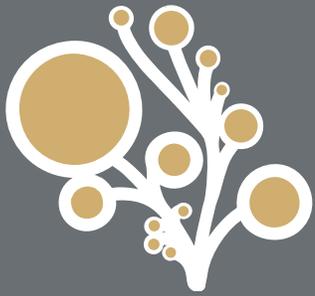
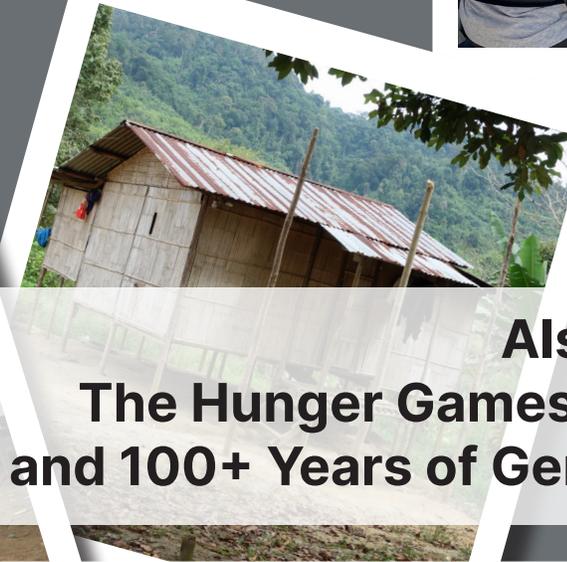


EVOLUTIONARY STUDIES



the magazine



**Also in this issue:
The Hunger Games: *E. coli* Edition
and 100+ Years of Genetics in Media**



*The genetic changes of moving
from rural to urban landscapes*

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VANDERBILT ESI

Greetings Alumni and Friends,

I am writing to you from the Heidelberg Institute for Theoretical Studies in Germany and am making plans to move to Oxford's Merton College in the UK, as part of my academic leave. The distance and change in surroundings provide valuable perspective in what we achieved in 2022. Without a doubt, we have had great year full of new successes and collaborations.

We have been incredibly fortunate to welcome three new faculty to our university and to Evolutionary Studies this semester. Gianni Castiglione has a dual appointment with Biological Sciences and Ophthalmology. Monica Keith joined the Anthropology department. Lin Meng joined the Earth and Environmental Sciences department and has already secured a pilot grant to work with Carl Johnson in Biological Sciences. We are also looking forward to welcoming Carlos Taboada when he joins the Biological Sciences department in 2023.

We just finished our application for a ~\$4.5 million dollar NIH grant to build our graduate training program on computational evolutionary approaches to the study of genetic and infectious disease. Through this grant application, which has been in the works for several months now, we worked with more than 30 labs across VU and VUMC. We also wrote a grant for the history of evolutionary research at Vanderbilt and are developing an expansion of a recently awarded outreach grant by the Society for the Study of Evolution.

Our pilot grants, the first cycle of which ended this past summer, are a huge success. You can read more about them in the pages below - our sole graduate student awardee, Audrey Arner is even featured on this issue's cover. Her project took her to Malaysia to study genetic differences among populations in rural vs. urban environments. Now that she's collected the data, we're anxiously awaiting some interesting results! We were also thrilled to financially support many of our undergraduate, graduate, and postdoctoral researchers to present at conferences around the world and spread the evolutionary research done at Vanderbilt University far and wide!

One, but by no means the only, measure of our growth and success is the ever-growing list of awards received by our amazing trainees and faculty. These include graduate student Jacob Steenwyk's Harold M. Weintraub Award (widely considered the top graduate award in the life sciences), Professor Amanda Lea's Searle Scholarship (recognizing exceptional young faculty in the biomedical sciences and chemistry), and Professor Ken Catania's American Association for the Advancement of Science/Subaru SB&F Prize for his Great Adaptations book.

We are really excited about our progress and for the future of Evolutionary Studies at Vanderbilt. In the pages of our magazine, you will find our list of seminar speakers (you will recognize many, so join us when you can!) and learn about much of the amazing science that our trainees are doing. This edition contains research from Biological Sciences, English, Astronomy, Medicine, Anthropology, and Earth and Environmental Sciences. I thank you for your support to our efforts and look forward to sharing our progress with you in the future. If you have questions or ideas, please do not hesitate to reach out.

Sincerely,

Antonis Rokas

Antonis Rokas, Director

Evolutionary Studies Initiative

Cornelius Vanderbilt Chair in Biological Sciences

Vanderbilt University



Dr. Antonis Rokas in Heidelberg



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SEMINAR SERIES

Fall 2022



10/26 - Ben Good

Stanford University, Assistant Professor
Applied Physics Department

Short-term evolutionary dynamics in rapidly evolving microbial populations



11/11 - Sohini Ramachandran

Brown University, Director of the Data Science Initiative, Professor
Department of Ecology and Evolutionary and Organismal Biology

Inferring aspects of population histories from extant genetic variation

Spring 2023



1/25 - Trisha Wittkopp

University of Michigan, Arthur F. Thurnau Professor
Department of Ecology and Evolutionary Biology

Genetic basis of phenotypic evolution



2/8 - Richard Lenski

Michigan State University, Hannah Distinguished Professor
Department of Microbiology and Molecular Genetics

Time travel in experimental evolution



3/29 - Scott Edwards

Harvard University, Alexander Agassiz Professor
Curator of Ornithology, Museum of Comparative Zoology

Exploring bird diversity through genomics, museums and a two-wheeled cross-country adventure



4/19 - Graham Slater

University of Chicago, Assistant Professor
Department of the Geophysical Sciences

Evolution of biological diversity in space and time

Find more information about our virtual seminar series on [Vanderbilt.edu/evolution](https://vanderbilt.edu/evolution)

Meet our new student board!

EVOS_t

Evolution at Vanderbilt Organization for Students



Tara Stanley
Undergraduate President



Joyce Sanks
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Graduate Chair

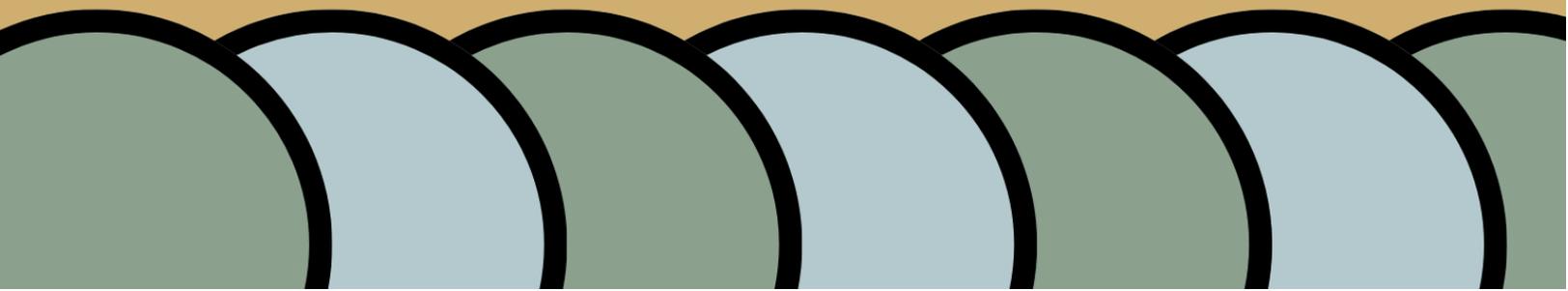


Student bowling night at Tee Line Nashville



Welcome

TO THE TEAM



Gianni Castiglione

Before pursuing a career in academia, Gianni Castiglione was a big fan of The Magic School Bus. He explained, “there was an episode of questionable ethics where they shrank down and entered a student’s body. It blew my mind and I’ve been interested in cell and molecular biology ever since!”

Castiglione is joining Vanderbilt University as an Evolutionary Biochemistry and as a member of the Evolutionary Studies Initiative (ESI).

Castiglione earned his Bachelor of Science degree from the University of Toronto in cell biology and philosophy working closely with Drs. Dinesh Christendat and Alan Moses. He followed up with a Ph.D. under Dr. Belinda Chang studying molecular evolution of rhodopsin in

fish. After finishing his Ph.D., he served as a lab manager for the Chang lab before moving on to a postdoctoral research position with Johns Hopkins School of Medicine under Elia Duh, M.D. at the Wilmer Eye Institute.

During his postdoctoral appointment at Johns Hopkins School of Medicine, Castiglione’s research expanded to include work with SARS-COV-2 infections. His work revealed a particular evolutionary pathway of an enzyme (ACE2) can provide resistance to infection in mammals. This evolutionary pathway had negative fitness effects during human evolution, and thus was likely impossible to occur. This interesting result points to the surprising directions research can take.



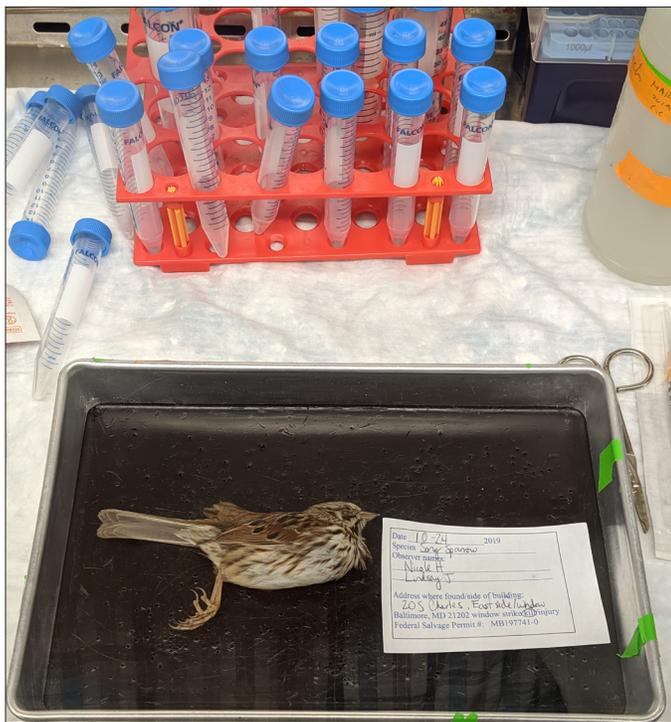
Gianni Castiglione poses with the evolutionary studies props.

Castiglione explained, “I would say most of my work was a surprise. There’s a winding road that leads to ‘ah ha’ moments, but the path is very frustrating and full of failure. I consider that to be a necessary part of the process! So much so that I now get nervous and suspicious when the evidence supports a hypothesis... there must be something else I’m missing!”

He is excited to start his own lab at Vanderbilt University. He is excited about the interdisciplinary nature of the ESI as he does both clinical research and evolutionary biochemistry.

“Having both these disciplines in such close proximity (both physically and intellectually) was a huge draw for me. It gives me the breadth of expertise to collaborate and execute on ideas that span ophthalmology and cancer to phylogenetics and crystallography,” said Castiglione.

Castiglione is excited about life in Nashville. He hopes to continue cycling, birding, and enjoying the occasional small batch whiskey – he is also eager to try Nashville hot chicken. Reach out and say hello next time you see him on campus!



Wild bird ready for dissection (Castiglione).

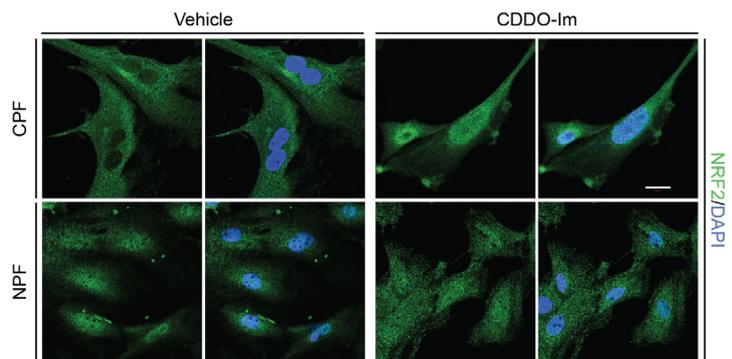


Image of the confocal microscopy of bird cells (Castiglione).

Monica Keith



Monica Keith

Monica Keith arrived at Vanderbilt University to start her new role as an assistant professor in Fall 2022 after a postdoctoral scholar position at the University of Washington. She completed her M.A. and Ph.D. in Anthropology at the University of Missouri and did her undergraduate work at Texas State University.

As an undergraduate, she majored in anthropology with a minor in biology. She received the Texas State Achievement and the University Honors Scholarships. At the University of Missouri, Keith studied the effects of genetic differences on humans and gorillas under the tutelage of Dr. Gregory Blomquist. While at Mizzou, Keith was awarded the Best Paper by a New Investigator award from the Evolutionary Anthropology Society. She also developed a keen interest in Bayesian modeling. During her postdoc at the University of Washington, Keith worked with Dr. Melanie Martin on reproductive ecology and expanded her expertise in Bayesian modeling.

Keith's current work focuses on human populations in Argentina, Bangladesh, Dominica, and the United States. She is particularly interested in how hu-



Monica Keith poses with the evolutionary studies props.

mans adapt and respond to environmental stressors, especially with respect to the role of maternal health on intergenerational outcomes. To this end, she has been developing causal pathway models of maternal health disparities in the US.

Her work is inspired by her family history.

According to Keith, “my father grew up in Bangladesh during a period of civil war followed by severe famine, mortality, morbidity, and widespread growth stunt-

ing. My drive to assess biosocial determinants of health in diverse contexts stems from an acute awareness that socioecological circumstances impact health and biology in myriad ways over a lifetime.”

Keith expressed excitement about moving to Nashville.

“Good food and live music are my top two extracurricular interests, so I look forward to exploring all that Music City has to offer!” she exclaimed.

Lin Meng

Lin Meng joined the department of Earth and Environmental Sciences in Fall 2022. She is a global change ecologist with a current interest in understanding the impact of climate change and human activities on terrestrial ecosystems.

Her interest in plant biology was sparked by a trip in China in 2015.

According to Meng, “the night before I planned to visit Central Park in Beijing to see cherry blossoms, snow came unexpectedly, and what I saw the next day was an almost complete loss of those emerging blossoms. Trees that grow in places experiencing such fluctuations in temperature can be at risk. This inspired me to study how plants respond to climate change.”

Meng joins us after completing a post-doctoral research position with the Lawrence Berkeley National Lab, in Berkeley, California. Before that, she completed her Ph.D. in environmental science and geology at Iowa State University. She also worked as a research intern at Oak Ridge National Laboratory. In 2016, she completed a master’s degree in meteorology at the Chinese Academy of Meteorological Sciences in China and in 2013 a B.Sc. in meteorology from Shenyang Agricultural University, also in China.

She has received a number of awards for her work including Grand Prize winner of the 2021 Science & SciLife Lab Prize for Young Scientists from AAAS and Science Magazine, 2020 E. Lucy Braun Award for Excellence in Ecology from the Ecological Society of America, a NASA Earth and Space Science and Technology award (FINESST) in 2019, as well as Best Teaching Assistant Award while at Iowa State University.

Meng enjoys teaching and is excited to be a part of the new Climate Studies major. She will teach Global Climate Change in the upcoming year.

According to Meng, “I will explore what climate and climate change is, and why climate change is happening. I will also talk about how a changing climate

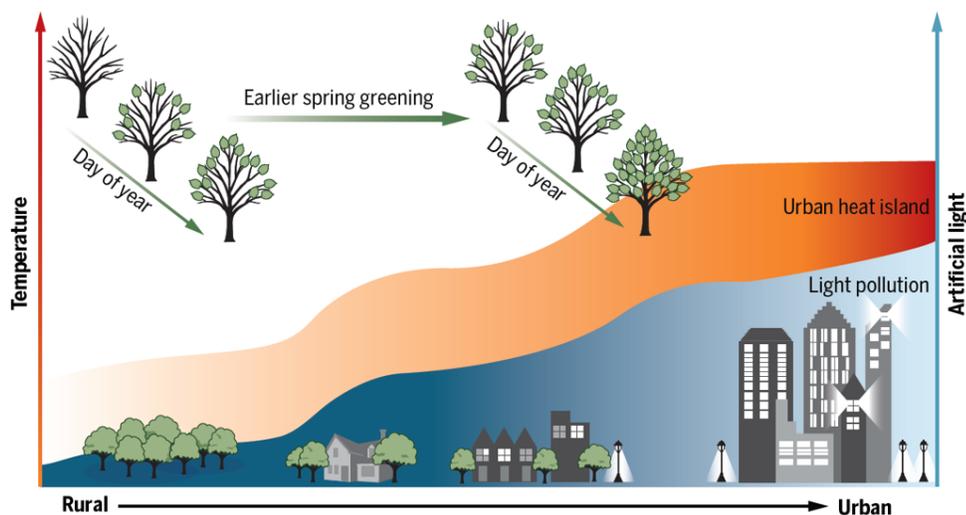


Lin Meng (left) and undergraduate student Tara Stanley (right) pose with the evolutionary studies props.

impacts ecosystems and human society, as well as the many ways in which we can all help reduce climate change and its effects, from individual and local actions to regional and global measures. I will give students suggestions and show that even small things add up to make a difference!”

Meng is as excited to be joining the Vanderbilt community as we are to have her.

“Vanderbilt is a great place to conduct interdisciplinary research by bringing together Earth science, social and political science, epidemiology, and engineering. This provides the perfect soil to grow my interdisciplinary research about urban plants and climate change. I am also impressed by the vibrant and friendly feel of the Vanderbilt community and by how welcoming everyone was. I am so excited to be here!”



The effects of temperature and artificial light on ecology (Meng)

Digging for Fossils

Faculty and trainees visit Coon Creek Science Center

On Saturday, 3/26/22, a handful of members of the Evolutionary Studies Initiative took a field trip to Coon Creek Science Center (CCSC) to dig for fossils. It was a beautiful day where many trainees that have never studied paleontology got to get out and do some field work.

Michael Gibson, a faculty at the University of Tennessee, Martin, runs the CCSC. He provided expert guidance as the group took a trip back in time to the Late Cretaceous epoch. ESI researchers present included Simon Darroch (EES), Rachel Racicot (BSCI), and Larisa DeSantis (BSCI). The trainees consisted of undergraduates, graduate students, and postdoctoral researchers. While several trainees in attendance are in the Earth and Environmental Science program (Paleontology) at Vanderbilt, others joined from a variety of non-paleontology labs, including those that study fungal

pathogens, neurobiology, and mathematical models of disease.

Gibson led the group in an hour-long information session about the fossils, how old they are, and where they came from. After a break for lunch around an open flame grill, the group broke to go fossil hunting.

The site features two areas to explore for those seeking a fun day trip (reservations required). In one spot, an earthmover comes along every couple of years to dig up some of the ground and deposit in a hill for easy access. The weather helps strip away some of the material surrounding the fossils. From this area, Darroch was excited to find and show the group the Tennessee state fossil straight away, a bivalve called *Pterotrigonion thoracica*.

The second area is in the creek itself, where slightly acidic water flows through

and degrades any exposed shells. The shells are calcium-based and break down in the water. The area of creek available to explore is about a half mile in length and has twists and turns through water never much deeper than a foot. Students found 70-million-year-old shrimp claws, oyster shells, and plenty of beautiful mother of pearl – though no mother of pearl were successfully retrieved without being damaged.

When one of the trainees asked about the dirt surrounding the fossils, Gibson explained that what the group was removing was not dirt at all, it was actually seafloor. The fossils were left behind as the Gulf of Mexico receded that once covered this part of Tennessee. Learn more about the CCSC following this link or find them on Facebook. Images credited to Tatum Lyles Flick.



Above: Graduate student Kerri-Ann Anderson walks down the creek toward the others. Right: clockwise from top left: examples of fossils found in the creek. Simon Darroch digs for fossils. Graduate student Kate Hudson stands over the creek. Undergraduates Joyce Sanks and Tara Stanley share fossils. Group photo in the creek. Stanley and site director Michael Gibson hunt for fossils in the creek. Postdoc Brant Gibson and research associate professor Rachel Racicot share fossils. Graduate student Thodoris Danis holds out his find.



Stassun Lab

Astronomers discover exceedingly rare star



Stassun Lab

A team of astronomers have made the discovery of a lifetime that will help answer burning questions on the evolution of stars. The group is led by Evolutionary Studies Initiative member and Stevenson Professor of Physics and Astronomy, Keivan Stassun.

Stassun's team generated a new model that greatly improved the way stars are measured in 2017.

"Being able to combine all of the different types of measurements into one coherent analysis was certainly key to being able to decipher the various unusual characteristics of this star system," Stassun said.

The model helps predict the types of planets orbiting distant stars – called exoplanets. It has been used to identify the characteristics of more than 100 stars

found by the TESS space telescope and 1,000s of others. But nothing prepared the team for what this new binary star system – which is actually two stars orbiting each other – could tell them about our universe.

According to Stassun, "this type of star is so extremely unusual that, frankly, we would not have thought to go looking for it – nobody has seen one before!"

Graduate student Dax Feliz, also played a major role in this project. He joined the lab as a fellow through the Fisk-Vanderbilt Masters-to-PhD Bridge Program.

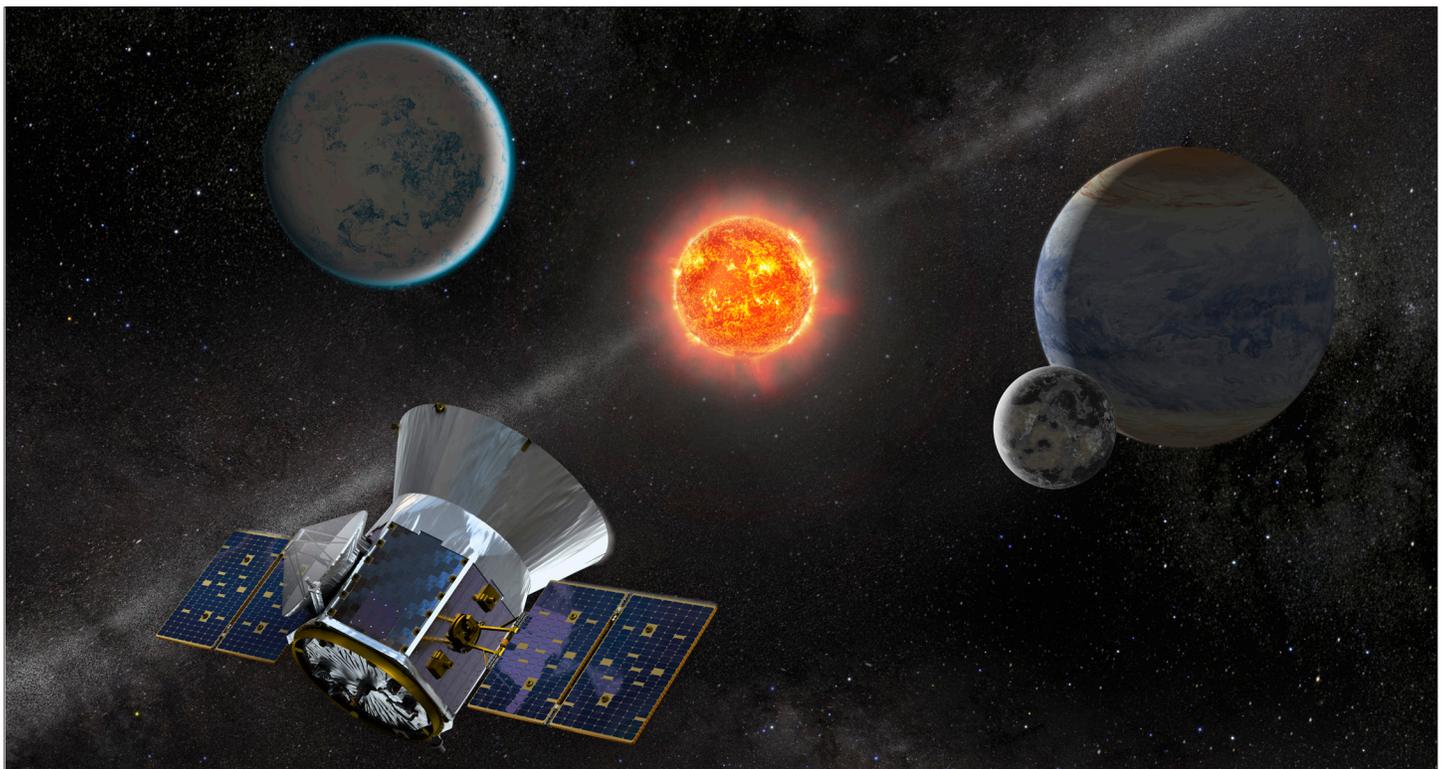
According to Feliz, "the discovery of this rare eclipsing binary star system provides a fantastic test bed for understanding how stellar binaries evolve over time. As the TESS mission continues ob-

serving large patches of sky, star systems like HD 149834 which are located in star clusters can help us further our understanding of stellar evolution."

When asked about the occurrence of Earth-like planets that could support life, Stassun said, "planets orbiting such systems would be about one in a billion... our galaxy contains about 200 billion stars, so within the Milky Way galaxy there would be a couple hundred Earth-like planets around such exceedingly rare binary systems."

The team received plenty of help from the Frist Center for Autism and Innovation. The center, founded by Stassun in 2018, works to understand and promote neurodiverse talents.

[Read more >>](#)



Artist concept of TESS observing an M dwarf star with orbiting planets. (NASA's Goddard Space Flight Center)

Clayton Group

Identifying attitudes toward genetics in TV and movies through 100+ years

Science's influence on pop culture is undeniable. Equally important is how popular culture affects people's understanding of science. Jay Clayton, Evolutionary Studies Initiative member and professor of English at Vanderbilt, and his group wanted to explore how the concept of genetics has been treated in literature, movies, television, and social media over the past century.

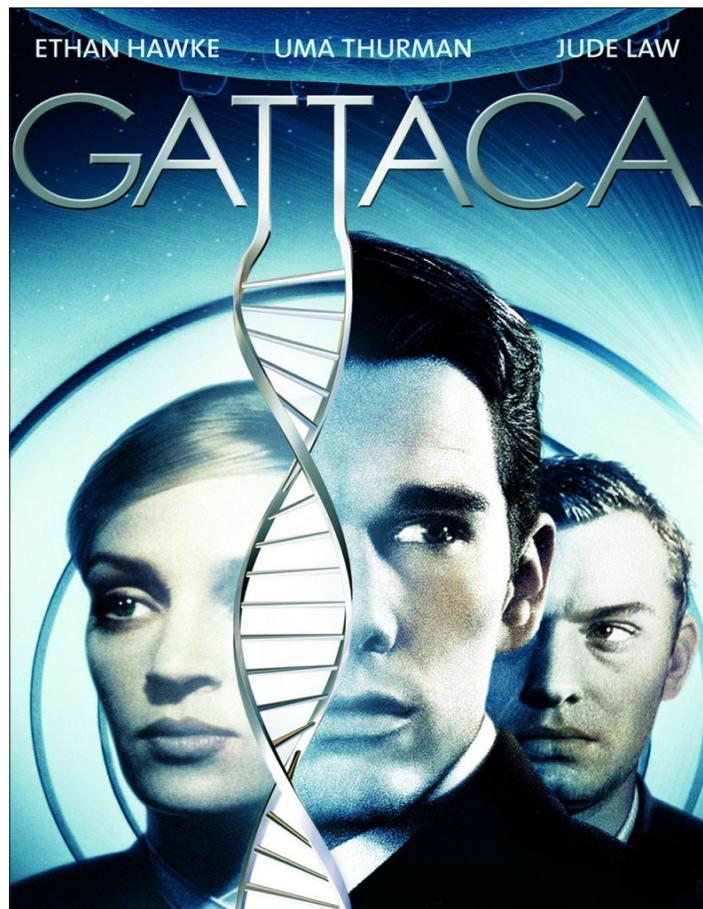
According to Clayton, "how genetics is represented in culture is enormously important. The images that circulate in popular culture both shape and reflect public attitudes toward science. Imagined worlds provide a space for reflection and depict the complex social

and ethical issues that can emerge around scientific discoveries."

This deep dive into genetics in popular culture was funded as part of a larger NIH grant.

"The grant brings together researchers from law, genetics, biomedical informatics, bioethics, the social sciences, and the humanities to look at genetic privacy in the age of big data," Clayton said. "Our team is charged with looking at how popular culture affects people's attitudes toward genetics."

To that end, graduate student Ethan Gibbons led a study that resulted in a new paper in the *Journal of Literature and Science* called "Genetics in Film and TV, 1912-2020." Gibbons, un-



Movie poster for the film *Gattaca*. The letters represent the four nucleic acids - ATGC.

dergraduate student Isaac Stovall, and Clayton analyzed more than 800 movies and TV episodes gauging the treatment of genetics. The team coded the data for 109 variables, including whether the show depicted genetics as 1) beneficial, 2) risky, or 3) mixed. They found that attitudes varied significantly over time, across media (TV vs movies), and by genre.

Films portrayed genetics as risky (70.6%) far more often than did television shows (42.7%). This difference stems from the preponderance of doctor shows, like *Grey's Anatomy*, which explore genetics' potential to improve medical care, and forensic detective

shows, like *CSI*, which use genetics to solve crimes. In terms of genre, horror and science fiction films were more likely to depict genetics in negative terms (74%) than were, say, dramas (20%), which often attempted to show both the benefits and the risks of genetics.

The group used logistic regression to test the effects of each of the predictors (era, medium, genre) on the likelihood of a risky portrayal of genetics. First, with genre and time held constant, movies were more than twice as likely to show genetics in a negative way compared to TV.

[Read more >>](#)



Left: Ethan Gibbons (Emily Dee) Right: Jay Clayton (Don Rodrigues)

Creanza Lab

Complex bird songs might require large populations

Growing up in a small community has its advantages, but if you want to learn from world experts, you may have better luck in a big city. This is the case in the world of birds as well. Large populations of birds might be better able to maintain complex songs than small populations – all because of access to high-quality tutors.

Two researchers associated with the Evolutionary Studies Initiative, postdoctoral researcher Emily Hudson and assistant professor of Biological Sciences Nicole Creanza, published their findings in the journal *Evolution*.

According to Hudson, “we hypothesized that a simple song can be maintained in a population of any size, whereas a complex song might only be maintained in a large population.”

Birds in large populations may have access to better tutors than those in small populations. Therefore, we would expect songs in smaller populations to have less complexity. This use of tutors mirrors how humans learn to make and use tools. The mathematical model that Hudson and Creanza built is based on the longstanding hypothesis that larger populations of humans might make more technological advances.

According to Creanza, “it is tempting to draw parallels between bird’s songs and human

music or language. However, a bird’s song is more than just beautiful music.”

Hudson continued, “a young bird often learns his songs from someone other than his father, particularly if his father sings a poor song. This is more like how humans learn to make tools – by finding someone who is good at making something and trying to copy them – than how humans learn language.”

This work builds off previous research in the Creanza lab exploring the role of mate choice in song evolution. The lab found that female bird preferences can drive the evolution of male song learning behavior. This work extends the previous results by showing a way that complexity could diminish in spite



Nicole Creanza (left) and Emily Hudson

of female choice.

“This mirrors the way that this type of model was originally used in human cultural evolution: to show why seemingly advantageous technologies disappeared from the archaeological record in some groups of people,” explained Creanza.

The pair of researchers are really excited about the future directions of this work.

“We believe our model also provides a potential null hypothesis for evolutionary biologists -- an expectation for how behaviors might change over time, even in the absence of changes in selection pressures,” said Hudson.

[Read more >>](#)



A songbird sings its tune on a branch.

Eichman Lab

New method to target potentially undiscovered beneficial therapeutic chemicals

A team of researchers from the Eichman lab and associated with the Evolutionary Studies Initiative led a project that was recently published in *mBio*. Graduate student Noah Bradley and undergraduate student Katie Wahl were co-first authors on the work studying chemical compounds produced by bacteria.

Specifically, the group was interested in a suite of chemicals known as natural products. These chemicals are produced by the organism for a specific purpose, but are often valuable because they may be used as antibiotics, anticancer agents, or other therapeutics. As new drug-resistant strains of diseases evolve, the importance of finding new weapons against resistant-diseases is ever increasing.

In this study, the researchers relied on a technique known as genome mining which Bradley describes as a useful tool in identifying gene

clusters and natural products they produce. Historically, genome mining targets a specific mechanism used to produce a natural product. However, several mechanisms may produce similar natural products, thus, the team's approach instead targets processes that provide bacteria with self-resistance towards a specific type of compound. Specifically, they were interested in mining for gene clusters that produce genotoxic natural products – those that can form a chemical bond to DNA.

The group paid special attention to two bacterial DNA repair enzymes known as DNA glycosylases. One, AlkZ, is found in *Streptomyces sabachiroi* while the other, YcaQ, is found in *Escherichia coli*. These enzymes – and those closely related – can remove DNA damage caused by genotoxins. However, the genomic environments and

functions of AlkZ and YcaQ are very different.

AlkZ-like (AZL) enzymes tend to localize within biosynthetic gene clusters and according to Bradley, “AZL proteins seem to be tailored for self-resistance to specific natural products.”

However, YcaQ-like (YQL) enzymes have not been found in clusters and according to Wahl, “YQL proteins might be general caretakers to remove a variety of DNA damage.”

The pair of co-first authors are excited about what the results mean moving forward.

“In the short term, we hope that the approximately 70 uncharacterized gene clusters we identified in our study can be screened for the targeted discovery of novel or useful genotoxic natural products,” said Bradley.

“In the long term, we are hopeful that our self-resistance-guided genome mining

framework will be applied in the scientific community for the targeted discovery of natural products of therapeutic benefit. We also envision the discovery of new DNA repair mechanisms through this approach,” added Wahl.

This project was borne out of creativity due to the COVID-19 pandemic forcing researchers out of the lab. Eichman reflected on the strong work ethic and positive attitudes of Bradley and Wahl.

“I enjoyed watching Noah and Katie execute a project that they designed specifically to be done while at home during the lab shut-down period. Not only did it help us all to stay engaged while being isolated, but this study has paved the way for an entirely new avenue of research for the lab,” he said.

[Read more >>](#)



Brandt Eichman



Noah Bradley



Katie Wahl

Darroch Lab

Bringing paleoecology into the 21st century

Science is an inherently collaborative endeavor. When a respected colleague courteously disagrees with your point of view, it can lead to great new papers, perspectives and collaborations.

In that same vein, feedback from editors and reviewers of academic journals is an often-understated driver of new research directions. Assistant Professor of Earth and environmental sciences Simon Darroch, found this to be the case for his new paper

examining the differences between geographic ranges of species historic and living.

In a precursor to the current paper, “Integrating geographic ranges across temporal scales”, an editor was hesitant that historic ranges and modern ranges could be defined as equivalent, since historic ranges are created using “time-averaged” records.

“This rankled us, so we’re hoping that this new framework will bring paleontologists and ecologists closer together and put us on a common conceptual footing,



so that we can work towards answering bigger questions in ecology and evolution,” said Darroch.

Darroch and Associate Professor of EES Malu Jorge published this manuscript in the journal *Trends in Ecology and Evolution* with colleagues from Oxford and Towson universities.

Darroch explained that the concerns did not take into account that current ranges are also time-averaged. It is easy to imagine a species range of buffalo in Yellowstone National Park. The range of those buffalo is the entire park. While an individual buffalo does not cover the entire park, it does not mean that all of Yellowstone National Park is not the range of buffalo. It means that the range is time-averaged over the course of several buffalos’ lives—or even several generations of buffalo.

Understanding how geographic ranges of extinct species can be related to geographic ranges of living species can yield great insights. “We’re hoping to use the fossil record to understand how geographic range size correlates with extinction and speciation and how geographic ranges of species

change in the aftermath of mass extinction events,” Darroch said. “This will help us understand the deep-time processes that are responsible for present-day patterns in biogeography.”

“Historical geographic range studies offer a deep time perspective and can tell us [for example] which species are most at risk over extinction events,” Darroch said. “I’m hoping that this framework encourages more collaboration between people who work with modern versus fossil organisms to answer these questions.”

To inspire future collaborations across the field, Darroch worked with Jorge, a conservationist who studies neotropical mammals, a set of animals including llamas, tapirs, deers, pigs, jaguars, pumas, a variety of opossums, many rodents and fishes and extremely rich insect and bird populations.

“Malu was crucial to putting these ideas together—she’s a modern ecologist and one who is learning to love the fossil record!”

[Read more >>](#)

Earlier origins for complex behavior

Graduate student in the Darroch Lab, Kat Turk, recently published a paper about life in the Ediacaran. Along with Darroch and colleagues at the University of Toronto, Mississauga, she found we might need to change when we believe some complex animal behaviors evolved.

Predatory behavior may have arisen earlier than previously thought. According to Turk, we don’t have a firm date on the first appearance of predation or when it really became wide-spread. Fossils from the Cambrian Period appear to show strong evi-

dence of predation, so we know it was around by this time. Turk’s research shows predation may go back even further.

According to Turk, “finding ecdysozoan trace fossils in the late Ediacaran means we probably had some level of active predation occurring during this interval. While priapulids today are not major predatory players in benthic marine ecosystems, in the Cambrian they were some of the earliest apex predators, with individuals found with preserved gut contents including other priapulids and

hard, shelly organisms that would have been a challenge to digest.”

Priapulids are worm-like animals that dig into the sediment and create holes. Before they evolved, the seafloor was predominantly covered with microbial mats. Their behavior of digging into the substrate may just put them in a class with beavers. Beavers are known as ecosystem engineers, as their behavior can change the landscape completely.

In the case of the priapulids, Turk explained, “they are like taking a hoe to an



Kat Turk having a blast in the field.

undisturbed plot of land – introducing that mechanical disruption results in aeration and makes the soil more hospitable for other organisms to develop.”

She continued, “I do think the gradual evolution of these bioturbators probably correlated with a slow decrease in matground cover, as their initial and then later more aggressive burrowing would have disrupted matground structural integrity and broken it into smaller and smaller pieces as time went on.”

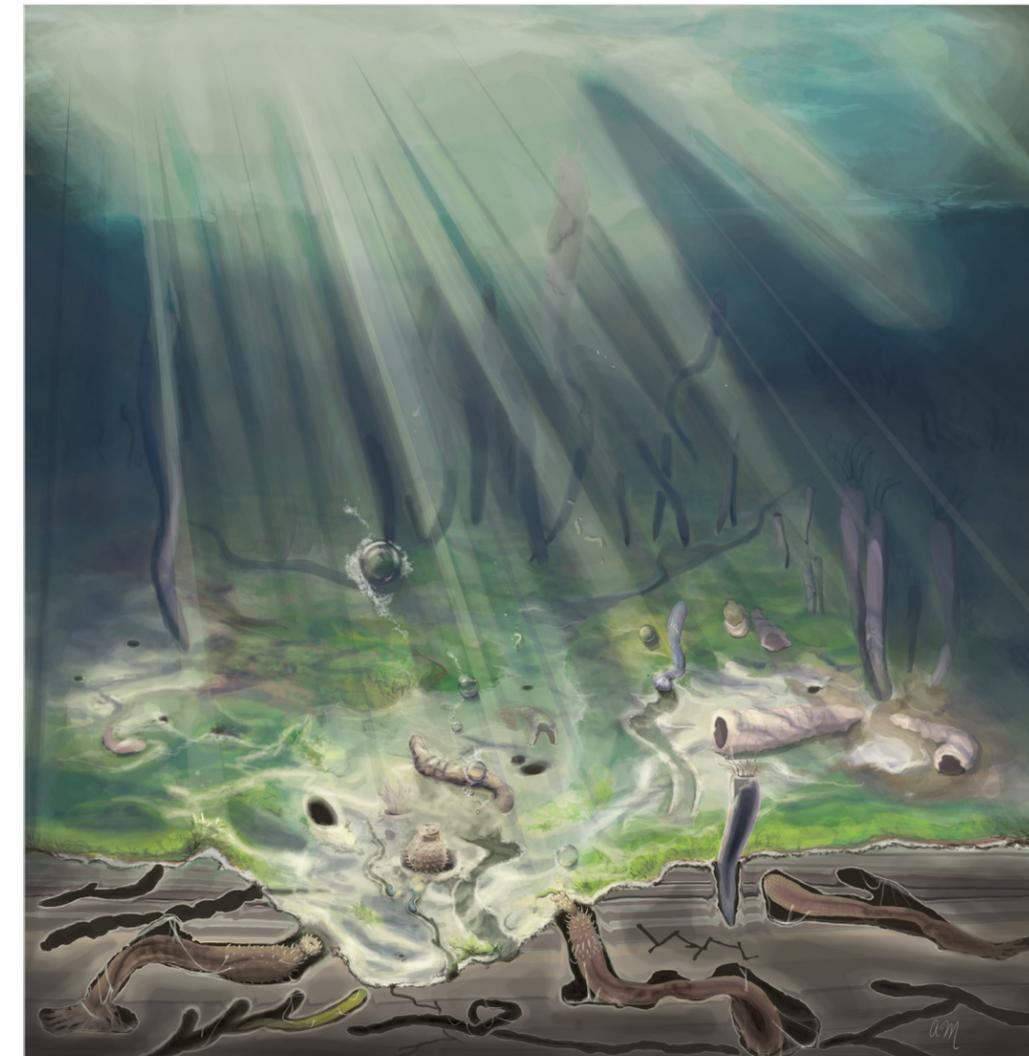
These fossils are found in an area of desert located in Namibia. The Namib Desert is full of hills, canyons, and relatively flat rock areas. Due to a lack of tectonic movement in the area and lack of human intervention due to desert-conditions, the fossils – that once covered a seafloor – have remained undisturbed through time.

“The Nama Group of southern Namibia is the best place to find late Ediacaran fossils anywhere in the world – so much so that this interval and its organisms are collectively referred to as Nama-type,” explained Turk.

[Read more >>](#)



Top right: Darroch shows off fossilized worms to students Kelly Tingle and Andrei Olaru. Center left: Students in the field under the guidance of Malu Jorge study pumas. Bottom left: Bison in a grass field.



Reconstruction of Ediacara by paleoartist Audrey Manuel.

Behringer Lab

The Hunger Games: *E. coli* edition demonstrates how mutualism and cooperative behavior shape species

Bacteria, not unlike humans, can take up more resources than necessary. When this happens, synthesized byproducts can leak into the environment. This allows the nearby bacteria to evolve cooperative behaviors, such as using the byproducts as nutrients. Cooperation in bacterial communities has also been previously observed with behaviors like altering the environment or forming new structures like biofilms.

“Making your own resources costs energy. Bacteria can evolve to rely on each other—and also conserve energy—through mutations that result in the loss of certain metabolic processes that can be supplemented by using these now public goods,” said Megan Behringer, an assistant professor in biological sciences.

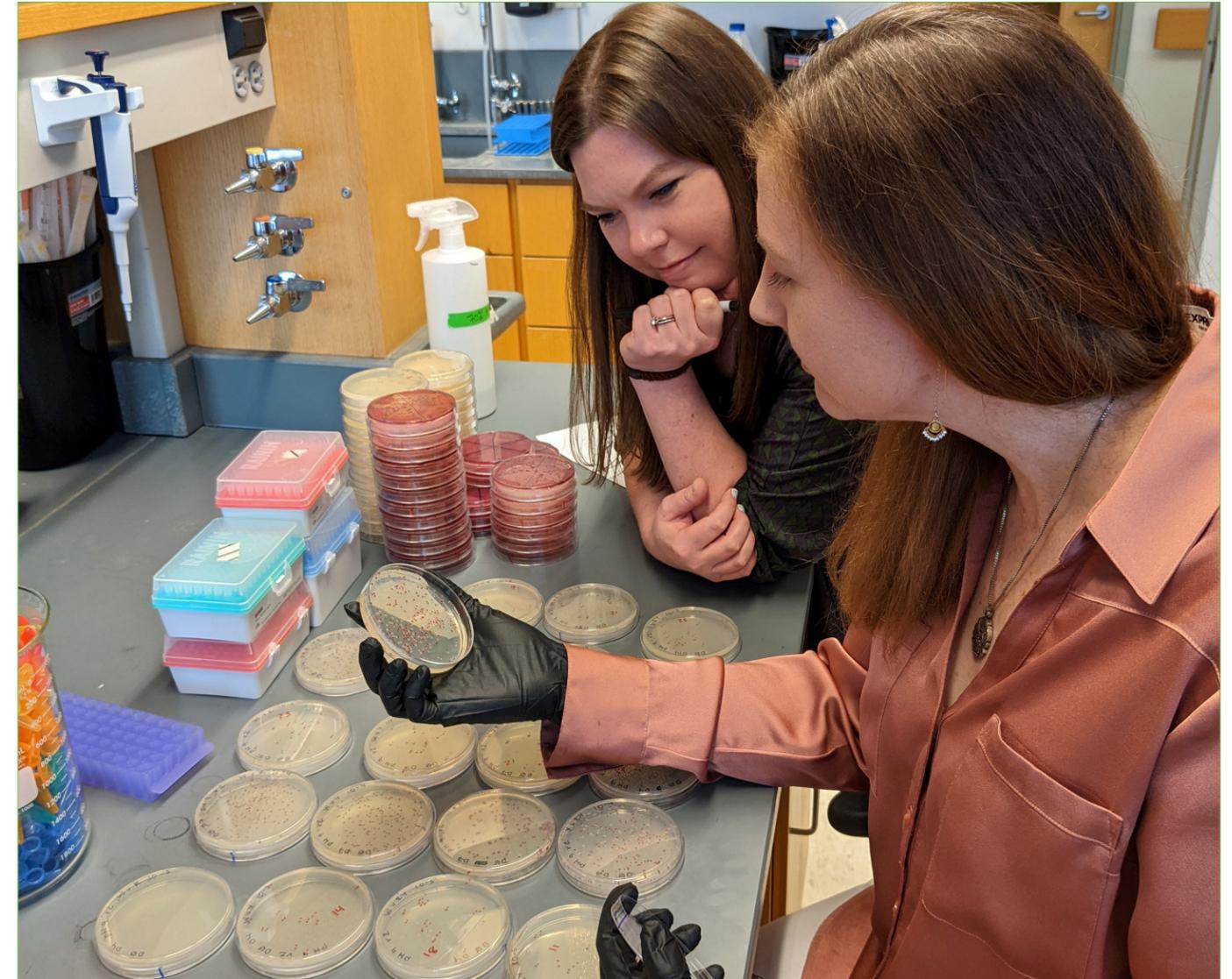
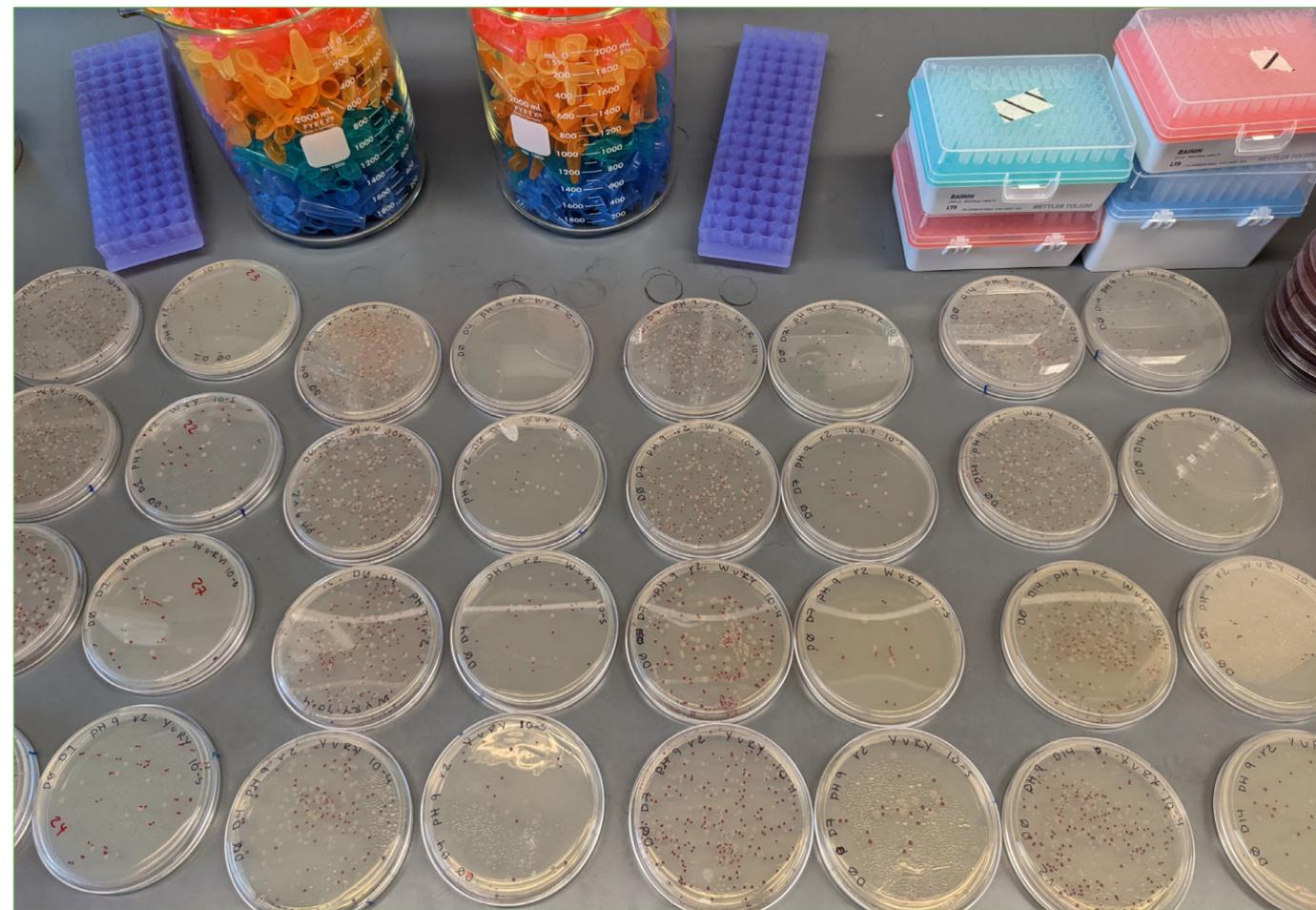
Behringer, also a member of the Evolutionary Studies Initiative, published the study,

“Complex Ecotype Dynamics Evolve in Response to Fluctuating Resources” in the journal *mBio* on May 16. The study explores the effects of feast and famine cycles within groups of the intestine-dwelling bacteria *E. coli*. The work was a collaborative effort between the Behringer lab and Wei-Chin Ho, a postdoctoral researcher at Arizona State University.

Behringer and Ho set out to test this cooperation in *E.*



coli under feast and famine conditions. They set up the bacteria with a broth medium to grow in. After 10 days, the bacteria were transferred to new broth medium. The bacteria used up most of the resources within the new broth after about one day.



Top: Megan Behringer smiles at the coast. Above: Petri dishes full of *E. coli* colonies growing. Opposite: Behringer explains her process to postdoctoral researcher, Sarah Worthan.

“*E. coli* grow very quickly and can exhaust their preferred nutrients within a day, so if we are transferring the cells every 10-days like in this experiment, they will spend the next 9 days scavenging for nutrients—including cannibalizing other *E. coli* that don’t survive the harsh, nutrient limited conditions,” Behringer said. “It’s kind of cruel really, because for us researchers it feels like we are just mixing up tubes every 10-days, but the bacteria are participating in The Hunger Games.”

Every 100 days for 900 days total, Behringer and

Ho sequenced the bacterial genomes. Following nine genome sequencing timepoints, the researchers confirmed that though the bacteria started as a group of highly similar individuals, they quickly evolved into two specialized kinds, or ecotypes. One ecotype spent energy gathering iron from the environment but did not put much energy into producing fatty acids. The other ecotype did not gather iron efficiently but did well producing fatty acids.

“While we know that cooperative interactions occur in our guts and in the wild, we

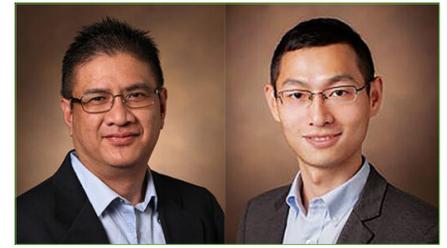
know less about how these interactions arise. To date, most of the study of cross-feeding in the lab has focused on microbes that have been engineered to cooperate or where the interaction has evolved in the lab, but it’s one-sided (A feeds B but B doesn’t feed A),” Behringer said. “In this study we found that through repeated cycles of feast and famine bacteria can evolve what appears to be bidirectional cross-feeding (A feeds B and B feeds A).”

This is exciting because until now evolution has trouble explaining this type of efficient cooperation. Feast and

famine are very natural fluctuations for bacteria. Even in our guts—an environment thought of as nutrient rich—bacteria can still be constrained for certain resources, like nitrogen. The study’s results suggest that these feast and famine dynamics can provide the conditions for bacteria to evolve these cooperative cross-feeding behaviors and provide insight into how the bacterial communities that reside in our guts, with our crops, in lakes and streams and beyond become so complex.

Gamazon Lab

New methodology for molecular mechanisms of disease



Eric Gamazon (left) and Dan Zhou

Eric Gamazon and his former postdoctoral researcher, Dan Zhou (now faculty at Zhejiang University), recently published new software and methodology for understanding the molecular basis of disease. They then applied their work to understanding the genetic basis for COVID-19 severity. The study is published in *npj Genomic Medicine*.

According to Zhou, “we developed a novel framework and metrics to evaluate the contribution of a genomic segment of interest to phenotypic variation.”

The pair then identified a specific phenotype to test their new method. They chose COVID-19 severity as their phenotype and used dif-

ferences among individuals as the variation.

“We applied our method to the host genetics of COVID-19 severity. In this case, the most significant association with the disease phenotype is a locus that contains a 49.4 Kb introgressed DNA segment from an archaic Neanderthal genome,” Gamazon said.

Genes that humans inherited from the Neanderthal genome may inform who gets severely ill during a bout of novel coronavirus. Specifically, they found a correlation between severe disease symptoms like inflammation and disturbances in smell and taste with archaic genes located on chromosome 3. In other words, people who

carry these genes inherited from Neanderthals are at higher risk to develop severe COVID-19 symptoms.

One feature key to this research was BioVU, a repository of DNA from clinical tests using blood housed at Vanderbilt. BioVU contains hundreds of thousands of samples that have been de-identified for research use.

According to Gamazon, “a large-scale electronic health records linked biobank such as BioVU provides a platform to investigate the effect of genes on potential complications.”

Gamazon concluded, “we hope that our new method will prove useful in helping future researchers identify relevant genes for other com-

plex diseases. We hope that this computational tool will be used to generate new insights into molecular mechanisms of disease.”

Zhou felt a strong sense of personal growth in the Gamazon lab, noting that the lab was inclusive of folks from all sorts of different backgrounds.

“People joined the lab from a variety of backgrounds, including human genetics, neuroscience, computer science, physics, molecular biology, pathology, epidemiology, etc. This diversity was fantastic for generating ideas and ways of solving scientific problems,” Zhou said.

[Read more >>](#)

Nashville Earth Day at Centennial Park



The DeSantis DREAM lab participated in Earth Day at Centennial Park. Undergraduate students Chamberlynn Barnett, Sola Johnson, Chuyuan Xu and Hannah Kirkham helped children excavate candy out of cookies and color in mammals. Also pictured are skulls showing differences among hominids and size of prehistoric teeth.

Rokas Lab

Evolutionary approach for finding proteins that interact

Jacob Steenwyk, along with several collaborators, published an article in *Science Advances*, the prestigious open-access journal of the American Association for the Advancement of Science. The article, titled “An orthologous gene coevolution network provides insight into eukaryotic cellular and genomic structure and function,” measured the evolution of pairs of genes shared across budding yeasts to identify those genes that participate in the same cellular or molecular functions.

The results of this work could fundamentally change the way we identify genes with similar functions.

“In this project, we examined nearly three million pairs of genes and identified instances where pairs of genes had strong evidence of coevolution. This allowed us to

draw a network diagram that reflected cellular and genomic structure and function,” said Steenwyk.

This project served as a proof of concept showing a new way to use the evolutionary histories of genes to inform our understanding of whether these genes and their protein products functionally interact inside the cell. The target group of organisms used were the budding yeasts, a group of microscopic fungi that have a plethora of evolutionary and genetic data available.

Using newly developed software - PhyKIT - and making use of evolutionary data, Steenwyk and his collaborators were able to demonstrate that genes’ evolutionary histories yield insights similar to those of genetic studies on model organisms. This is a hugely important step be-

cause evolutionary analyses are often far less challenging and require fewer resources.

According to Steenwyk, “our project sets the stage for examining gene coevolution networks in emerging model organisms, lineages with less functional data, or lineages that are not yet genetically tractable.”

Another interesting result is that the team found evidence that gene function, rather than gene location within a chromosome, drives the co-evolution of genes. According to the authors, genomes may best be viewed as extensively linked groups of genes.

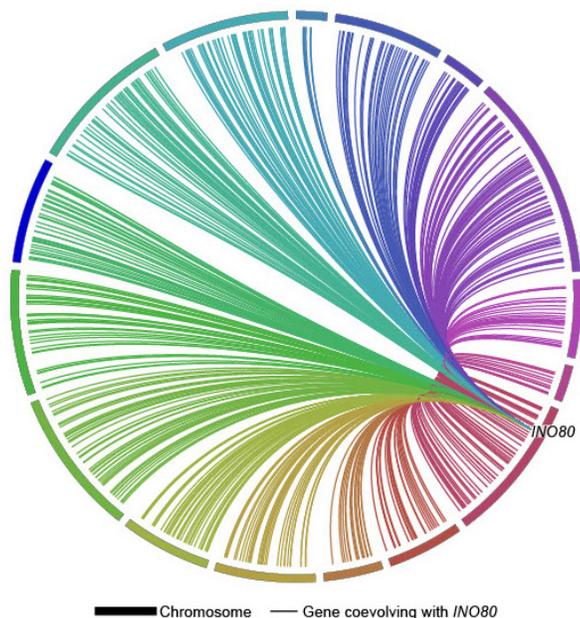
Steenwyk recently received the 2022 Harold M. Weintraub Graduate Student Award, an international award for outstanding achievement in graduate work in biological sciences, and defended his

Ph.D. in the lab of Antonis Rokas, Cornelius Vanderbilt Chair in Biological Sciences and director of the Evolutionary Studies Initiative.

Steenwyk is becoming something of an expert software developer. While Steenwyk remains humble – noting that this area is something of “novel terrain” – his software products have been downloaded tens of thousands of times. No small achievement.

According to Rokas, “Jacob saw a need among evolutionary biologists for user-friendly, robust software – he not only rose to this challenge by developing numerous pieces of software but integrated software development into his approach for asking how the evolution of genes can inform us about their function.”

[Read more >>](#)



Left: A simplified genome-wide map of genes coevolving with INO80 (Steenwyk). Right: Jacob Steenwyk and Antonis Rokas at the 30th Fungal Genetics Conference in Asilomar, California (Matt Sachs/Genetics Society of America).

Johnson Lab

Circadian clocks and climate change

Lúisa Jabbur published a review in *Frontiers in Physiology* with advisor, Carl Johnson. The new paper, “Spectres of Clock Evolution: Past, Present, and Yet to Come,” reviews the evolution of circadian clocks – focusing specifically on cyanobacteria.

“Circadian clocks are responsible, for example, for making it so that we fall asleep at night, or that sunflowers face the sun in the morning – even before they’ve seen the sun!” said Jabbur.

These clocks are easily explained for plants and animals that are relatively long-lived. For example, plant species need to use photosynthesis during the day and respiration at night. If these two processes acted at the same time, there would be no benefit to the plant. If photosynthe-

sis happened at night, again, there would be no benefit for the plant. To thrive, a plant must be able to sense its conditions and respond accordingly. Given the repetitiveness of daily cycles, it is much easier to rely on daily cycles via circadian clocks (like the sunflower) than wait until the conditions change and respond.

Jabbur, from Brazil, got into this work in Johnson’s lab while studying on a Science without Borders fellowship in the US. This fellowship allowed her to gain lab experience working on the evolution of circadian clocks.

According to Jabbur, “his lab was the perfect place to learn more about the intersection of chronobiology (circadian clocks) and evolution.”

Jabbur knows that the secrets to circadian clocks can give us insights into how species adapt, especially to things like climate change as important life-history events like reproduction and migration are tied to circadian clocks.

According to Jabbur, “research into how circadian clocks work, how they are selected by the environment, and how fast they change when subjected to new selective pressures will be crucial if we want to predict and mitigate the effects of climate change on different species.”

Importantly, Jabbur speculates that, “historical changes in circadian clocks, particularly those that were brought upon by changes in a species’ habitat, such as moving to new localities due to domestication, can give us a glimpse of what might happen as the climate changes.”

Differences caused by migration may be similar in nature to differences caused by climate change. For example, a species moving toward the equator may experience warmer temperatures, which might also be expected in the future for the individuals that didn’t migrate. This line of thinking is known as a space-for-time substitution, where changes in location can be well-correlated with future or historical events.

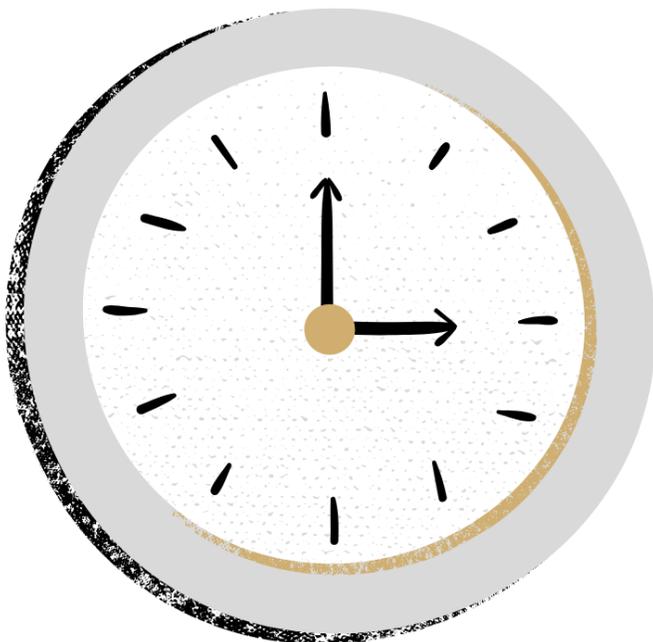
However, space-for-time substitutions have pitfalls. Jabbur uses Nashville as an example. She imagined that local squirrels might forage

until about 60°F. Average high temperatures in Nashville at 60°F or lower occur sometime in November, when daylight covers just 10.5 hours. If that same squirrel were put in Duluth, MN and stopped foraging at 60°F, it would need to have enough resources stored to survive starting a full month earlier, at the beginning of October. If, instead, the squirrel waited until there were 10.5 hours of light, it would be foraging in weather conditions that were unsuitable and may not find enough resources to survive the winter.

Jabbur says, “looking at how species have responded to this mismatch between day length and temperature in the past (e.g., through migration) can teach us about what they might do to respond to a similar mismatch in the future.”

Finally, Jabbur is really excited to be finishing up some of her Ph.D. work.

“In my Ph.D., I’ve discovered that cyanobacteria are also capable of the photo-periodic responses that we mention in the review (such as migration, flowering, etc.) that will likely be affected by climate change. This is a very exciting discovery because it means both that this might be much more evolutionarily ancient than we thought, and because cyanobacteria could potentially be a great model organism to study how clocks might evolve in response to climate change!”



Tate Lab

The effects of coinfection on community dynamics

A new study in *The American Naturalist* models how parasites interact to affect their host's behavior. The results of the research, conducted by Faith Rovenolt, BA'20, and assistant professor Ann Tate, reinforce an understanding of the influence of disease in community dynamics.

The pair created a new model to study coinfection of hosts and developed a table of known interactions between parasites infecting the same hosts.

"I wanted to create a model that involved resistance and tolerance to parasites, since they should have different impacts on host ecology and evolution," said Rovenolt, now a graduate student at

the University of Pittsburgh. "We already had some experimental data suggesting that our hosts, two flour beetles (*Tribolium*), fared differently under infection, so it made sense to incorporate it all under the same framework."

"It blew my mind just how difficult it is to define interactions," Rovenolt said. "In one context, like high host food availability, two parasites might facilitate each other, while under low food they might compete."

"It is important to know the relative strength of within versus between species competition in the absence of parasites, and whether the two hosts are sharing one or both parasites, since it affects feedbacks on prevalence and

transmission to each host," said Tate, also a member of the Evolutionary Studies Initiative.

Flour beetles are a great system to test questions about parasitic interactions and community dynamics because they are well-studied and frequent agricultural pests. "The rich body of literature on natural history and population biology of *Tribolium* is complemented by a modern molecular genomics toolbox and the ease of collecting beetles and their parasites in the 'wild' — like in grain elevators and feed mills around the U.S. and the world," Tate said. "It makes it an ideal system to test these cross-scale feedbacks."

This work was partly in-

spired by a 1948 study focused on the interactions between two species of flour beetles. The paper was among the first to suggest that parasites could alter community dynamics of their hosts. "I've known about and been inspired by this paper for as long as I've worked on the beetles, so it was fun to resurrect it to serve as a motivating example for this study," Tate said.

While Rovenolt wrote this paper as part of her senior honors thesis, she and Tate will soon test their model's usefulness as they design new lab experiments that aim to predict coinfection and community dynamics.

[Read more >>](#)



The Tate lab at MegaMicrobe 2019

Bonami and Georgiev Labs

Cellular and antibody responses to COVID-19 vaccine

By Leigh MacMillan
Writer VUMC Reporter

In a technical tour de force, a collaborative team of Vanderbilt researchers has characterized the antigen-specific immune response to the Pfizer SARS-CoV-2 RNA vaccine.

The group used multiple single-cell technologies, unbiased machine learning, and traditional immunological approaches to track cellular and antibody responses in samples collected over time from a cohort of healthy participants. The findings, published in *Nature Communications*, could guide testing for vaccine response and booster timing.

“There is a lot of debate in the clinical immunology field about what is an appropriate vaccine response: What actually protects someone against disease?” said Erin Wilfong, M.D., Ph.D., instructor in Medicine and one of three co-first authors of the paper with Kevin Kramer, Ph.D., and Kelsey Voss, Ph.D. “How do we know who’s had a good response, and who hasn’t? How do we know when people need a booster?”

When VUMC began vaccinating its workforce against SARS-CoV-2, the virus that causes COVID-19, in December 2020, the collaborative team was in a unique position to explore these questions.

The researchers — including the groups of Jonathan

Irish, Ph.D., Ivelin Georgiev, Ph.D., Rachel Bonami, Ph.D., and Jeffrey Rathmell, Ph.D., all co-senior authors of the *Nature Communications* paper — had been working together through the Human Immunology Discovery Initiative (HIDI), which was funded in 2019 by a Vanderbilt Trans-Institutional Programs (TIPs) award.

“The TIPs grant brought together researchers with disparate technologies and expertise focused on trying to understand how the human immune response works,” said Rathmell, director of the Vanderbilt Center for Immunobiology, which coordinates HIDI.

Kramer, who was a graduate student in Georgiev’s lab, suggested that the group study the response to the SARS-CoV-2 vaccine in healthy volunteers who had not had the disease COVID-19.

Within hours of getting Institutional Review Board approval and sending out an email to a faculty list, the team had volunteers ready to donate blood samples ahead of being vaccinated, and several times afterwards.

Irish and Georgiev have both pioneered single-cell technologies and unbiased analytical approaches to find and identify the rare immune cells directed at specific antigens — in this case the SARS-CoV-2 viral spike protein. Bonami is a B cell biologist who developed single-cell an-

alytical pipelines to identify which of the functionally distinct subsets or “flavors” of antigen-specific B cells expanded with vaccination.

Using these technologies alongside other single-cell and traditional approaches, the group identified and characterized the SARS-CoV-2-directed B cells that instruct T cells and produce antibodies and the T cells that can kill virus-infected cells and also help direct antibody production.

“Right now, the way that we test if vaccines are working is by measuring antibodies,” Rathmell said. “You really need both antibody-producing B cells and T cells for an effective immune response, and we’re not measuring either of the cells.”

The team was able to develop strategies for using a more common technology — flow cytometry — to find the B and T cells that respond specifically to the SARS-CoV-2 vaccine.

“We’re still a long way off, but this is a first step towards being able to test whether someone had a good cellular

response,” Wilfong said.

The researchers expect such measurements will be useful, particularly for determining the vaccine response of high-risk individuals and for defining if and when booster doses might be beneficial.

One of the participants who did not have the identified vaccine-induced cell populations had a breakthrough COVID-19 infection, they reported.

The group was also intrigued that the vaccine-induced T cells they identified had unique characteristics that didn’t match previously described categories of T cells.

“I think we found a new phase in an immune response,” Rathmell said. “It’s going to be an interesting set of cells to study in the future. These cells are the ones that correlate best with the antibody response.”

Rathmell noted that the “cellular analysis platform” the group developed can be broadly applied to study cellular immune responses, for example in patients with kidney cancer who are being treated with immunotherapies, patients on immunosuppressant therapies following cardiac transplant, and patients with lupus.



The team: (front row, from left) Kelsey Voss, Rachel Bonami, Erin Wilfong, (back row, from left) Jonathan Irish, Jeff Rathmell, and Ivelin Georgiev (photo by Susan Urmey).

Hillyer Lab

Genetic pathways linking the immune and circulatory systems of mosquitoes during infection

Vanderbilt biologists have discovered the genetic pathways that link the immune and circulatory systems of mosquitoes during the fight against infection. A mosquito fighting infection of malaria or bacteria attracts immune cells to its heart that filter microbes that are flowing in its blood, called hemolymph. The discovery of two pathways that link immunity and hemolymph circulation is a major contribution to the understanding of how mosquitoes, which are themselves disease vectors, respond to infection.

Julián F. Hillyer, professor of biological sciences, and his research team investigate the physiology of mosquitoes and, specifically, how the mosquito heart pumps hemolymph, how its immune cells fight infection and how these processes interact.

In some cases, mosquitoes beat infection through im-

munologically active cells in the heart. Because the circulatory system of mosquitoes contains only one contracting vessel and no arteries or veins, their hemolymph flows freely throughout the body. “Insects deploy a powerful immune response against infection, with immune cells aggregating on the heart to destroy passing microbes. Yet, the genetic mechanisms that guide these immune cells to the heart remained unknown,” said Yan Yan, Ph.D. 21, a lead researcher on the project.

Hillyer’s team studied the expression of every gene in the mosquito heart and identified the genetic pathways that become significantly activated on the heart when an infection occurs. By disrupting these pathways using a technique called RNA interference, the researchers discovered how the genetic pathways are involved.

The immune deficiency

pathway, which produces and secretes immune proteins, also recruits free-floating immune cells to settle on the heart. The team also found that a pathway that plays a role in longevity, reproduction and defense brings immune cells to the heart. Immune cells that arrive on the heart eat and digest microbes, increasing a mosquito’s likelihood to overcome infection.

Hillyer, Yan and their team hypothesize that the genetic pathways identified in this study drive immune responses on the hearts of other insects — including disease vectors, agricultural pests and crop pollinators—because the immune and circulatory systems are functionally integrated throughout the insect tree of life and are evolutionarily conserved in the insect lineage.

“This research could lay the foundation for novel strategies that protect beneficial

insects or harm detrimental ones,” Hillyer added.

To continue this advance in knowledge, Hillyer’s team is investigating how pathway disruption affects insect heart contractions and is looking for heart-specific factors that act as “homing signals” for the arrival of immune cells on the heart.

The article, “The immune deficiency and c-Jun N-terminal kinase pathways drive the functional integration of the immune and circulatory systems of mosquitoes” was published in the journal *Open Biology* on Sept. 7.

The work was conducted in the department of biological sciences and the Evolutionary Studies Initiative at Vanderbilt University. The research was funded by National Science Foundation grants IOS-1456844 and IOS-1949145. Members of the research team include first author Leah Sigle, PhD’18, postdoctoral scholar David Rinker and research assistant Tania Estévez-Lao. Former Vanderbilt faculty member and current associate professor of epidemiology and biostatistics at University of California at San Francisco John A. Capra also participated in the research.



Yan Yan



Julián Hillyer

PILOT GRANTS

New research avenues abound in evolutionary studies

With the funding of seven pilot grant projects last year, there are numerous new research avenues across evolutionary studies. Check out the precursor to this story here.

Arner experiences anthropological field research for the first time

The sole graduate student recipient last year was Audrey Arner of Amanda Lea's lab. Arner used the funds for a 5-week trip to collect preliminary data on how changes in ecological and cultural environments impact health- and fitness-related traits in the Orang Asli, the indigenous peoples of Malaysia.

While in Malaysia, Arner sampled blood, conducted lifestyle interviews, and even supported efforts to provide free health care while collecting research data. Arner's original task was to learn about blood sample collection and processing. However, Arner was not satis-



fied at simply learning sample processing and wanted a deeper understanding of the indigenous people she was studying.

Since her pilot grant was funded, Arner successfully wrote for an NSF Graduate Research Fellowship Program grant.

Racicot expands research scope

Rachel Racicot used her pilot grant funds to help offset the cost of industry standard Avizo software. Access to Avizo has not only contributed to the originally proposed work but has also



expanded the lab's reach into two additional projects. Racicot used Avizo to train several students in her lab in methods of inner ear studies. Of note, Sydney Rosen, leveraged her work with the new software into an NSF-REU opportunity at the American Museum of Natural History studying the inner ears of animals including and related to horses and rhinoceroses.

Patel lab identifies causative agent for evolutionary trade-off between maintenance and reproduction

The Patel lab put in a true team effort to uncover the mechanism behind a mitochondrial stress response. The project was led by graduate student James Held, who discovered 12 mutant lines from a forward genetic screen. These dozen mutant lines were then examined more closely through the pilot grant funds. Held got help from undergraduate students and research assistants Nadir Dbouk and Adrianna Strozak. The team discovered one of the genes responsible for the mutant lines from the original screen and, according to Patel, "can now proceed with characterization of this gene within the context of the reproductive-soma evolutionary tradeoff."

Tate lab discovers new role of regulatory immune genes

Assistant professor Ann Tate, graduate student Justin Critchlow, and undergraduate student Katherine Zhong completed work testing an array of regulatory immune genes for their role in the creation of antimicrobial peptides. Of the four genes they tested, only cac-

rus showed significant results. After silencing the expression of cactus in flour beetles, the team exposed the beetles to a common, fungal pathogen (*Bacillus thuringiensis*). These beetles showed higher rates of survival after infection. However, these beetles also had a lower rate of survival compared to the control group without infection.

Behringer and Bratton develop new phenotypic biosensors for E. coli

The Behringer and Bratton labs acquired seven fluorescent biosensors that will allow for the detection of six different molecular phenotypes. They used the biosensor pHluorin, along with a pH sensitive dye, to test the effects of environmental pH on intracellular pH levels with four strains of *E. coli*.

The DeSantis lab explores the Smithsonian Museum of Natural History

While visiting the Smithsonian Museum of Natural History, Larisa DeSantis and two of her undergraduate trainees, Ashley Rogers and Kristen Koehler, collected dental microwear samples from a

crabeater seal, leopard seal, and bottlenose dolphin, among others. More than 200 samples were collected and will be used for undergraduate research projects moving forward. Rogers is a MARC scholar and will use the data for subsequent dietary analyses.

The Creanza and Benn Torres labs funded an undergraduate researcher and published a paper in Evolution

The funds helped a collaborative research project between the Benn Torres and Creanza labs. This project investigates genetic admixture along with Creole and Creole-source languages. The grant paid for an undergraduate student, Toluwani Star David, to work on analyzing data as part of her Immersion research project. One interesting result from her work so far is that non-European words are less likely to be adjectives compared to pronouns, interrogatives, or quantifiers.

Read more >>



Top Left: Audrey Arner sampling blood in Malaysia (Ian Wallace); Top right: The Racicot lab stands around a CT scan machine; Bottom: The Patel lab poses with the evolutionary studies props (from left, back row: James Held, Lantana Grub. Front row: Marleigh Canter, Adrianna Strozak, Sam Schaffner, Nikita Tsyba, Maulik Patel).



Left: Ashley Rogers (left) and Kristen Koehler (DeSantis Lab, photo credit Larisa DeSantis); Right: Justin Critchlow (Tate Lab) pipettes at the bench



PILOT GRANTS

2022 Awardess feature anthropology, biological sciences & Earth and environmental sciences

Evolutionary Studies at Vanderbilt selected four exciting, new proposals for pilot grants. Graduate students Samantha Schaffner (biological sciences, Patel Lab), Taiye Winful (anthropology, Benn Torres Lab), and Katie McCormack (anthropology, Benn Torres Lab) have all been awarded funding, along with new professor in Earth and environmental sciences, Lin Meng who will be working with biological sciences professor Carl Johnson.

This year's lone faculty application, led by assistant professor Meng collaborating with Johnson, will focus on the effects of artificial light at night (ALAN). Meng studies ALAN and Johnson studies the molecular mechanisms of timekeeping. The pair will compare the effects of ALAN on two plant species with different life-history traits. The first, *Arabidopsis thaliana*, is a long-day plant,

meaning it needs less nighttime to induce flowering whereas the second, *Schlumbergera* is a short-day plant and will not flower with less than 12 hours of night. They will use multiple ALAN treatments to tease apart effects of ALAN on each species.

Excitingly, Evolutionary Studies will be funding two pilot projects in the anthropology department this year. The first, led by graduate student Taiye Winful, will study the effects of chronic stress on physiological conditions in a Nigerian population. Many studies investigate how genetics can control the levels of stress hormones in the body, Winful's will be one of few that incorporates the impact of environmental factors. Winful's dissertation has thus far focused on data available through Bio-VU and other sources; this grant will allow collection of data at Lagos State University Teaching



Sam Schaffner

Hospital in Nigeria. According to Winful, "this approach further contextualizes how genetic and social factors influence health outcomes." This project will be in collaboration with senior lecturer

Modupe Sorunke of Lagos State University.

McCormack will lead the second project from the anthropology department. McCormack's research will focus on calcified dental plaque

from individuals that lived in the years 600-1200 from Santa Rita Corozal in Belize. McCormack is specifically interested in the microbiome associated with the human mouth. According to McCormack, "analysis of this sample of individuals will also inform future exploration into the disease ecology of Classic and Postclassic Mayan populations in Belize." McCormack will collaborate with Assistant Professor Rick Smith at George Mason University.

For the second straight year, a graduate student in the Patel Lab will receive funding to research *Caenorhabditis elegans* evolutionary biology. Schaffner's project looks at the genetic abnormalities associated with a protein required for meiosis in *C. elegans*. The abnormality in this case is that a specific gene necessary for meiosis in *C. elegans* is missing in related species. Schaffner hypothesizes that this gene is present not as something generally required, but something required to negate the presence of an additional, deleterious gene.

According to Evolutionary Studies director, Antonis Rokas, "we are beyond excited to support these fascinating and diverse projects from these three departments. The funded projects showcase the amazing talent within our group and collaborative nature of evolutionary studies at Vanderbilt."



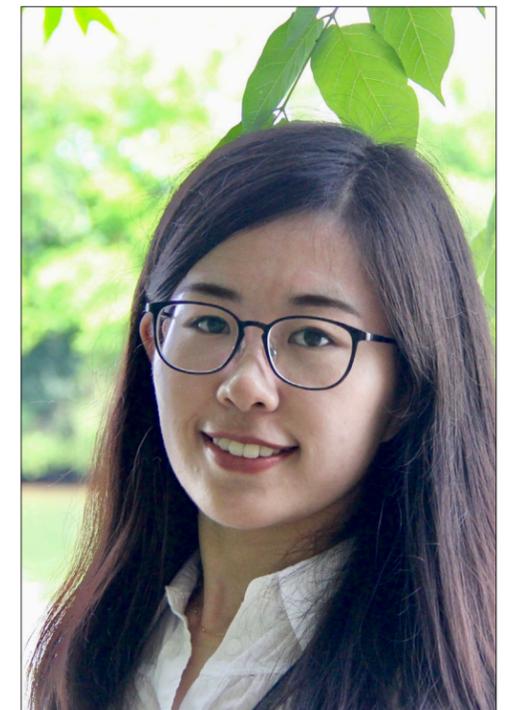
Katie McCormack



Taiye Winful



Carl Johnson



Lin Meng



A map of the US showcasing artificial light at night.

Undergraduate Research Fair Participants

Charu Balamurugan '25
Biological Sciences; Medicine,
Health & Society

**Characterization of a Toxic Secondary
Metabolic Gene Cluster in *Penicillium* Fungi**
Mentor: Professor Antonis Rokas, Biological Sciences

Rachel Haselkorn '23
Neuroscience

**Organization of Cortical Connections of Complex
Movement Domains in the Squirrel Monkey Brain**
Mentor: Professor Jon Kaas, Psychology

Sarah Hourihan '24
Biological Sciences; Music

**Significant Song and Genetic Differences
Between Subspecies of the Dark-Eyed Junco**
Mentor: Professor Nicole Creanza, Biological Sciences

Kristen Koehler '24
Ecology, Evolution & Organismal
Biology

**Re-evaluating the Paleoecology of the West Coast of
South Africa through Dental Microwear Analysis of Bovids**
Mentor: Professor Larisa DeSantis, Biological Sciences

Anika Mahajan '24
Medicine, Health & Society;
Spanish

**Identifying Binding Attributes of Insuling-Binding B
Cell Receptors**
Mentor: Professor Rachel Bonami, Medicine

Kayla Prowell '23
Psychology

**Hanging with Herbivores: A Survey of Dental
Microwear Analyses of Alaskan Bovids**
Mentor: Professor Larisa DeSantis, Biological Sciences

Wonder Wei '24
Biological Sciences; Ecology,
Evolution & Organismal Biology

**Reconstructing the Dietary Ecology of Lynx Throughout
Time**
Mentor: Professor Larisa DeSantis, Biological Sciences

Veronica Wroblewski '22
Biological Sciences; Secondary
Education

**Toxicity of Yeast Encapsulated Phoyosensitive Insecticides
on *Anopholes gambiae* and *Aedes aegypti* Mosquito Larvae**
Mentor: Professor Julián Hillyer, Biological Sciences

Michelle Yin '23
Biological Sciences

Mutation Accumulation of *Lactobacillus* Sp.
Mentor: Professor Megan Behringer, Biological Sciences



Kristen Koehler collects dental microwear samples of marine mammals at the Smithsonian Museum of Natural History in Washington, D.C. (DeSantis)

Awards

Faculty

- Amanda Lea - Searle Scholar, Dean's Faculty Fellow, CIFAR Azrieli Global Scholar
- Kenneth Catania - AAAS/Subaru SB&F Prize for Excellence in Science Books, 25 Years of Service
- Megan Behringer - Dean's Faculty Fellow
- Alex Bick - Pew-Stewart Scholar for Cancer Research

Graduate Students

- Jacob Steenwyk (Rokas Lab) - Harold M. Weintraub Award, Edward J. Ferguson Jr. Graduate Award
- Noah Bradley (Eichman Lab) - Edward J. Ferguson Jr. Graduate Award
- James Held (Patel Lab) - Graduate Student Research Excellence Award in Biological Sciences
- Reese Martin (Tate Lab) - Itchy

Finger Award, Ann Bernard Martin Award for Excellence in Graduate Research, NSF GRFP Honorable Mention

- Cole Meier (Hillyer Lab) - Hickory Stick Award for Outstanding Teaching Assistant, Gisela Mosig Best Presenter Award
- Lantana Grub (Patel Lab) - Biological Sciences Annual Retreat Best Poster Award, Three Minute Thesis Finalist, Department of Defense NDSEG Fellowship
- Annie Hatmaker (Rokas Lab) - F31 Predoctoral Fellowship National Eye Institute, NIH, Summer Research Award, Hickory Stick Award for Outstanding Teaching Assistant
- Carla Gonçalves (Rokas Lab) - GSA Fungal 22 Poster Award
- Audrey Arner (Lea Lab) - NSF GRFP Award
- Kat Turk (Darroch Lab) -

President's Prize at Paleontological Association Conference, Best Oral Presentation, GSA, "Respekt & Wertschätzung" Scholarship

- Christina Chavez (Rokas Lab) - Graduate Leadership Anchor Award

Undergraduate Students

- Joyce Sanks (Darroch Lab) - Best Poster at NABG Conference
- Kayla Prowell (DeSantis Lab) - Excellence in Research Poster Award
- Anika Mahajan (Bonami Lab) - Excellence in Research Poster Award
- Charu Balamurugan (Rokas Lab) - Excellence in Research Poster Award
- Andrei Olaru (Darroch Lab) - Best Poster Award, GSA



Undergraduates

Spring 2022

- Chamberlyn Barnett - Bachelor of Science from Peabody College in Cognitive Studies
- Micayla Cochran - Bachelor of Arts in Ecology, Evolution & Organismal Biology (honors)
- Ziwen Guo - Bachelor of Arts in Ecology, Evolution & Organismal Biology
- Calla Reed - Bachelor of Arts in Ecology, Evolution & Organismal Biology
- Navya Thakkar - Bachelor of Arts in Ecology, Evolution & Organismal Biology



Cheers

TO THE NEXT CHAPTER



Graduates

Summer 2021

- Abin Abraham - Doctor of Philosophy - Human Genetics - Quantifying preterm birth risk and heterogeneity using evolutionary history and electronic health records
- Yan Yan - Doctor of Philosophy - Biological Sciences - Integration between the mosquito immune and circulatory systems: from genetic mechanisms to evolutionary conservation

Fall 2022

- Brian Gitschlag - Doctor of Philosophy - Biological Sciences - How adaptive strategies of cooperation and cheating define the population dynamics of mitochondrial mutations

Spring 2022

- Noah Bradley - Doctor of Philosophy - Biological Sciences - Characterization of bacterial DNA glycosylases involved in interstrand crosslink repair and antibiotic resistance
- Evonne McArthur - Doctor of Philosophy - Human Genetics - The contribution of 3D genome to gene regulation, human evolution, and disease
- Jacob Steenwyk - Doctor of Philosophy - Biological Sciences - Fungal genome evolution and software for the life sciences

Alumni Update

Sam Smith – Undergraduate (EEOB, '17) – Rokas Lab

Sam Smith just finished his Ph.D. at Brown University in Sohini Ramachandran's lab. He spent 2016-'17 as an undergraduate researcher in the Rokas lab. He is now a postdoctoral researcher at the University of Texas, Austin, in Arbel Harpak's lab. Sam took time for a Q&A:

How did you find your way to Vanderbilt?

I grew up in Nashville and went to elementary school at Eakin, just about a block or two from campus. Vanderbilt has always been a part of my life. Both of my parents are alums of the Divinity School. I chose to come to Vanderbilt because of that intimate knowledge of the university that was born of proximity and I have been so grateful for that opportunity.

What was your favorite academic and non-academic experience at Vanderbilt?

My favorite academic experience was the Evolution course that I took with Antonis Rokas and Dan Funk. In An-

tonis' half of the section I got my first taste of how mathematical modeling can be used to understand evolutionary phenomenon. The course was incredibly challenging but rewarding in the way it reshaped my thinking around what pursuits in population genetics can look like through a research lens.

My favorite non-academic experience has to be the friendships that I formed while I was on campus. They are lifelong friendships that superseded backgrounds or current interests – many of those friends were with me when I got married over the summer and I talk to them almost every week.

What is your favorite part about research and why?

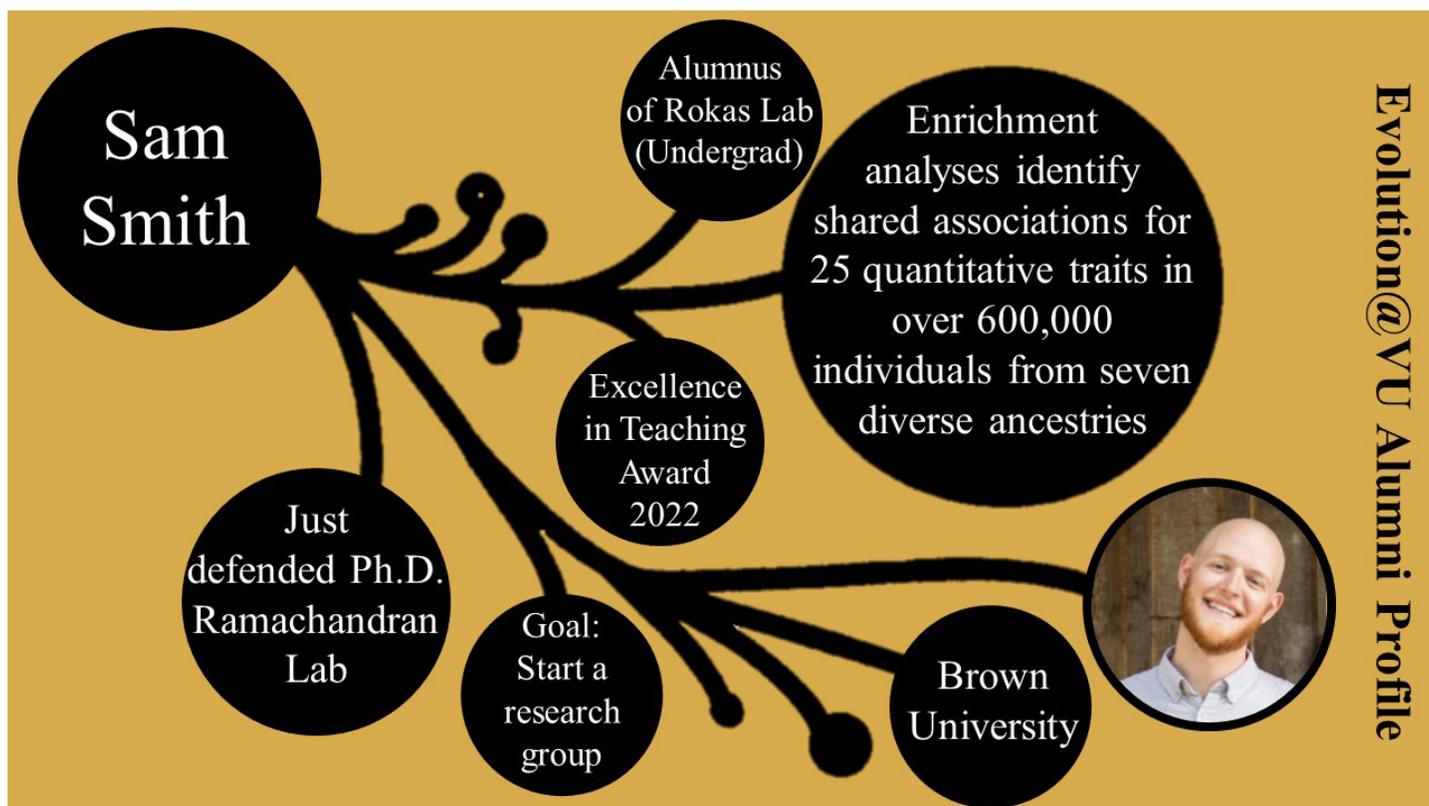
My favorite part about research is the intellectual liberty that it facilitates. It offers the unique opportunity to transition from learning foundation knowledge to applying that knowledge to open questions. I also believe that it becomes more

rewarding and exciting the longer that you are involved in a particular field because you begin to establish connections between questions that you may have initially believed to be unconnected.

How did your experiences at Vanderbilt prepare you for graduate school?

I started in the Rokas Lab as an undergraduate research assistant the summer after my Sophomore year (2016). Antonis created an environment of curiosity that I became enamored with quite quickly. I also think that he put so much intention into scientific communication with the lab which really helped me understand what other lab members were talking about and minimized imposter syndrome. Additionally, Antonis really invested in the work that I was doing by reading drafts and offering feedback on presentations.

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RECRUITING NOW

Brian O. Bachmann (Biochem)

Biosynthesis, Secondary Metabolites, Directed Evolution, Drug Discovery

Megan Behringer (BSCI)

Population genetics, genomics, microbiology, *E. coli*

Benjamin Bratton (PMI)

Bacterial evolution, microscopy, cell shape, quantitative biology

Gianni Castiglione (BSCI)

Molecular evolution, vision, oxidative stress, evolutionary medicine

Simon Darroch (EES)

Extinction, origination, paleontology, ecology, biogeography, Ediacaran, Cambrian

Larisa DeSantis (BSCI)

Vertebrate paleontology, paleoecology, paleoclimates

Monica Keith (Anthro)

Biological anthropology, data science, Bayesian modeling, maternal health disparities

Amanda Lea (BSCI)

Gene regulation, biological anthropology, genotype x environment interactions, early life effects

Lin Meng (EES)

Climate change, plant ecology, remote sensing, light pollution

Maulik Patel (BSCI)

Mitochondria, adaptive evolution, genetic conflict, selfish DNA, female reproduction, disease inheritance

Rachel Racicot (BSCI)

Marine mammals, evolutionary morphology, sensory systems, 3D visualization, development

Antonis Rokas (BSCI)

Evolutionary genomics, molecular evolution, phylogenomics, fungi, mammals, fungal diversity

Carlos Taboada (BSCI)

Treefrogs, camouflage, biochemistry, protein evolution, animal fluorescence, visual ecology, optics

Ann Tate (BSCI)

Immune system, virulence, systems biology, coinfection, host-parasite coevolution, life history evolution

UNIVERSITY POSITIONS

Research Assistant Professors:

Biological Sciences

Physics & Astronomy

Professor of the Practice:

Computer Science

Electrical and Computer Engineering

Mathematics

Assistant Professor:

Biochemistry

Clinical Psychology

Cultural Anthropology

Pharmacology



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