzyme. Which sigma factor is used depends on the needs of the cell and the environment around the cell (Davis et al. 2017; Helmann 2019). They are crucial to the initiation of transcription. Sigma factors recognize specific promoters in the DNA sequence and open the DNA strand to allow RNAP to bind. Without the sigma factor, RNAP would bind at random locations on the DNA strand and create mRNA that did not encode for the correct proteins. Sigma factors help to regulate gene expression because they only allow RNAP to bind to promoters.

Promoters have a specific sequence that regulates how frequently the genes they correspond to are transcribed (Rye et al. 2016).

SigN was originally a sigma factor homologue, ZpdN, that was found on an ancestral strain of *B. subtilis* (Burton et al. 2019). Laboratory strains of *B. subtilis* have lost the plasmid, pBS32, that encodes for the factor because it was not copied frequently enough to survive in laboratory strains (Burton et al. 2019). Dr. Burton helped to verify that ZpdN was in fact a sigma factor through various biochemical assays and molecular genetics. This led to ZpdN being called SigN and further research into its promoters and how its expression is regulated.

Dr. Burton continued her research and was able to identify three different promoters that initiate SigN's transcription, P_{sigN1}, P_{sigN2}, and P_{sigN3} (Burton et al. 2019). She was also able to figure out that when DNA damage occurred in the cell, SigN expression was no longer repressed and the increase in the expression of SigN created a positive feedback loop. Though it is known that plasmid pBS32 can cause cell death when DNA damage has occurred, it is unknown exactly how SigN helps the process or why the plasmid is part of the bacterial genome (Burton et al. 2019).

Connection to the Biology Curriculum

Dr. Burton's work characterizing SigN connects to the genetics curriculum. SigN is a sigma factor and those factors help to control gene expression in bacteria. In our genetics classes we learn about transcription and gene expression in bacteria before we move on to those same processes in animal cells.

We learn that RNAP is the main enzyme involved in transcription that uses a DNA template to produce RNA that will later be used to create proteins. It is an essential part of the central dogma of biology. We also learn about some of the components of RNAP in prokaryotes, such as a brief mention of the sigma subunit

of RNAP. However, we don't go into much depth or detail about what composes RNAP. Dr. Burton's work helps to expand on the knowledge of RNAP. The sigma factor that she has characterized can teach how most other sigma factors work. Sigma factors work to ensure the RNAP enzyme finds the correct promoter region in the DNA to start transcription. It is crucial in ensuring that the RNA molecule that is made is the correct one that the organism needs. In this way it also helps to control gene expression.

In genetics we learn that promoters are located in the DNA and regulate when a certain gene should be expressed. However, the promoter alone is not the only thing helping to ensure the correct genes are transcribed at the correct time. The sigma factor is just as important as the promoter. This is because without sigma factors promoters would be useless. RNAP would start transcription wherever it wanted regardless of where in the DNA the promoter was located. The sigma factor is required because they only allow RNAP to bind to promoters. This means that they are also helping to control gene expression. Dr. Burton's work helped to identify another sigma factor which will help scientists understand another way that bacteria transcribe their DNA and control their gene expression.

Sigma factors also help us understand gene expression in how different genes can be transcribed depending on environmental factors and needs of a cell. This understanding comes from the fact that there are different sigma factors that can be part of a RNAP molecule. The sigma factor that is chosen to be part of the RNAP molecule depends on the environmental conditions around a cell and the needs of the cell at that time. This means that no transcription occurs in the cell until a sigma factor is signaled to bind to the core RNA complex. The sigma factor that Dr. Burton identified is one that acts when the cell undergoes stress, so her work can help us understand how stress impacts gene expression. Dr. Burton's

work and sigma factors in general all expand upon and help to better understand transcription and gene expression, which are both things that are part of NEIU's genetics curriculum. Seeing Dr. Burton's work being used to help explain the principles of transcription and gene expression would be very meaningful to me. As a minority student in STEM most of the scientists that I learned about did not look like me. So, being able to learn concepts using work from a scientist who looks like I do makes it easier to believe that I could also do work in the same field. Seeing representation in the subject that I choose to study makes it feel like I do belong and can make a difference in the field.

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Colleen Cavanaugh

Cell/Molecular Biology (Microbiology)

by Sadia Khanam

Scientist Story

Dr. Colleen Cavanaugh is an experimental microbiologist working at Harvard University. Prior to receiving a PhD in organismic and evolutionary biology from Harvard in 1985, Dr. Cavanaugh earned her Bachelor of General Studies (BGS) in biology from the University of Michigan. At Harvard, Dr. Cavanaugh currently serves as co-director of the Microbial Sciences Initiative and as the Edward C. Jeffrey Professor of Biology in the Department of Organismic and Evolutionary Biology. Her research group examines the symbiotic relationships between bacteria and marine invertebrates, such as those found in coastal sediments, methane seeps, and deep-sea hydrothermal vents. She was elected as a fellow of both the American Academy for the Advancement of Science and the American Academy of Microbiology. Through her research excursions around the globe and on board the *Alvin* submersible, she has been able to describe several chemosynthetic symbiotic relationships in the marine biome.

When we sat down to talk over Zoom on April 14, 2023, she shared with me that the first time she used a microscope was in the third grade, when her science teacher brought a sample of pond water from somewhere and she observed a rotifer for the first time, falling in love instantly. Growing up in an Irish Catholic neighborhood in Detroit, she was one of five children, and when she and her siblings got home from school, their mother would instruct them to go outside and play. When it rained, she would pass the time by making dams in rivers, playing with roly-polies, and capturing bees. When she got a little older, she attended an

all-girls Catholic high school, which she now values looking back, since, in her words, it helped her stay focused at that problematic age and allowed her to become more educated and knowledgeable. Although open-book exams were uncommon back then, her high school biology teacher "Sister Martina" used them to encourage her students to "Think about answers instead of regurgitating them," which helped her develop a deeper interest in the topic.

She took a term off in her sophomore year of college, when she was pursuing a biology degree, because she wasn't sure where she wanted to go from there. Around that time, a friend of hers noticed a poster at the university advertising a marine biology/ecology course in the marine biology lab for undergraduates, so she decided to enroll in the course. Three primary professors were involved, and there were around 60 total students—half undergraduate and half graduate. She considers this to be the moment when she fell in love with research. An opportunity finally came for her to work in the field while she was waiting tables at a restaurant. She began her research career in the field of marine biology, working with arthropods. From that she moved on to marine environment research and eventually to microbiology. In the end all of these fields helped her find her calling in the study of symbiotic relationships between marine invertebrates and chemoautotrophic prokaryotes.

I came across Dr. Cavanaugh's work almost by chance, while reading about microbiology. While most work in microbiology is done in a lab setting, I was pleasantly surprised to see how close Dr. Cavanaugh's work was to the deep sea, the native environment of her subjects of study. Once I actually got to talk to Dr. Cavanaugh, she transmitted to me her love and admiration for the natural world and all of the life it hides from plain sight.

Contribution to Science

In deep-sea vents, Dr. Cavanaugh discovered chemosynthetic bacteria residing symbiotically in tubeworms. The observed lack of guts in the trophosome (feeding organs) of *Riftia pachyptila* Jones prompted her to investigate how it was possible for it to process nutrients despite a missing digestive system. Therefore, to find this out, she went on to collect *Riftia* samples from the deep sea, with the help of the *Alvin* submersible. She examined a sample under the microscope and discovered sulfur crystals, which indicates that sulfide has likely been oxidized. When she discovered this, she concluded that chemoautotrophic reactions must also be present. A chemoautotrophic organism is a living thing that gets its energy by chemosynthesis, usually a bacterium or a protozoan. Oxidizing inorganic molecules (like reduced forms of sulfate) allows the organism to produce energy. She then utilized a dye that specifically and sensitively stains DNA to determine whether a bacteria or protozoa was present in the trophosome tissue. She discovered DNA granules within the cells, and these granules were distinct from the worm nuclei. Then, she wanted to know if this DNA belonged to a bacterium, so she performed a test and discovered the presence of lipopolysaccharide (LPS), a substance that is unique to the outer cell wall of gram-negative bacteria.

This was the first time that the symbiosis between an animal and a chemoautotrophic bacterium had ever been discovered. Before, scientists studied independently in their own fields since they did not believe that two different categories (such as animals and chemoautotrophic bacteria) could engage in symbiosis. Following these discoveries, it had a significant impact on how other fields might cooperate. Symbiosis is a crucial biological term because it enables us to comprehend how intricate interactions between species have evolved through

time. Throughout the study of biology we have documented symbiotic relationships between a large range of animal species and in a wide range of habitats. In the water, symbiotic connections play a significant role in life. Different species of plants or animals may be dependent on one another to survive in such partnerships. This dependency allows for the process for coevolution to take place. Two organisms that are intimately intertwined are more likely to evolve their relationships throughout time.

The theory symbiogenesis suggests that eukaryotic life originated from two prokaryotic species that initially engaged in symbiosis and were dependent upon one another, eventually evolving to form one complex organism. Plants, for instance, use their mitochondria and chloroplasts to produce energy. The fact that these organelles are able to independently produce energy suggests they may have evolved from an independent organism over millions of years (Bunney et al. 2001). Furthermore, mitochondria and chloroplasts have double membranes, which makes them resemble a cell that has been endocytosed. Also, they have their own DNA that resembles bacterial DNA in size and in shape. These observations suggest that these organelles could have evolved from an independent organism over time. Studying the progress of symbioses like the one present on *Riftia* can further our understanding of the symbiogenesis theory, perhaps by studying the phenomenon in real time.

Connection to the Biology Curriculum

Evolution could be described as the differential survival of organisms following their naturally existing variation. As an environment changes, features that help survival in that environment will likewise gradually change, or evolve and be naturally selected, so that the organisms with best features will pass down their genetic material to the next generation. The environmental changes will also

include the interactions with other organisms. An example of this would be an evolutionary partnership that is advantageous to both organisms. This is called mutualism (Leigh 2010). In this sort of symbiotic relationship, the participating species cooperate so that each species provides something that the others need to thrive. If such a relationship goes on for long enough the evolutionary path of the organisms will converge to improve on it. This is what we know as coevolution (Barricelli, 1963; Wernegreen, 2004).

Just like the work of Darwin is crucial to the understanding of evolution in complex life forms, work done by scientists like Dr. Cavanaugh shed a light on evolutionary processes that took place in the earliest and simplest organisms millions of years ago, to give rise to the grand biodiversity that exists on the planet today. It is important to learn about what early evolution looked like so that we can better understand the factors that have always driven it.

In the case of *Riftia* and chemoautotrophs it is theorized that their relationship is one of mutualistic nature. Without a digestive system, the deep-sea hydrothermal vent tubeworm *Riftia* is likely to require carbon fixation. The bacteria that were found inside the worm trophosome are capable of getting their carbon from CO₂ and their energy from the oxidation of reduced inorganic sulfur compounds like hydrogen sulfide, thiosulfate, or elemental sulfur, a process known as chemosynthesis. We know this to be true because there was evidence of bacterial enzymes present in the trophosome tissue that is involved in oxidation of sulfur and CO₂ fixation (Cavanaugh et al. 1981). One of the benefits of chemoautotroph-invertebrate partnerships for the host is an internal supply of the organic compounds produced by the chemoautotrophic bacteria. An additional benefit is production of oxidized sulfate, which reduces toxicity for the *Riftia*. Chemoautotrophic bacteria also use this oxidation process to generate ATP. On

the other hand, protection from the environment and potential predators is one possible benefit that *Riftia* offers to chemoautotrophic bacteria. Living inside *Riftia* is also advantageous because it gives chemoautotrophic bacteria the nutrients they require, such as CO₂ and sulfur, in a steady, vascular flux.

It's possible that *Riftia* and chemoautotrophic bacteria are coevolving based on some of the available evidence (Cavanaugh 1983). The hemoglobin present in *Riftia* is advantageous to the bacteria because it carries oxygen as well as sulfur, which the bacterium consistently uses for energy. Since sulfur is not of use to *Riftia*, the hemoglobin could have evolved to help the bacterium thrive by providing a better source of sulfur. One can hypothesize that the bacteria that produce carbon products for the benefits of *Riftia* are evolving to become more efficient in carbon fixation and anabolism. Likewise, the evolutionary pathway of these bacteria could be directing them to improve the rate of sulfur oxidation to help *Riftia* thrive. This means we could be looking at a current living example of the early stages of coevolution.

Another example would be members of the *Solemya* genus discovered in the 1800s (Kellogg 1892), whose mechanism of nourishment was also poorly understood and which also happened to have poor digestive tracts. After looking at several tissues from this genus, they found results that were comparable to those of *Riftia* and also revealed intracellular gram-negative bacteria (Krueger et al. 1992). Since then, over 100 species of marine invertebrates have been proposed to have similar symbiotic relationships with sulfur-oxidizing chemoautotrophs (Fisher 1990). The fact that this is present in so many different kinds of organisms speaks to the importance of symbiosis in the marine environment. Since the marine environment is thought to be the origin of life then the importance of symbiosis extends to complex life as well.

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Kizzmekia Corbett

Molecular Biology

by Nahid (Nina) Irani

Scientist Story

Recognition and representation are critical aspects of professional growth and development, but this is different for Dr. Kizzmekia Corbett. The 37-year-old American viral immunology expert played a crucial role in the development of the Moderna, or mRNA-1273 SARS-CoV-2 (COVID-19), vaccine (ASM [accessed 2023]). She was born in Hurdle Mills, North Carolina, and her fascination with science started at an early age. She excelled academically throughout her schooling and graduated from the University of Maryland, Baltimore County (UNBC) with a B.S. in biological sciences (ASM [accessed 2023]). Dr. Corbett enrolled at the University of North Carolina at Chapel Hill (UNC) where she earned her doctoral degree in microbiology and immunology (ASM [accessed 2023]). After graduating, Dr. Corbett joined the Vaccine Research Center (VRC) at the National Institutes of Health (NIH) in Bethesda, Maryland. In 2020, when the COVID-19 pandemic hit, she and her team at VRC collaborated with Moderna to develop the mRNA-1273 vaccine against SARS-CoV-2 (COVID-19) (ASM [accessed 2023]). It is interesting to note that Dr. Corbett's interest in science started when she was accepted into the SEED program. This led to her taking on the highly challenging task of developing an mRNA vaccine against COVID-19 and she continued to be one of the top researchers at the National Institutes of Health. Being a woman of color and being recognized in the scientific community as the leading expert in the race to create a SARS-CoV-2 vaccine at such a young age is truly phenomenal. Dr. Corbett will not only be remembered as being a major contributor to the advancement of the science that

put an end to the pandemic but also someone who paved a path for many girls and women in STEM.

Dr. Corbett is currently working at the Harvard T.H. Chan School of Public Health as an Assistant Professor of Immunology and Infectious Diseases. She is committed to promoting diversity and equity in science. She is a vocal advocate for increasing the representation of underrepresented minorities and women in science and has worked to inspire the next generation of scientists (Kamin 2023; Moderna 2023).

Contribution to Science

Dr. Corbett's contribution to the development of the mRNA-1273 SARS-CoV-2 (COVID-19) vaccine was recognized and praised by Dr. Anthony Fauci on national news (Corum and Zimmer 2021). Moderna announced the development of the mRNA-1273 COVID-19 vaccine in January 2020, attracting the attention of scientists worldwide (Corum and Zimmer 2021). Dr. Barney Graham, a colleague of Dr. Corbett, chief of the Viral Pathogenesis Laboratory, and deputy director of the Vaccine Research Center acknowledged Dr. Corbett's efforts in developing the COVID-19 vaccine and noted that her previous research, which had focused on coronavirus since 2015, was crucial to the vaccine's rapid development (Corum and Zimmer 2021; Kamin 2023). Dr. Corbett was also part of a research team led by Dr. Lingshu Wang that studied the Middle East Respiratory Syndrome Coronavirus (MERS-CoV), a dangerous zoonotic virus that causes severe pulmonary infections (Wang et al. 2018).

The development of the mRNA-1273 vaccine against COVID-19 began when Dr. Corbett and her colleagues, including Dr. Graham, saw a rise in COVID-19 cases in Wuhan, China, in January 2020 (Kamin 2023). They contacted Chinese scientists and urged them to share the widespread Wuhan virus' genetic makeup (Kamin

2023). Based on Dr. Corbett's previous extensive research on SARS, MERS, and other coronaviruses, the information provided by the Chinese scientist allowed Dr. Graham, Dr. Corbett, and her team to determine which part of the virus would activate the body's immune system to provide protection against the virus (Hsieh et al. 2021; Kamin 2023).

In a study done in mice, Dr. Corbett and her team found that the spike protein of the virus acts as an antigen to the host immune cells, which is sufficient to mount an immune response against the virus (Hsieh et al. 2021). As Dr. Corbett had the prototype ready for the virus, Dr. Corbett and her team identified the sequence that encoded the spike protein of the SARS-CoV-2 virus and added some mutations to stabilize it (Hsieh et al. 2021). They collaborated with Moderna and used Moderna's mRNA technology to develop nucleoside-modified mRNA that was encapsulated in lipid nanoparticles to aid in efficient delivery (Corum and Zimmer 2021; Hsieh et al. 2021). This led to the development of the mRNA-1273 COVID-19 vaccine by Dr. Corbett and her team in March 2020 (Corum and Zimmer 2021; Kamin 2023). Upon injecting the mRNA-1273 COVID-19 vaccine into the host, the nucleoside-modified mRNA uses the host's translational machinery to synthesize the viral spike protein (Corum and Zimmer 2021; Moderna 2023). The nucleoside-modified mRNA is degraded after being translated; however, the newly synthesized viral spike protein is recognized as a foreign antigen by the host immune system, eliciting an immune response (Hsieh et al. 2021; Moderna 2023). The immune cells recognize the antigen and destroy it, thereby providing protection against the virus (Hsieh et al. 2021; Moderna 2023). The development of the Moderna vaccine was a collaborative process that involved Dr. Graham, Dr. Corbett, and many other teams of scientists working on various aspects of the vaccine's development and testing (Corum and Zimmer 2021; Kamin 2023). The

vaccine was highly effective, easily manufactured, and approved by the FDA for phase 1 first-in-human trials just 66 days after the release of the virus' sequence (NIAID 2020). After successful clinical trials, the FDA granted emergency use authorization for the vaccine in December 2020 (NIAID 2020; Corum and Zimmer 2021). In 2021, Dr. Corbett and a team of scientists at NIH, including Matthew Gagne, Danielle A. Wagner, and Sarah O'Connell, sought to understand whether the developed vaccine against COVID-19 could provide sustained immunity. They assessed the immune reactions in non-human primates that were inoculated with a primary vaccination series of mRNA-1273 and received B.1.351 Beta variant boosters six months later. Improved protective effects were observed in the boosted animals, compared to those that did not receive the booster (Corbett et al. 2021). Dr. Corbett and colleagues' studies suggested the importance of booster vaccinations in maintaining protection and immunity (Corbett et al. 2021). Additionally, Dr. Corbett teamed up with other NIH scientists, including Anne P. Werner and Juan I. Moliva, to explore the efficacy of the mRNA-1273 vaccine against spike mutants from worldwide coronavirus variants (Wu et al. 2021). The team found that while neutralization was reduced in specific mutants, it was still significant in all those that were tested (Wu et al. 2021).

Dr. Corbett is a groundbreaking scientist whose contributions to the field of immunology and infectious diseases have saved countless lives. Her dedication to science and commitment to diversity and equity have inspired many, and she continues to be a role model for aspiring scientists around the world.

Connection to the Biology Curriculum

Dr. Corbett's work on developing the Moderna mRNA-1273 SARS-CoV-2 vaccine involved designing and optimizing the sequence of mRNA that encodes the viral protein (Corum and Zimmer 2021). This process involves the "central

dogma”—a fundamental topic in any molecular biology curriculum. The central dogma explained in the molecular biology curriculum is the process of DNA being transcribed into RNA, which is subsequently translated into proteins (Li and Zhao 2013). Unlike the DNA vaccine, which needs to enter the nucleus to get transcribed, the mRNA vaccine is translated within the cytosol. So, to develop the mRNA-1273 SARS-CoV-2 vaccine, Dr. Corbett selected the appropriate mRNA sequence encoding the viral spike protein that is usually present on the surface of the virus and, using the mRNA technology, developed nucleoside-modified mRNA that is wrapped in nanolipid (Hsieh et al. 2021; Moderna 2023). Once the mRNA-1273 SARS-CoV-2 vaccine is injected into the host, the mRNA-1273 enters the cytosol of the target host cell where it is translated into viral spike protein using the host’s translational cell machinery (Hsieh et al. 2021). Following translation, the mRNA is degraded. The newly synthesized viral spike proteins are recognized as antigens by the host immune cells, resulting in the production of antibodies against the viral spike protein that attach to the antigen and destroy it (Hsieh et al. 2021).

Dr. Corbett’s success in developing the Moderna COVID-19 vaccine was based on her extensive knowledge and years of research on respiratory syncytial virus, dengue virus, influenza virus, and, more specifically, coronavirus (Corum and Zimmer 2021; ASM [accessed 2023]; Kamin 2023). More importantly, Dr. Corbett’s research on the mRNA vaccine will not only provide clear insights into its mechanism of action but will also help confront misinformation and mistrust of the vaccine. Through the curriculum, students will gain a deeper understanding of how mRNA vaccines work and the immune response elicited by the vaccine.

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Esther Lederberg

Cell Biology

by Ivan Morales

Scientist Story

Esther Lederberg was born on December 18, 1922 in the Bronx, New York. She graduated from high school at 16 years old and attended college in New York City. She originally wanted to study French or literature but decided to study biochemistry because it was her passion. She was able to complete her undergraduate degree at the age of 24. She later attended Stanford University where she was offered a fellowship for a master's course in genetics (Marks 2015).

There were many challenges that she faced, and one of the biggest was money issues, which caused her to eat frogs' legs that were left over from laboratory dissections and to wash her landlady's clothes. In 1946 she met her husband Joshua Lederberg and completed her master's degree. Once she finished her master's, she went to the University of Wisconsin and received her doctorate in 1950. After her doctorate she continued to do research at the University of Wisconsin (Esther...2022).

During her research, she discovered lambda phage viruses and developed the replica plating technique. These huge discoveries helped scientists have a better understanding of molecular biology. In 1956 she and her husband received a Pasteur Award from the Society of Illinois Bacteriologists. Then in 1958 her husband received a Nobel Prize for Physiology or Medicine for the discoveries that Esther Lederberg made (Piqueras 2014).

The reason why I chose Esther Lederberg as my underrepresented scientist was because she is a scientist whose discoveries help scientists in understanding

molecular biology. Her work also provided a way to replicate bacteria colonies at a fast rate. Another reason was she did not receive any credit for her discoveries, but her husband received the credit and awards for her discoveries instead.

Contribution to Science

During her doctorate in 1950 she was studying bacteria culture and observed that there were strange patterns, such as missing segments on the *E. coli* colonies. Upon further investigation she found that it was a virus that caused the *E. coli*'s inability to grow, leading to the missing segments. The virus was called lambda phage (Marks 2015). She noticed that this virus acted differently from other viruses. For instance, the lambda phage would inject its own DNA into the bacteria, which would allow the virus to replicate itself within the bacteria and into the future generations of bacteria. This type of virus was one of the first viruses to be classified as lysogenic, meaning that the virus does not automatically kill the cell host (Piqueras 2014). Lambda phage would not kill the bacteria host unless it was under stress. The use of this virus was safe because it was only pathogenic to bacteria.

Before the discovery of the virus, scientists believed that all viruses were lytic, which means that the virus would infect the cell, use the cell functions to replicate itself, and then burst the cell in order for the surrounding cells to be exposed to the mature cells and also be infected. The discovery of the Lambda phage made it possible for a better understanding of genetic material between bacteria, the process of gene regulation, and the steps that DNA does to break apart to make new genes (Marks 2015). Before the discovery of Lambda phage scientists had difficulty observing changes in bacteria colonies due to environmental changes. Scientists would use different methods, such as blotting paper and metal brushes with small prongs, but it all ended in failure. Scientists would also spread bacteria

throughout entire plates containing different experimental variables like antibiotics. While this method worked, it was time consuming and difficult to identify and reproduce individual colonies. Joshua Lederberg, who was Esther's husband, did discover a way to replicate colonies with toothpicks, but it was a difficult process. This changed when Esther invented a simpler process called replica plating technique. She believed that copying the original petri dish will help the replication of bacterial colonies be easier, so she used a velvet cotton pad, which acted as a small inoculating needle and helped transfer the bacteria in the same position as the original plate. She then washed the velvet cotton pad with a detergent that she had determined washes the best (Esther...2022). This new technique helped scientists to produce bacteria colonies in agar plates that have the same spatial configuration. Having the same bacteria being replicated helped compare the reactions that bacteria have to environmental changes, such as nutrition and temperature.

Before her discovery, scientists believed that bacteria resistant to antibiotics were not affected by all antibiotics. Once she discovered that there is a specific antibiotic responsible for bacterial resistance, it changed scientists' understanding of bacterial resistance. A Nobel Prize was given for her discoveries, but it was given to only her husband with no credit given to her (Kashani 2020).

Connection to the Biology Curriculum

When I took Cell Biology, I learned about DNA interactions inside different types of cells and how it is able to repair itself when it is damaged. I also learned how to use different materials in lab experiments and the similarities and differences between prokaryotic and eukaryotic cells. These things that I learned in Cell Biology can be connected with Esther Lederberg and her discoveries. For example, the work of Esther Lederberg can be connected to cell biology, specifically

DNA, microscopy, and molecular biology. The discovery of Lambda phage could be used when discussing bacterial DNA, especially during the process of DNA replication. This will give some history of what helped further our understanding of the process that viral DNA undergoes in order to lie dormant in bacteria. There will also be a better understanding of how prokaryotic cells' genes are evolving when the Lambda phage is in the bacteria. We can also observe how Lambda phage is able to stay hidden inside the cell and interacts in the environment. This would connect to the discussion of prokaryotic cells. It will help us understand how viruses are able to attack a bacterium.

Another way that Lambda phage can be used is in a molecular biology lab. *E. coli* can be used to grow Lambda phage, since *E. coli* has a fast growth rate; it would not take long for Lambda phage to be replicated and used during lab. This virus will only infect *E. coli* and is not pathogenic to humans, which would make it safe to use when following common safety precautions. This virus could also help students better understand the genetic material that bacteria contains and the central dogma of how the DNA code is used to create proteins.

The replica plating technique can be used to provide bacteria in the lab to show during microscopy and study the structure and reproductive behavior of the bacteria. Performing the replica plating technique would show how fast bacteria cells can replicate, and it can help students understand how to replicate bacteria in a short amount of time. It can also be used to test how bacteria act against environmental changes, such as changing temperature or to see how bacteria acts against Lambda phage. Another way to use the replica plating technique would be to use the multiple colonies of bacteria in the lab, let the bacteria undergo different environmental changes and observe it under a microscope to check if the bacteria have any changes in appearance or behavior. While this experiment can take a

couple hours, it would show the bacterial resistance to the environmental changes that they are exposed to. As a student, these experiments would help me better visualize bacteria interaction with the environment, creating a better understanding of how the environment plays a role in the changes that bacteria experience.

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Sandra Lopez-Vergès

Anatomy and Physiology

by Carla M. Amaya

Scientist Story

Born into a family of clinicians, you could say that Sandra Lopez-Vergès' journey into medical research started quite early. Her father worked in public hospitals and often for free, while her mother, a pediatrician at a public hospital, really valued women and children's health. According to Sandra Lopez-Vergès (Video call, 30 Mar 2023), her mother believed that the family and education of the mother was very important for the health of a child. Her mother also believed that the community played a huge role in the wellbeing of their children and that the community members were just as important as the doctors for the overall good health of their children. There was one particular instance however, that became truly eye opening for Sandra Lopez-Vergès. While accompanying her parents during medical visits in the most rural areas of Panama, deep in the mountains where it was not accessible to cars, she got to experience first-hand the injustices of the world. Visiting communities where due to the poverty and lack of education, there was more than a 10 year difference in life expectancy and for their women - even less. These outings with her parents were the motivation to look into virology as her field of study.

Sandra Lopez-Vergès was raised to believe that she could do as she pleased, and since both her parents were doctors, getting into the sciences was a given. Thanks to Sandra Lopez-Vergès' French roots from her mother's side, she had the opportunity to study in France and eventually earned her PhD in Virology from the Université Paris 7 Denis Diderot, Ecole Normale Supérieure d'Ulm and Pasteur

Institute. Sandra Lopez-Vergès also completed post-doctoral training in Immunology at the University of California San Francisco. As a winner of the “UNESCO L’OREAL International Fellowship for Young Women in Science 2014” award and the “Exceptional Woman of Excellence 2019 by Women Economic Forum (WEF) and All Ladies League (ALL)” award (Sandra Lopez-Verges 2023), Sandra Lopez-Vergès is appropriate for this book because she is a woman in power. She is a Latin American woman scientist who is a big proponent of women in the sciences. According to Sandra Lopez-Vergès, your work will speak for you and will put you on the radar of those who matter, regardless of your gender and ethnicity (Video call, 30 Mar 2023). As a Latin American woman in science myself, seeing someone like me in a position to enact change in the world of research is what first drew me to look into her work. What kept me interested is the reinvestigation of a cell that is part of the very foundational teachings of anatomy and physiology, rousing hope in me that the answers to many of our scientific questions may be in what we think we already know.

Contribution to Science

The innate defense system is considered our first and second lines of defense. Respectively, it is composed of surface barriers such as skin and mucous membranes as well as internal defenses such as antimicrobial proteins, phagocytes, other cells, and chemicals (Marieb et al. 2013). It is always prepared and ready to respond within minutes to any and all foreign substances to protect our body, making it a nonspecific defense system. The adaptive defense system, which is composed of a separate set of internal defenses such as antibodies and the cells that produce them, lymphocytes, including B and T cells, is considered our body’s built-in specific defense system. It is our third line of defense made up of an elite

fighting force that is equipped with high-tech weapons to attack a wide variety of specific foreign substances, making it a specific defense system (Marieb et al. 2013).

Sandra Lopez-Vergès' work challenges what we thought about immunity. Through her work, we are discovering that the relationship between non-specific (innate) and specific (adaptive) immunity is not as cut and dry as we thought. She does this through her work on Natural Killer (NK) cells. NK cells are considered part of our innate defense system, specifically part of the second line of defense. They belong to a small group of large granular lymphocytes, which are a type of immune cell. Unlike the lymphocytes of the adaptive defense system, NK cells are not specific and can eliminate a variety of bad cells, or pathogens, indiscriminately. They patrol the body in blood and lymph and kill pathogens by inducing them to undergo apoptosis (programmed cell death) before the adaptive defense system is activated (Marieb et al. 2013).

Sandra Lopez-Vergès' work demonstrates that just like the B and T cells of the adaptive defense system, NK cells undergo a selection, cloning, and creation of memory cells that help mediate a stronger response to previously encountered pathogens. These were all characteristics associated only with the cells of our adaptive immune system before the work of Dr. Lopez-Vergès and others. Essentially, her works suggest that NK cells may fundamentally be closer to the lymphocytes of the adaptive immune system than the immune cells of the innate system (Sun et al. 2011).

Sandra Lopez-Vergès' work on NK cell response to cytomegalovirus (CMV) in solid-organ transplantation recipients was an attempt to determine whether immune memory could exist in virus-specific NK cells. CMV is a common virus that is part of the *Orthoherpesviridae* family. Once infected it stays in a person's body for life and can reactivate. In healthy people it rarely causes problems. However, if one

is pregnant or has a weakened immune system (immunocompromised), CMV could lead to severe complications and may even be lethal to the fetus or the immunocompromised host (Cytomegalovirus...2022). Unfortunately, CMV is the most common viral complication after solid-organ transplantation. Through research Sandra Lopez-Vergès' group conducted, they were able to detect a unique NK cell population that preferentially responds to acute CMV infection, multiplies in response to the infection, and can still be detected in CMV+ healthy adults years after their initial infection by the virus (Lopez-Vergès et al. 2011). This means that this unique population of NK cells was specifically targeting the CMV cells, a behavior only previously recognized in the cells of the adaptive immune defense system. In addition, this unique NK cell population's ability to make perfect CMV-targeting NK cell copies and multiply is again a characteristic previously only associated with cells in the adaptive immune response. Finally, their presence years after the primary acute CMV infection suggests "memory". Normally, cells of the innate immune defense are indiscriminate and tend to be short-lived, so once their job is done, they are done. Seeing this unique subset of NK cells years later in CMV+ healthy adults implies that just like the cells of the adaptive immune response, their body is armed and ready for a subsequent CMV infection, again, a characteristic not associated with the innate immune response but to the adaptive immune response.

Prior to this research, Sandra Lopez-Vergès and her group had previously studied a particular marker on NK cells called CD57. CD57 is a marker that is generally associated with cellular maturity nearing the end of NK cell life (Nielsen et al. 2013). However, it is recognized that more research is needed on this CD57 marker as there is very little known of its role in NK cells. Seemingly, in agreement with Sandra Lopez-Vergès' research, the CD57 marker on NK cells is not just a

useful indicator of NK cell maturation but also helps identify a stable subset of NK cells that increases with age and exposure to pathogens. NK cells with the CD57 marker have more potent cytotoxic potential (ability to kill bad cells) and are consistently associated with better outcomes in cancer and autoimmune disease despite their decreased sensitivity to cytokines (immunity mediators that influence cell development, differentiation, and response in the immune system) and reduced replicative potential (Nielsen et al. 2013). Previously, through Sandra Lopez-Vergès and her group's research on this CD57 marker, they proposed that CD57 may be a potential indicator of "memory" NK cells. Her team argued that CD57 does indeed correlate with NK-cell maturation, however this maturation should not be seen as an indication of "exhaustion" but an indicator of "expertise" in the NK cell. They have not necessarily lost their ability to react to cytokines but just simply acquired a greater sensitivity to what's needed to respond. Furthermore, as a result of responding to pathogens or cytokines, NK cells with CD57 have lost their proliferative capacity due to having undergone more cell divisions as a strategy to have a more potent specific "bad cell" destroying ability. (Lopez-Vergès et al. 2010). Remember that unique subset of CMV specific NK cells? Well, those cells carry this CD57 marker. Unlike what her previous research on the CD57 marker suggested, her later research on NK cell response to CMV in solid-organ transplantation recipients did suggest that NK cells with the CD57 are likely to proliferate *in vivo* in response to viral infection. This means that having CD57 may truly not be indicative of the loss of proliferative ability.

So what does this all mean besides more research being needed on NK cells? Sandra Lopez-Vergès belongs to a group of scientists that is challenging what we thought we already knew about our immune system in her attempts to find a reliable marker to define memory in NK cells. Just the simple fact that NK cells

marked with CD57 of the innate immune defense may have this “memory” goes against a fundamental concept taught in biology, let alone providing targeted cell response and targeted multiplication. Her work has brought to light an additional role NK cells may have in the human immune system.

Connection to the Biology Curriculum

When learning about our immune system and how it works in physiology class, one of the first concepts taught is that the immune system relies on two intrinsic defense systems that act both independently and cooperatively to provide resistance against pathogens. These two systems, essentially being our immunity, are called the innate defense system and the adaptive defense system. The adaptive defense system takes longer to prepare because it works from a set of “instructions” that allows the adaptive immune response to recognize a specific invader from memory and mount an even stronger attack. This ability to recognize specific pathogens of the adaptive immune response is the hallmark that distinguishes the adaptive defense system from the innate defense system. This is thanks to two very important cells of the adaptive immune system, the B and T cells. These two cells undergo rigorous selection to make sure they are ready to turn on and take on the jobs of inactivating, destroying, or even calling other cells to handle the pathogens they encounter. Once turned on, B and T cells are able to multiply (cloning), generate effector cells (cells that directly fight infections), and create memory cells (cells that allow for the quicker response after any following encounter with the same pathogen) which keeps the adaptive defense system armed and ready when facing that specific pathogen again (Marieb et al. 2013).

Until further research is done to expand on Sandra Lopez-Vergès’ work, the ideas that she brings to the table could be used to show anatomy and physiology students that our immune systems are still not perfectly understood. Her work

could open up their minds to the possibility that the fundamental knowledge they are learning today, regarding the specific roles immune system cells have, could change tomorrow. Her work on NK cells possibly having characteristics previously only associated with B and T cells is alluding to the idea that the two intrinsic defense systems are more intertwined than previously imagined. Though it is clear that these two defense systems cooperate together, when studying the immune system the difference between the innate and the adaptive response is emphasized most. A small addition could be made at the end of this section that allows for the students to be brought back to the concept of these two systems working in conjunction. That is when Sandra Lopez-Vergès' work could be highlighted in support. Perhaps, learning about the specifics regarding NK cellular markers may be too in-depth for your average anatomy and physiology undergraduate lecture. In spite of that, having a section relating to "current research" at the end of the immune system lecture could be an interesting idea, especially for professors who earned their specialization in the areas of microbiology or virology. NK cells could serve as a connection between the innate and adaptive defensive systems, bringing the concept of specific and non-specific together. Opening up questions such as "Does our adaptive immune system eventually become more innate-like?" or "The adaptive system needs information from the innate defense system, could NK cells also be among the cells that provide such information?" After going through the immune system lecture, attention could be called to the NK cell's potential ability to not be as "non-specific" as previously thought. They seem to have the ability, at least when studied responding to a herpes virus (genus *Cytomegalovirus*), to behave like cells of the adaptive immune response. As a student, the idea that our bodies are still not perfectly understood is always of interest. Concepts such as cellular marker CD57 on NK cells not meaning end stage cell life could reveal that other cell

markers we previously thought we understood could be erroneous. Sandra Lopez-Vergès' work not only inspires curiosity and brings about questions such as "what else could possibly be misunderstood about our immune system?" but also gives hope surrounding possible future organ transplant rejection solutions.

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Maria de Lourdes Cabezas Tapia

Cell/Molecular Biology

by Eduardo Vaca

Scientist Story

After receiving their Bachelor of Science degree at University of Texas at Austin, Maria de Lourdes Cabezas Tapia received her PhD at Northwestern University, where she worked as a research fellow for the Jewett Lab. There, Cabezas and their colleagues make use of a variety of high-throughput technologies and techniques, utilizing the latest in automated liquid handling systems, next-generation genome sequencing, computational analysis, cell expression systems, and genome mining (Heiden 2022). Genome mining is a process of creating large data sets of genomic sequencing information with the intention of discovering novel biosynthetic pathways that can uncover unknown biosynthetic routes and molecular structures in natural products (Yee et al. 2023). Liquid handling systems give their researchers the ability to automate the tedious, but necessary, process of pipetting hundreds or thousands of samples in a short amount of time. These automated liquid handling systems allow for the experimentation, processing, and validation of these unknown natural biosynthetic products at a large scale and in a fraction of the time. The combination of innovative technology and platforms for the advancement of timely and vital medical solutions, is what drew me the most to Cabezas' work.

Contribution to Science

By utilizing cutting edge cell-expression systems and genome mining, Cabezas and the Jewett lab have invented platforms for discovering molecules to

facilitate future *in vivo* biomanufacturing, biosensing, and biosynthetic engineering for medical therapies. Their lab recognizes the urgent need to discover faster methods of developing antibiotics to address the threat of antibiotic resistance to our health and are using the latest technologies and techniques in biosynthesis and molecular biology to accomplish these goals.

Up until recently, advances in high-throughput genome sequencing and computational analysis demonstrated that the amount of known natural products are only a fraction of those that exist. Cabezas was a contributor to a publication on the exploration of the natural product chemical space using cell-free means to explore the tools at our disposal to combat the threat of antibiotic resistance (Bogart et al. 2020). The acceleration of natural product, enzyme, and cryptic pathway characterization discovery is essential to keep up with the acceleration of antibiotic resistance, but knowledge gaps in individual and multiple biosynthetic enzyme function and assembly pathways still exist.

In 2022, Cabezas and colleagues published the development of a novel high-throughput platform that leverages engineered DNA libraries, cell-free protein synthesis, emulsion droplet microfluidics, standard flow sorting, and next generation sequencing, for regulator part prototyping and analysis. Using this novel platform, they successfully prototyped a large randomized ribosome binding site mutant library (Gan et al. 2022). These cell-free metabolic engineering approaches could be used to accelerate the discovery of natural products. Ultimately, contributing to the development of robust catalytic networks that can be repurposed for accessing new chemical scaffolds and enzymes. The discovery of which has the potential to serve as flexible biocatalytic tools that may lead to the discovery of essential antibiotics and other therapeutics. These tools may be a vital part of preventing our world

from entering a post-antibiotic era.

What makes this significant is that antibiotic resistance is on the rise and has increased in prevalence in all parts of the world. Bacteria have been able to develop new resistance mechanisms that are spreading at an alarming rate globally. This threatens medical professionals' ability to effectively treat the most common and, as of yet, typically non-threatening infectious diseases.

Connection to the Biology Curriculum

The variety of high-throughput technologies and utilization of next generation genome searching and sequencing for discovering novel natural products and molecules is what initially attracted me to their work. I had just completed a genomics and proteomics course at Northeastern Illinois University, where we utilized KBase software linked with supercomputers across the country to analyze genomes and the products that result from it. After hearing about the altruistic goal and motivation of Cabezas' work, to help combat the threat of antibiotic resistance and other microbial threats, I found it incredibly inspiring.

In molecular biology, natural products and secondary metabolites are responsible for some of the most transformative advances in medicine, agriculture, and biotechnology. One of the most transformative discoveries in medicine was in 1928 with the discovery of penicillin by Alexander Flemming (Tan and Tatsumura 2015). Since its discovery, antibiotics have proven to be one of the most indispensable medications used clinically. However, today many of the world's top infectious disease specialists have been ringing the alarm bells of an imminent existential threat, antibiotic resistance. Cabezas and their colleagues at the Jewett lab have been researching ways to address this urgent threat with advanced techniques in molecular biology.

Antibiotic resistance is the process by which bacteria adapt, evolve, and

resist in response to the antibiotic medicine being used to treat or eliminate the bacterial infection. As a biology student with a concentration in the biomedical sciences, learning about antibiotic resistance and the urgent need for a timely solution for hospitals and patients today is such an engaging topic because of its connection with a variety of issues faced today, such as increased medical costs, hospital stays, and mortality. Cabezas is working to establish cell-expression and genome mining systems to discover natural products for the purpose of accelerating the discovery of novel molecules that may have antimicrobial properties to be repurposed for other therapeutic applications.

Due to the lack of standards and common over-prescribing and availability of antibiotics for human and animal use, the spread and emergence of antibiotic resistance has been made worse. This is especially true in countries that lack any prescription standards or where the public, due to lack of medical resources, education, and standards, accesses antibiotics and tend to use them incorrectly by over- or under-using them. The frightening truth is that without urgent action, a post-antibiotic era, in which even the most “insignificant” infections and minor injuries can once again kill, is very likely on the horizon. A growing list of infections including pneumonia, tuberculosis, gonorrhea, and many more have become harder, and even impossible, to treat due to the increasing ineffectiveness of our current antibiotics (Antibiotic...2020).

One of the fundamental issues we have when attempting to address bacterial resistance to antibiotics is that we cannot develop novel antibiotics at a rate fast enough to keep up with the evolving bacteria. As a result, new high-throughput methods of sequencing and analyzing the genome and proteome of organisms has become a focal point of research in this area. By utilizing these next generation sequencing and analysis techniques researchers

like Cabezas, are able to compile and process large volumes of biological and genomic data for the purposes of finding these novel antibacterial molecules and ultimately treatments. Such products, like enzymes for example, may be able to serve as tools to expand the chemical space of natural products and secondary metabolites. This can ultimately provide a more sustainable and efficient route for the discovery and manufacture of these molecules.

Finally, with this in mind it is clear that the need to incorporate novel ways of accelerating the discovery of antibiotics in today's biology curriculum is two fold. Not only would the topic provide a much needed headstart for many up-and-coming scientists to begin thinking about innovative solutions to these challenges, but also engage them with a topic that can provide them a sense of meaningful discovery and advancement in the biological sciences. I think that if this topic were included in our curriculum it would be of interest to my classmates and I because not only would we see an opportunity to discover innovative solutions to tackle modern biology issues but we would also recognize the importance of scientist like Cabezas, who are using their understanding, knowledge, and education for an altruistic end.

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Elba Serrano

Genetics

by Sumaiya Ahmed

Scientist Story

Dr. Elba Serrano is a neuroscientist who acquired her PhD in biological sciences from Stanford University. She completed her bachelor's in physics from the University of Rochester, where she was only one of two women in her graduating class of 80 students. She is also a first generation college graduate. Currently, she is affiliated with New Mexico State University, where she works and conducts her research as a Regent's Professor. Dr. Serrano's work stood out to me because it immensely improves the quality of life for individuals affected by hearing loss through trauma or genetic disorders. She also mentors underrepresented students such as women with aspiring STEM careers similar to me.

Contribution to Science

Some notable research of Dr. Serrano focuses on neural regeneration to restore hearing loss and the effects of phenobarbital on the nervous system. She used her expertise to study the formation of sensory organs, in particular how sensory cells acquire their specific phenotypes. The genus *Xenopus* makes a significant animal model because it has a unique amphibian quality of tissue and organ regeneration (Powers et al. 2012). Using a cDNA library, Serrano and her team of researchers analyzed the prevalence of orthologous genes in both the human cochlea and *Xenopus* inner ear. Based on these data, Serrano et al. determined that the physiological processes essential for inner ear function must be shared between the two species because of genetic similarities (Powers et al.

2012). Specifically, these similarities were observed in sensory cells of the ear which prompted Dr. Serrano to conduct further studies on her findings (Freeman 2005). Using GeneChip and various *X. laevis* probe sets, they analyzed gene expression which could be related with deafness. They found certain proteins such as EEF1A1, TPT1, PMP22, SPARC, and CLU corresponded the most with transcripts also found in the human fetal cochlea (Powers et al. 2012). The findings from this study were significant because these similarities had not been identified before. Dr. Serrano's work enables researchers to potentially focus on specific proteins and genes identified through her work to study and curate treatment options for hearing loss.

Building upon her previous research, Dr. Serrano conducted an RNA-seq and microarray which led to the identification of candidate scaffold regions of the *Xenopus tropicalis* genome to investigate hearing loss and restoration in humans. Scaffold regions are parts of DNA which attach chromatin to the nuclear matrix and have been found to impact gene expression (Narwade et al. 2019). Dr. Serrano and her research team used GeneChips, *Xenopus* 2.0 genome arrays, to conduct RNA sequencing of the *X. tropicalis* inner ear transcriptional profile. They found 108 genes which contain orthologs to human genes in terms of deafness and vestibular disorders (Ramirez-Gordillo et al. 2015). Her work has paved the way for conducting in depth genetic analysis of auditory and vestibular function using *X. tropicalis*, citing this organism as an ideal animal model for auditory and neuronal research.

Apart from studying restoration of hearing loss, Dr. Serrano's expertise also lies among other parts of the nervous system. She has also researched how neuronal development can be altered by the use of certain drugs. Her research has also shown the effects of phenobarbital (PB), an anti-epileptic drug, on neuronal characteristics in a developing human nervous system. For this research, they analyzed the effect of increasing PB concentration on neuronal cell cultures from

mice. Their results demonstrated decreased dendritic branching frequency upon increased PB exposure and reduced survival (Serrano et al. 1988). Her study also indicated how the extended use of PB can negatively impact neuronal morphology and survival. The use of PB during pregnancy has been linked with various birth defects such as low birth weight, cognitive impairment, and learning disabilities (Swanborough 2021). Dr. Serrano's work regarding the use of PB is significant because it demonstrates neuronal alteration in a mammalian model. The neuronal alteration seen in the murine cell cultures can be applied to further *in vivo* experiments for the analysis of the symptoms associated with this drug. Her research on phenobarbital and the restoration of hearing loss makes her a remarkable neuroscientist.

Connection to the Biology Curriculum

Dr. Serrano's work fits into the NEIU biology core curriculum in many ways. Her research using *X. tropicalis* integrates well into the genetics courses taught at NEIU. In General Genetics at NEIU, there are many experiments conducted using *Drosophila melanogaster* since it shares orthologs of human genes. The research conducted by Dr. Serrano analyzes orthologs related to hearing between humans and *X. tropicalis* to study restoration of hearing loss. Based on the results from her research, she has found 70 orthologs that are responsible for deafness and vestibular disorders and proposed the use of *Xenopus* models with the target genes to investigate hearing loss restoration. The use of model organisms to study diseases with target genes is a significant objective of genetics at NEIU. As taught in the course, much of what we know about science, medicine, and treatments has been through the use of animal models to conduct genetic studies. Dr. Serrano's work fits well into NEIU's curriculum, because it could potentially provide a deeper insight into how studying animal models and genomic similarities can improve our

understanding of disease in humans. Personally, it helps me learn the material in a more advanced manner when examples from the real world are incorporated into lectures and discussed in class.

Her research on neuronal alterations from the administration of PB also correlates with the overall curriculum of Cell Biology. Cell Biology at NEIU details how cell interactions can be mediated and impacted by various elements. Certain drugs can also impact the structure and functionality of our cells. Dr. Serrano's research of PB on neuronal characteristics highlights this importance of drug/medication interaction with our cells. As a student, learning how drugs interact with our cells and why they prompt the effects associated with the drugs would help bridge the gap of vocational lectures and an applied learning approach. This approach facilitates discussions among peers and results in a more engaged classroom experience. It also supports one of NEIU's core visions of supporting diverse opinions and discussions. Stimulating discussions would be valuable to me and my peers as it promotes engagement and allows critical analysis of the material presented to us. By doing so, it strengthens the overall understanding of the concept.

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