EVOLUTIONARY STUDIES

the magazine

Kate Snyder: Evolution & Birds

The Evolution of Excercise in Horses

The Scopes "Monkey" Trial Centennial Symposium

Fall 2025

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VANDERBILT UNIVERSITY

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Greetings ES Members, Alumni and Friends,

I hope this semester's magazine finds you well. As the year is coming to a close, I can't help but feel excited about all that we have accomplished in 2025.

In July 8-10, we hosted the International Society for Evolution, Medicine, and Public Health meeting. More than 150 researchers from around the world joined us in Nashville to talk all things Evolutionary Medicine. The meeting was a resounding success that included three-days of non-stop science with a lovely conference dinner at Acme Feed and Seed.

The following weekend, we partnered with the National Center for Science Education to host the Scopes "Monkey" Trial Centennial Symposium (p. 22). We brought world-class experts on the trial, on creationism, on modern challenges to the teaching of evolution, on the relationship of religion and the teaching of evolution, on the evolutionary process and its applications and so on – all the talks are freely available on YouTube (you can find links on our website at https://www.vanderbilt.edu/evolution/scopes-symposium/). It was a huge success – as one of our speakers quipped, "the only other people […] who succeeded in getting this strong a lineup to come to Tennessee in the middle of the summer was Scopes' defense team." I am sure they were being too kind, but I'll take it!

To cap it all off, at the end of the symposium, Amanda Townley, executive director of NCSE, presented the Evolutionary Studies Initiative with the Friend of Darwin award recognizing that our Initiative "is a model of interdisciplinary focus on the importance of evolution in higher education." It's a tremendous honor for our young initiative to receive this award, and so special that it happened in the year that marks the Centennial of the Scopes "Monkey" Trial.

In the middle of the summer, we learned that our National Institutes of Health T32 grant to build our graduate program on computational evolutionary approaches for the study of disease was funded. We began this semester with selecting the first two students on the program, Layla Brassington (Lea Lab) and Josh Eis (Castiglione Lab). We matched these two slots with a pair supported through ESI funds. These new students are the ESI CoEvoD fellows, Abby Rose (Zhu Lab) and Ashlynn Bruder (Behringer Lab). We are excited to bring this new evolution-oriented program to Vanderbilt!

This past year, more than twenty of our faculty served as mentors for undergraduate researchers; you can get a flavor of those research projects and the amazing undergraduate students that led them in this edition (p. 30). Of note is recent alumna Lauren Solecki, now at Epic in Madison, Wisconsin, who worked one year with physician scientist Tim Cover and a second year with bioarcheologist Tiffiny Tung.

We also had many exciting research publications, such as the ones from Gianni Castiglione's group on the evolution of oxygen metabolism in horses (p. 10), and from Amanda Lea's group on human adaptation to extreme environments (p. 14). Both stories ended up in the journal *Science* and Amanda's got the cover as well!

We are thrilled by the strides we've made and the bright prospects for Evolutionary Studies at Vanderbilt. In this issue, you'll discover exciting research from Biological Sciences, Medicine, Chemistry, and Earth and Environmental Sciences. We are grateful for your unwavering support and look forward to keeping you updated on our progress. Please feel free to contact us with any questions or ideas you may have.

Sincerely,

Antonis Rokas

Antonis Rokas, Director
Evolutionary Studies Initiative
Cornelius Vanderbilt Chair in Biological Sciences
Vanderbilt University

Photo credit Wesley Elsberry

Rokas with the NCSE Friend of Darwin award.

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SEMINAR SERIES

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John Gibbons
University of Massachusetts, Associate Professor
Department of Food Sciences
Microbial Domestication of Traditionally Fermented Foods

Natasha Vitek
Stony Brook University, Assistant Professor
Department of Ecology & Evolution
Evolution of Variation within and between Species using the Fossil Record

Jennifer Wisecaver
Washington State University, Associate Professor
School of Biological Sciences
The Genomic Basis for Evolutionary Innovation in Algae

Spring 2026

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Arizona State University, Professor and Center Director
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Evolution across Scales

Tyrone B. Hayes - J.T. Scopes Lecture 3/18
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Department of Integrative Biology
Evolutionary Effects of Environmental Contaminants

Greg Wilson Mantilla - Earth Day 4/15
University of Washington, Professor
Department of Biology
Evolution and Ecology of Early Mammals

Find more information about our seminar series on Vanderbilt.edu/evolution

*Submitted photos

Welcome, Chance Meers

Evolutionary Studies is excited to welcome Dr. Chance Meers, who joins Vanderbilt University from Columbia University, where he served as an NIH postdoctoral fellow in the Sternberg Lab. His research investigates how ancient mobile genetic elements gave rise to RNA-guided molecular machines and how those systems have been repeatedly reinvented by life, and now by scientists, for genome defense, regulation and engineering.

Meers studies mobile genetic elements, often called selfish DNA. These segments of genetic material move, copy, and insert themselves across genomes. Although they act in their own interest, their relentless drive to spread has seeded the origins of some of biology's most powerful molecular systems. In bacteria, this includes the ancestors of CRISPR.

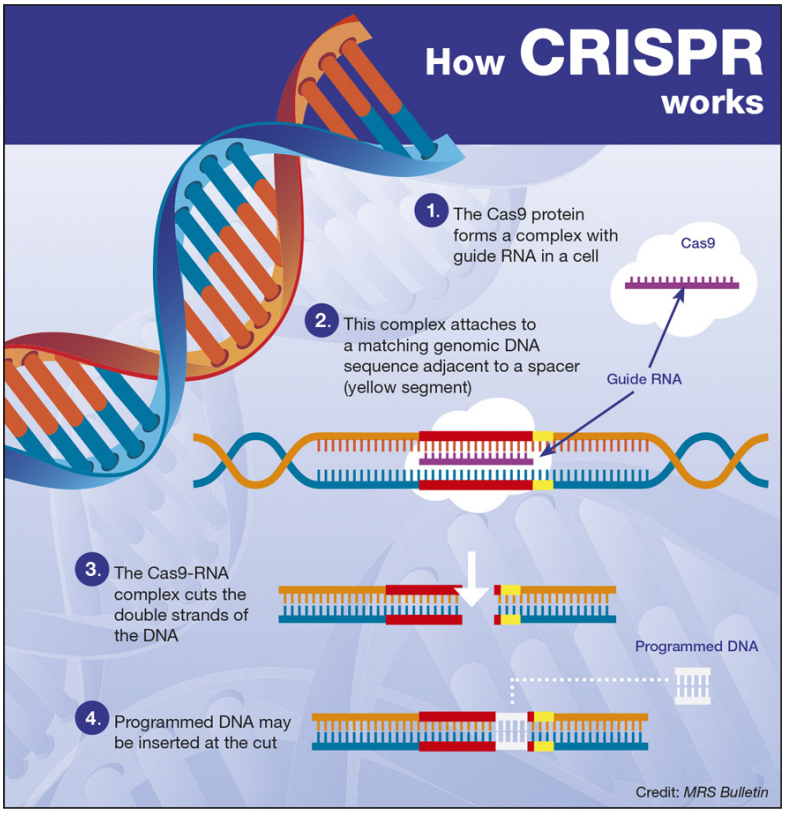
During his postdoctoral work, Meers showed that CRISPR-Cas enzymes did not originally evolve to fight viruses. Instead, they first served transposons, the "jumping genes" that hop through genomes. Working in the heat-adapted bacterium *Geobacillus stearothermophilus*, he developed experimental approaches to watch transposons move in real time and discovered that without their RNA-guided DNA-cutting enzymes, these elements quickly disappeared. His findings reveal that early CRISPR-like systems evolved as a transposon survival strategy, guiding reinsertion to ensure persistence. This work helped resolve a longstanding evolutionary question and uncovered thousands of CRISPR-related enzymes that may eventually expand the genome-editing toolkit.

Meers blends biochemistry, genetics, and evolutionary analysis to understand how mobile DNA has shaped genome architecture and how its molecular machinery can be repurposed. His work extends beyond CRISPR: he has also contributed to uncovering the evolutionary roots of snoRNA-guided RNA modification and highlighted parallels to the V(D)J recombination system that generates immune receptor diversity in humans.

At Vanderbilt, the Meers Lab will explore how selfish DNA drives genome innovation, how organisms tame and co-opt these elements for essential cellular processes, and how these domesticated systems can be adapted for biotechnology and precision medicine.

Meers earned his B.A. from Berry College and his Ph.D. from the Georgia Institute of Technology. Music city is a good fit as Meers enjoys hiking and playing the guitar. His arrival strengthens Vanderbilt's growing community in genome biology, molecular evolution, and the development of evolution-informed approaches to genome engineering.

Chance Meers (Harrison McClary / VU)



CRISPR in Action: The guide RNA directs the Cas9 'scissors' to the matching sequence of DNA, where it makes a precise cut. Image credit: MRS Bulletin

Giant Sloths and Ecological Losses

Giant ground sloths were more than just Ice Age oddities. They were ecosystem engineers whose disappearance reshaped the landscapes they once roamed. A new study from Vanderbilt University's DREAM Lab reveals just how diverse these megaherbivores' diets were, highlighting the **ecological roles that vanished when they went extinct.**

Led by recent alum Aditya Kurre ('25 Molecular and Cellular Biology; D1 Penn Dental Medicine) and Associate Professor Larisa DeSantis, the study shows that giant sloths were not simply oversized versions of today's tree-dwelling sloths. Instead, they filled **complementary ecological niches**, helping to disperse plants and fungi, dig for roots and tubers, and keep woody vegetation in check. These were services that no other species fully replaced.

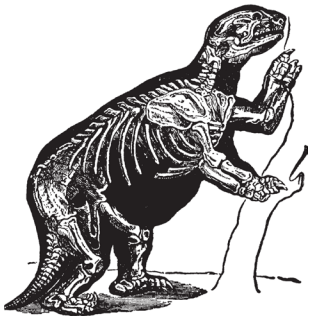
"When we think about modern sloths, we think of lethargic, gentle creatures. And while it is hard to imagine that their ancestors were some of the most gigantic and diverse mammals to inhabit the Western Hemi-

Opposite page top: Kurre (right), DeSantis (center), and Chancellor Diermeier look at Kurre's research model (Harrison McClary).

Opposite page bottom: From left, Juniper Koehler, DeSantis, Sola Johnson, and Kurre posing with a saber-toothed cat skeleton cast.

This page top: Giant ground sloth skeleton cast on display at the museum at the La Brea Tar Pits (photo credit: DeSantis). Cartoon from *Vintage Illustrations* with body outline.

This page bottom: DALL-E representation of what the dinner table might need to look like if you wanted to feed the different species of Pleistocene giant sloth.



sphere, layers of evidence show us that their diets and behaviors reflected these characteristics," Kurre said.

The paper, published in *Biology Letters* and titled "Lost giants, lost functions: paleodietary insights into the ecological niches of Pleistocene ground sloths," used dental microwear analysis to reconstruct these ancient diets.

"Sloth teeth do not have enamel like ours do, which makes them tricky to study," DeSantis explained. "But by focusing on the dentin layer, we can still see microwear textures and compare them to both living sloths and other animals like armadillos with known diets."

The team made molds of fossil teeth, created clear casts, and scanned them under a 3D microscope. Computer software measured tiny scratches and pits that act as dietary fingerprints and reveal what these animals were really eating thousands of years ago.

Although once thought to be grass-eating grazers, evidence shows *Paramylodon harlani* specialized in hard foods such as roots, tubers, or fungi. Its powerful forelimbs and claws would have aided this behavior, making it a crucial forager of underground resources. *Nothrotheriops shastensis*, on the other hand, was a selective browser, feeding on desert plants like yucca, agave, pine, and saltbush and shaping shrubland habitats in the process.

"Modern sloths are exclusively arboreal leaf-eaters, and that is all they do," DeSantis said. "But giant ground sloths were not simply ecological replicates of other herbivores at the La Brea tar pits. They played **unique and complementary roles,** and when they disappeared, entire ecological functions were lost."

Their extinction reminds us that when we lose species, we also lose the ecological services that keep ecosystems functioning.

A New Look at Gestation Length in Mammals

New research sheds light on a key driver of evolution in mammals: the length of pregnancy. By examining the diverse gestation periods across 845 species of eutherian mammals, including everything from mice to whales, scientists have uncovered surprising patterns that hint at how these varying timelines evolved and adapted to environmental pressures over millions of years.

The work, led by graduate student Thodoris Danis, was published in the *Proceedings of the Royal Society: B* on October 30th, 2024. "The Evolution of Gestation Length in Eutherian Mammals," was a collaborative effort between Danis and his advisor, Cornelius Vanderbilt Chair in Biological Sciences Antonis Rokas.

Contrary to popular belief, Danis found that gestation length does not strongly depend on body size across all mammals. This popular belief was not unfounded; though, most studies of gestation length and body mass looked at relatively few species from well-studied groups, such as the primates. Following that, the pair found many groups of mammals did have strong, positive relationships between body mass and gestation lengths. These groups included primates, rodents, carnivores, and artiodactyls like elk and bison. However, the link between the two traits is simply absent in many other groups.

For example, the team found that bats, seals, and perissodactyls like zebras and rhinos did not have any correlation between body mass and gestation length.

Why does the relationship between gestation length and body mass vary between mammals?

According to Danis, key shifts in evolutionary trajectory often coincide with major splits in the tree of life. Notable shifts occurred when mammals returned to the water – gestation lengths become longer -- likely as an adaptation to marine life. Conversely, when mammals took to the skies, gestation lengths shortened.

This seems to occur, in Danis' mind, because the ecological environments of marine and flying mammals are vastly different from those of terrestrial mammals.

Danis presents his work at the Society for the Study of Evolution annual conference in 2024 in Montreal, Canada.

Global Diversity of a Pathogenic Fungus

Annie Hatmaker, Ph.D., has spent the better part of a decade studying fungi and their secondary metabolites – small molecules they use to communicate, defend, and thrive. Her new publication, "Population structure in a fungal human pathogen is potentially linked to pathogenicity," closes her dissertation work and opens up a world of possibilities. Her fungus of choice is the *Aspergillus* genus, in this study, *Aspergillus flavus*.

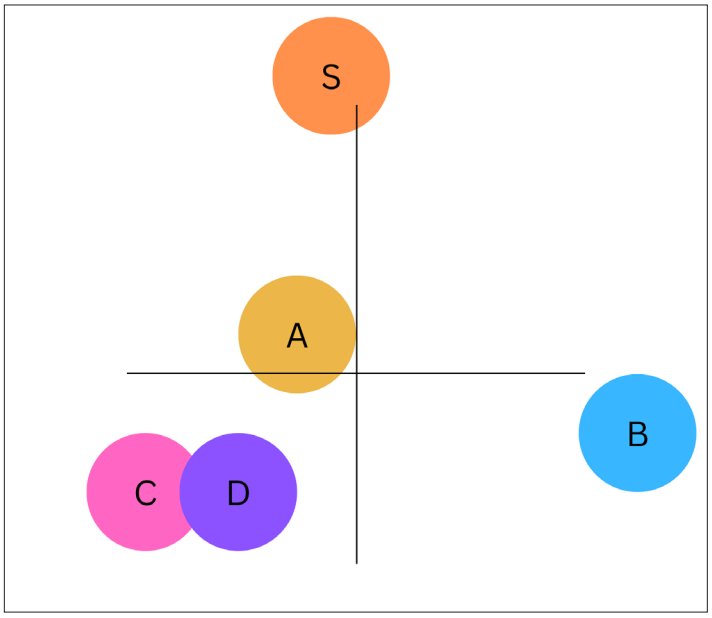
This story is based on clinical and environmental data from more than a dozen countries. Using genomic methods on 300 collected isolates of *A. flavus*, the team created an evolutionary tree suggesting that the isolates consist of five distinct populations.

Hatmaker was excited about the potential research prospects offered by the *A. flavus* system and other projects in her Ph.D. advisor Antonis Rokas' lab.

"Several studies had published whole-genome sequencing of *Aspergillus flavus* isolates just as I was considering topics," she said. "I was incredibly interested in how it was a human pathogen and also of agricultural interest due to its ability to produce aflatoxin (a type of secondary metabolite called a mycotoxin)."

Providing broader context on mycotoxins, collaborator from the Rokas Lab, postdoctoral researcher Thomas Sauters, explained that mycotoxins are toxic chemical compounds produced naturally by certain fungi, including *A. flavus*, which can contaminate crops such as corn, peanuts, and tree nuts. Aflatoxins are among the most potent naturally occurring carcinogens known, posing serious risks to human and animal health when ingested. Their production is influenced by environmental factors such as temperature, humidity, and nutrient availability, and while they are a major concern in agriculture, their role in human infections remains less clear.

"We know that aflatoxin production is reduced at the temperature of the human body, possibly indicating it is not necessary or important for human infections," explained Hatmaker. "In other studies, however, there's evidence that strains lacking the capability to produce aflatoxin are able to produce other metabolites which might play a role in infections. There's plenty of future work to be done regarding aflatoxin, so this remains a mystery!"



Above: Simplified reproduction of Figure 1B from the manuscript, showing five genetically distinct populations of Aspergillus flavus. Populations A, C, and D cluster closely, while Populations B and S are more divergent. Below Hatmaker poses with the evolutionary studies outreach casts.

Horses Run Faster by Ignoring an Ancient Mutation that Says 'Stop'

Evolution often makes a deal with the devil, creating challenges for treating human disease. By mass, the muscles of thoroughbred racehorses consume more than twice the oxygen of elite human athletes. Yet, oxygen produces free radicals, which damage organ tissues. Balancing energy production with oxidative stress is also a major challenge for extending lifespan, as well as treating epilepsy and Parkinson's disease. How did horses overcome this ubiquitous challenge to become paragons of athleticism? The answer, according to Gianni Castiglione, assistant professor of biological sciences and ophthalmology, seems to be by using a genetic trick previously thought to occur only in viruses.

New work from the Castiglione lab and that of collaborator, Elia Duh (Johns Hopkins), is shaping the way we understand the evolutionary limits of energy production. The team discovered that the horse, an oft-studied, physiological powerhouse, evolved an enigmatic and ancient mutation that enables horses and their relatives to produce extreme amounts of energy while avoiding deleterious side effects.

The new work, "Running a Genetic Stop Sign Accelerates Oxygen Metabolism and Energy Production in Horses," was published in *Science* on March 28, 2025. The team discovered that a rare mutational phenomenon known as opal recoding—occurring in only 0.1% of proteins—evolved in a horse ancestor millions of years ago. Unlike those other 0.1% of proteins, this opal recoding event facilitates adaptation, specifically by enhancing exercise performance by altering the biochemistry of muscle cells. This biochemical pathway also has major effects on lifespan and neuronal disorders.

Castiglione's work was assisted by the well documented fossil record of horses, which chronicles their ascent from dog-sized ancestors into modern physiological powerhouses. This record is one of the earliest examples used in biology textbooks to showcase evolution and transitional forms. In fact, in the first books used that covered evolution at Vanderbilt, Nicholson's Textbook of Zoology (1883), notes, "all the varieties of Horses appear to be descended from the single species *Equus caballus*." Certainly, this is a proper system to showcase the power of evolution.

The team investigated a pathway that is well-known by both the exercise science and clinical communities to enhance energy production but avoid the tissue-damage associated with excessive metabolic activity, such as that seen during exercise, and in energy demanding tissues, such as neurons.

This pathway (NRF2/KEAP1) senses free radicals, and then mounts a cellular response.

According to Castiglione, "oxygen metabolism produces energy for cells, but a side effect is free radicals (molecules with unpaired electrons) that cause extensive cellular damage, dysfunction and death if not counterbalanced by antioxidants. This oxidative stress damage accumulates over our lives, leading to aging. Our bodies produce antioxidants, and these are proteins and small molecules regulated by the transcription factor, NRF2."

He continued, "importantly, NRF2 cannot always be active, because too much antioxidant activity can trigger cancer and can even be lethal. Thus, KEAP1 evolved to mitigate NRF2 activity by binding to it and destroying it. When KEAP1 senses free radicals, it physically releases NRF2, allowing it to trigger cytoprotective antioxidant gene expression."

According to the manuscript, NRF2/KEAP1 is a major target in chronic diseases like emphysema, but

has also facilitated the vertebrate transition from aquatic to terrestrial life by protecting against UV light-induced oxidative stress, and more recently, as Castiglione previously found, during the evolution of birds to counterbalance the highly energetically demanding flapping during flight. The team found that horses have exploited this system as well. They show that a KEAP1 mutation present in all horses, donkeys and zebras, makes muscle cells more resistant to free radical damage.

The mutation has an additional benefit: it increases energy production through the muscle cell's mitochondria, giving horses and their ancestors the best of both worlds.

Castiglione said, "in 99.9% of known proteins, this mutation in horse KEAP1 would stop protein production (opal stop codon), However, we found that the opal stop codon is recoded into the amino acid cysteine, and it is this amino acid's unique sulfur group that favorably alters horse biochemistry. Previously, it was thought that this opal recoding was only adaptively useful in viruses as they adapt to selection pressures. It seems that predatory selective pressures imposed on ancient horses were so intense that they had to dig deep into the evolutionary bag of tricks to enable novel locomotion capabilities."

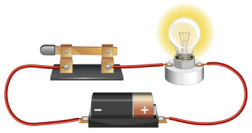
Beyond understanding the evolution of horses and their relatives, this work can pave the way for novel treatment strategies for multiple diseases. In fact, Castiglione explained, about 11% of all human diseases are caused by the premature stop codons that horse KEAP1 have evolved to overcome through additional adaptations in other proteins and RNA-based mechanisms. Castiglione's team is developing gene therapies that deliver these horse molecules into mice to improve stop codon recoding. Moreover, KEAP1/NRF2 is a goldilocks pathway, where its therapeutic benefit becomes a cancer-causing agent if it is too active.

The horse mutation in KEAP1 hits that sweet spot of moderate activity, creating a new molecular target to modulate NRF2/KEAP1 to a desired level of activity. This can therefore inform strategies targeting NRF2/KEAP1, such as in the treatment of emphysema, Parkinson's and epilepsy.

Read more >>

Opposite left: Castiglione poses for photo day in the lab. Opposite right: a DALLE-2 representation of a horse blowing a stop sign. This page: Castiglione analyzes respiration data in the lab.

A Conservative Defense: Cellular NFLs Resist Evolutionary Blitzes



In football, defense keeps the opposing team in check. A similar strategy is at play inside our cells. Negative feedback loops (NFLs) help regulate how cells respond to signals, for example, dialing down activity when things get too intense. A new study from Vanderbilt University reveals that these molecular "defenders" evolve differently depending on where they sit in the signaling pathway.

Danial Asgari, a postdoctoral researcher in the Tate Lab, and Ann Tate, associate professor of Biological Sciences, recently published a study in *Molecular Biology and Evolution* titled "How the Structure of Signaling Regulation Evolves: Insights from an Evolutionary Model." Their findings show that NFLs acting closer to a cell's final decisions, such as turning genes on or off, are especially resistant to evolutionary change.

Downstream feedback loops operate near the cell nucleus, where small changes can significantly affect how genes are turned on or off. Upstream loops act earlier in the pathway, often at the cell surface, where they respond to signals from outside the cell.

"Our model predicts robust evolution of downstream negative feedback loops under all conditions, which signifies their crucial role in controlling gene expression," said Asgari. "This aligns with empirical observations showing a slower rate of change for proteins involved in downstream negative feedback loops."

Upstream regulators, by contrast, evolved only under narrow conditions.

"I was surprised that upstream negative feedback loops evolve only under very specific conditions," Asgari said. "I was expecting the evolution of upstream negative feedback loops under a broader set of conditions."

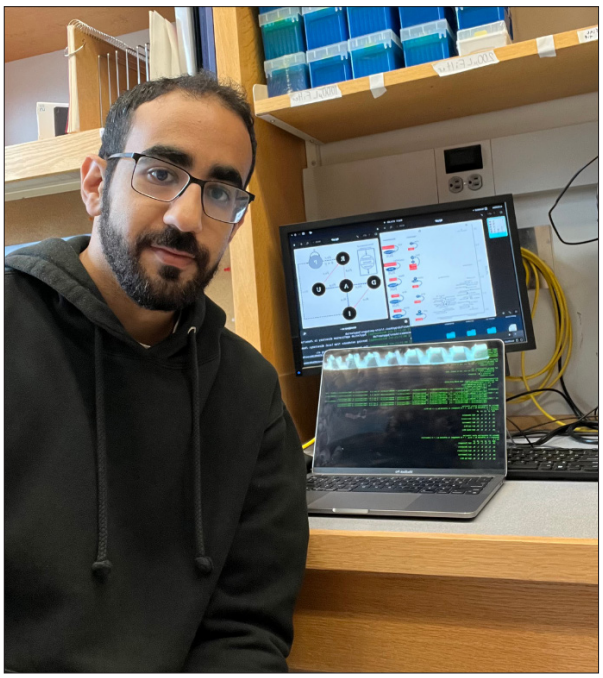
To make the concept more accessible, Asgari offered an analogy. "Imagine an electric circuit. An upstream negative feedback regulates how much electricity flows into the circuit, which ultimately affects how much the LED lights up. A downstream negative feedback directly regulates the LED brightness without changing the input."

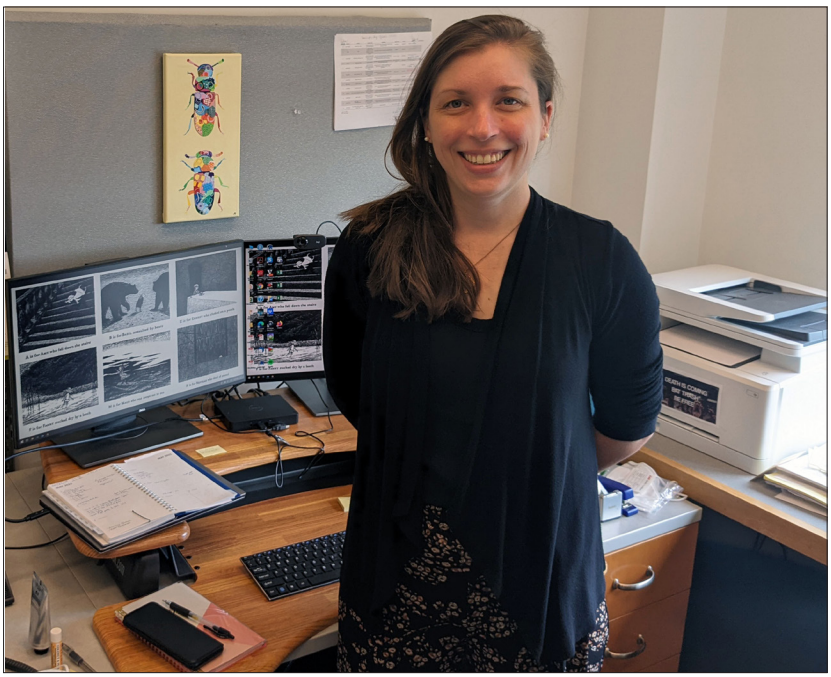
Tate sees the work as a key step in understanding how immune systems balance cost and control. She touched on the importance of pathway topology or the structure and order of interactions within a signaling pathway, essentially, how the molecular parts are connected.

"Our study suggests the strength of selection predicted by the model aligns with evolutionary rate statistics for NFL genes in real animals," said Tate. "Until now, most studies on immune gene evolution have discussed variation in these statistics in terms of host-parasite arms races or trade-offs driving protein evolution; here we show that this variation could instead be driven by pathway topology."

These insights could have broader implications for understanding disease.

"We think that multiple layers of feedback regulation provide the opportunity to fine-tune this balance," Tate added. "But we should figure out the contribution of each layer in different disease contexts before we start messing with them in the clinic."





Top: An electric circuit controlling a light. Left: Asgari working on the new models (submitted photo). Right: Tate posing in front of her desk on picture day.

Older Genes Take on More Roles

New research from Reese Martin and Ann Tate has uncovered a fundamental pattern in genome evolution: older genes tend to perform more jobs for the organism than younger ones.

In the paper, published in *Evolution Letters*, first author Martin and his advisor Tate examined six model organisms, ranging from *Arabidopsis* to humans. They found that the number of traits a gene influences, a property known as pleiotropy, steadily increases as genes get older, eventually leveling off at a plateau that may represent the functional carrying capacity of a gene.

Martin explained, "using public databases I was able to demonstrate the the 'prevalence of pleiotropy' (how many jobs a group of genes does) rises with evolutionary age. Put another way: the older a gene is the more it does for the organism. This general pattern holds across multiple multicellular species from *Arabidopsis* to *Homo Sapiens*, and across multiple measures of pleiotropy."

The study also revealed that genes involved in immune and developmental processes tend to be among the most pleiotropic, while metabolic genes are less so. Surprisingly, even genes with duplicated copies (paralogs) generally remained pleiotropic, challenging the expectation that subfunctionalization reduces their overall functional reach.

This style of change may have implication on genomics and organismal biology.

In the paper, the authors point to immune system genes as some of the most pleiotropic in the genome, reflecting the complex, interconnected nature of immune signaling networks. Developmental genes showed a similar trend, steadily accumulating new functions as they aged. This finding helps explain how relatively small genetic toolkits can generate such diversity of body plans across multicellular life.

While exploring the effect of gene duplication on pleiotropy, they found that duplicated genes frequently retained overlapping functions rather than partitioning them entirely. In mice, for instance, the muscle-regulating genes MYOD1 and MYF5 remain associated with many of the same biological processes despite specializing in different aspects of muscle differentiation. This suggests that duplications can preserve or even enhance a gene's complexity, providing organisms with a kind of "backup copy" while still allowing for innovation.

Finally, Martin and Tate showed that these patterns hold across a diverse set of model organisms — including plants like *Arabidopsis thaliana* and invertebrates like *Drosophila melanogaster* indicating that the relationship between gene age and pleiotropy is a general feature of multicellular evolution, not limited to animals or humans.

This broad perspective opens the door to using gene age as a predictive tool for understanding gene function and disease relevance across species.

Martin working on pleiotropy models in the lab.

Natural Selection and Extreme Environments

From UC Berkeley with edits by Andy Flick

Through a collaboration between US and Kenyan researchers and Turkana communities of northern Kenya, scientists have uncovered key genetic adaptations underlying survival in hot and dry environments, revealing how natural selection has enabled this pastoralist population to thrive in a challenging landscape.

A new analysis of Turkana genomes through a collaboration between US and Kenyan institutions shows how the activity of key genes has changed over millennia to allow them to thrive in extreme desert conditions. The comprehensive study, published in *Science*, reveals how the Turkana people have evolved extraordinary physiological adaptations to survive in their harsh homeland, where water scarcity and extreme heat have shaped their lifestyle.

Amanda Lea, assistant professor of Biological Sciences, is a co-principal investigator of the study.

The Turkana Way of Life

The Turkana homeland stretches across a vast arid landscape in Northern Kenya where shade is rare and water even rarer. While their nomadic existence takes them around East Africa—into Uganda on the west, South Sudan on the northwest and Ethiopia on the north—this is one of the most arid regions of the world. Rainfall arrives in short, unpredictable bursts, and in this environment, securing enough water for themselves and their herds of goats and camels is a daily chore. The journey to fetch water can take several hours each day, often across terrain that is hot and devoid of vegetation.

The traditional pastoralist diet reflects both resourcefulness and adaptation to scarcity: for those adhering to a nomadic pastoralist lifestyle, it is estimated that 70–80% of their nutrition comes from animal sources, mostly milk, blood, and meat. This reliance is a common solution among pastoralist societies around the world, in environments where crops cannot grow and markets may be far away on foot.

Through years of documenting the Turkana community's lifestyle and studying blood and urine samples to assess their health, researchers found a striking paradox: "About 90% of the people we assessed were dehydrated but generally healthy." said the Project co-PI, professor of integrative biology at UC-Berkeley Julien Ayroles.

"The Turkana have maintained their traditional way of life for thousands of years, providing us with an extraordinary window into human adaptation," Ayroles continued.

Genomic Discoveries, Community Partnership

After consultation with the communities' elders, area chiefs and local health officials, the team asked for permission to sample the communities' DNA. Working with the Turkana community, the researchers sequenced 367 whole genomes and analyzed over 7 million genetic variants to identify regions showing evidence of natural selection.

The genomic analysis found eight regions of DNA that had undergone natural selection, but one gene, STC1, stood out with exceptionally strong evidence of selection. STC1 is expressed in the kidneys and plays two vital roles that directly reflect the ecological challenges of both arid living and pastoralism.

First, it helps the body conserve water by responding to antidiuretic hormone, allowing the Turkana to concentrate their urine and retain more water. Second, it may also play a role in protecting the kidneys from the waste generated by purine-rich foods like red meat. These waste products, such as urea and uric acid, must be filtered by the kidneys and in many people, too much dietary purine can lead to gout; a problem that appears to be rare among the Turkana.

Ancient Climate, Modern Genetics

Intriguingly, the timing of these genetic adaptations appears to coincide with the

This page: A traditional Turkana boma at sunset (Turkana Health & Genomics Project). Opposite top: Turkana bomas stand amid the savanna, sheltering families and livestock. (Wenfei Tong). Opposite Bottom: Turkana women carrying water back to their village (Turkana Health & Genomics Project).

aridification of northern Africa, suggesting that as the climate became increasingly dry about 5,000 years ago, natural selection favored genetic variants that enhanced survival in desert conditions. This finding provides a compelling example of how human populations have evolved in direct response to major environmental changes. The genetic analyses show that these changes are also present in neighboring groups, including the Rendille, who live in this arid environment.

"This research demonstrates how our ancestors successfully adapted to dramatic climate shifts through genetic evolution," noted Dr. Epem Esekon, the County Executive for Health and Sanitation in Turkana County, Kenya.

Evolution Meets Urbanization

But the story doesn't end in the desert. As more Turkana migrate to towns and cities, a striking pattern emerges: the very genetic traits that aid survival could now carry hidden costs. This phenomenon, known as evolutionary mismatch, occurs when adaptations shaped by one environment become liabilities in another.

By comparing biomarkers and gene expression in the genomes of city-dwelling Turkana compared to their pastoral kin, the researchers found an imbalance of gene expression that may predispose them to chronic diseases, such as hypertension or obesity, which the researchers have also found to be more common in urban settings, where diets, water availability, and activity patterns are radically different.

"With more people shifting from rural to urban lifestyles, we are also seeing a change in disease patterns," said the Acting Director General, KEMRI, Prof. Elijah Songok.

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Learning to Sing: Kate Snyder on Birds, Culture, and Evolution

Like the songbirds she studies, Kate Snyder's scientific journey has been one of learning, adaptation, and discovery. She earned her Ph.D. from Vanderbilt University in Spring 2023, working in the Creanza Lab, where she explored how ecology, culture, and communication shape evolution across species. Her path traces an arc from early undergraduate research on population dynamics in beetles and cooperation in microbes to wide-ranging studies of human kinship systems and birdsong, connecting themes of survival, culture, and the power of social behavior.

Before Vanderbilt: Population Ecology and Cooperation

Snyder's early research examined population stability and the conditions that allow cooperation to persist.

Working with Joan Strassmann and others on the social amoeba *Dictyostelium discoideum*, the team demonstrated how genetic drift during colony growth can create zones of clonemates. Even in the absence of kin recognition, these patterns of relatedness promoted cooperation and altruism, providing insight into how social behaviors persist in microbes.

She then led a study in T.E.X. Miller's lab on sex-selective harvesting in beetles — a project firmly grounded in population ecology. She showed that removing females destabilized populations far more than removing males, and that dispersal from harvest refuges could rescue declining groups. Together, these projects highlighted Snyder's interest in how demographic pressures and structural context shape survival and reproduction.

Vanderbilt: Human Culture and Comparative Frameworks

At Vanderbilt, Snyder expanded her scope to cultural evolution and cross-species comparisons.

In a global study of human kinship systems, she and her collaborators explored why matrilineal descent, where children belong to their mother's family and inheritance flows through the maternal line, is relatively uncommon, yet still found in diverse societies around the world. Their analyses revealed that subsistence practices, animal domestication, and inheritance rules strongly influence whether matriliny persists or shifts to patriliny, reframing a longstanding anthropological puzzle in evolutionary terms.

She also drew explicit parallels between humans and

birds. In a commentary on birdsong and music, Snyder argued that studies of duetting birds, where individuals synchronize songs with precision, offer a unique window into the neural basis of rhythm and coordination, shedding light on the evolutionary roots of human musicality.

Vanderbilt: Birdsong, Social Behavior and Sexual Selection

Much of Snyder's work at Vanderbilt has focused on birdsong as a cultural and evolutionary trait.

In a large-scale comparative study, she showed that polygyny, where one male mates with multiple females, accelerates song evolution. Instead of pushing repertoires to extremes, polygynous lineages tended to converge on moderate levels of complexity, challenging assumptions about how sexual selection operates.

Snyder and collaborators are also preparing a revised manuscript on cooperative breeding and birdsong evolution, where they present evidence for an unrecognized evolutionary pathway to female song.

In addition to females joining males in territory defense or pair-bond maintenance, their results suggest that female song may sometimes be used for broader social cohesion, particularly in cooperative systems, a finding with exciting implications for understanding the evolution of female signaling.

She further examined how lifelong learning shapes birdsong. Across 67 species, she found that adult song plasticity was linked to **more evolutionarily flexible mating systems**. The results suggest that sexual selection can influence not just song traits but also the learning strategies that sustain them across evolutionary time scales.

Environmental Stress and Climate Change

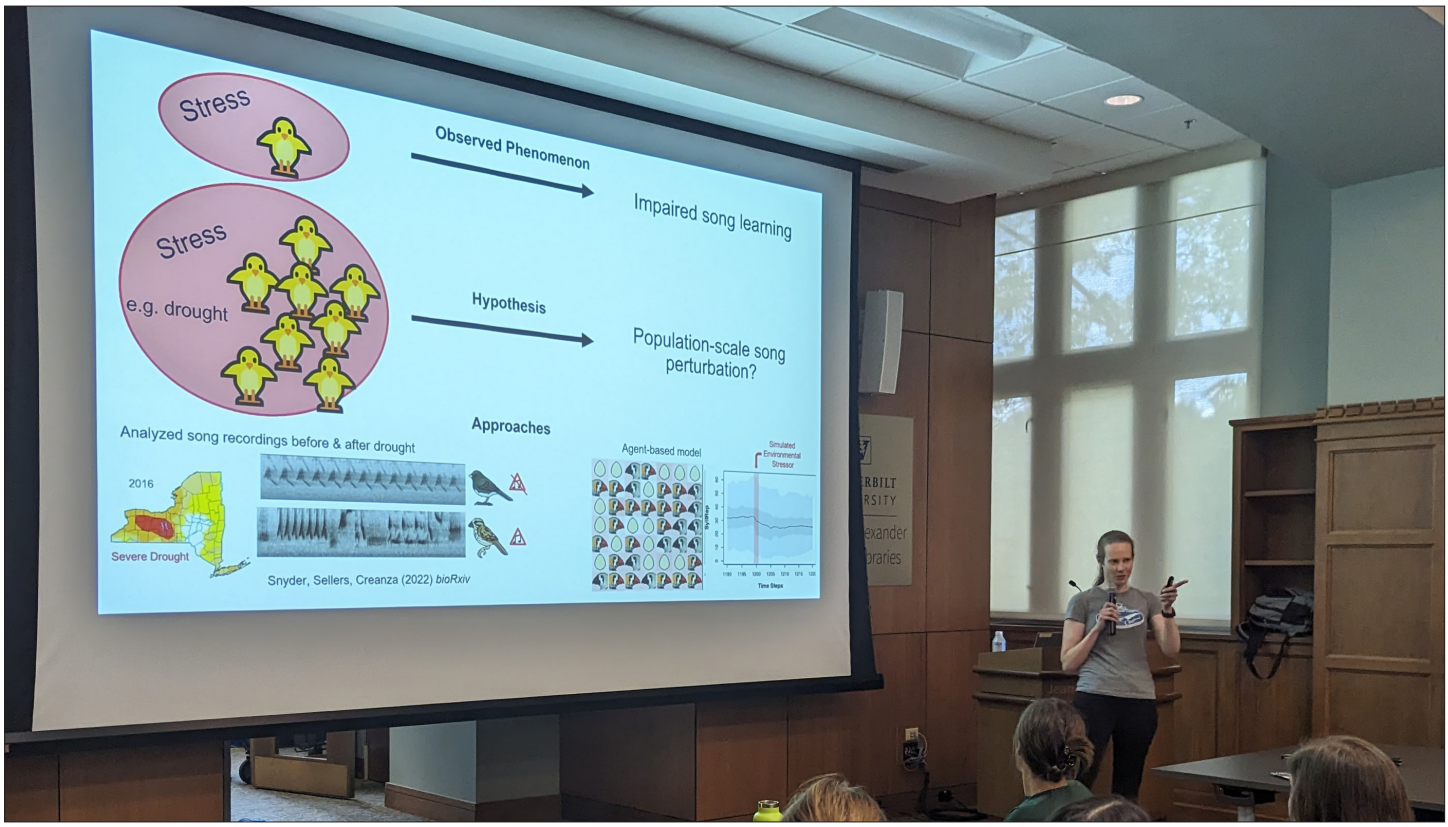
Building on prior knowledge that birds stressed during development show impaired learning as adults, Snyder proposed that widespread stressors, such as drought, could measurably alter songs on a population scale. Using citizen-science recordings from a region experiencing increasingly severe droughts, she captured the first hints that a changing climate might drive the evolution of simpler, easier-to-learn songs — with potential consequences for mate choice and reproductive success.

Computational Approaches to Birdsong

Snyder has also been an advocate for applying computational tools to behavioral research. In a *Nature News & Views* commentary, she offered a critical perspective on a deep-learning study of birdsong, cautioning that some methods may not capture biologically meaningful variation. While much of her piece focused on clarifying methodological issues, she emphasized that deep-learning approaches, when applied appropriately, hold enormous potential for advancing the study of communication and culture in animals.

Summary

Snyder's career evolved from population ecology in beetles and microbes to the cultural and evolutionary dynamics of birds and humans. Whether exploring the fate of matriliny, the evolution of female song, or the parallels between music and communication, Snyder's work illuminates how both biological and cultural forces drive evolutionary change.



Opposite page: Snyder investigates a fossil she has found at the Coon Creek Science Center. This page: Snyder presents her work at the inaugural ESI retreat.

Genes + culture: Exploring how our first language is echoed in our genes

By: Mary Lou Watkinson, VU Arts & Science communicator

A person's native language is often referred to as their "mother tongue." But does a first language always come from your mother?

In a new study conducted by Associate Professor of Biological Sciences Nicole Creanza, postdoctoral student Yakov Pichkar, and alumna Alexandra Surowiec BA'19, they found that certain cultural factors, such as being born in a matrilineal or patrilineal society and where a child grows up after parents separate from their respective households, may affect linguistic and genetic evolution.

If children learn their language primarily from their mother, language transmission might follow the evolutionary patterns of their maternally inherited genes (such as X chromosomes and mitochondria) more closely than their genomes as a whole. When children grow up surrounded by the language of their mother's extended family, the researchers hypothesized that these maternal gene-language associations might be even stronger.

These matrilineal influences on the sounds in languages, which the researchers detected by comparing the associations between genes, languages, and geography, were particularly strong in areas in Africa, however, there was no consistent global pattern. The association between maternal genetics and linguistic sounds had not previously been tested worldwide.

"Overall, we found that this phenomenon seems to occur in some geographic regions but not others, indicating that cultural practices can affect how languages and genes are transmitted, but that it is difficult to make global predictions about these cultural practices," Creanza said. "In particular, matrilineal populations in Africa appear to have a closer association between language and mitochondrial genetic variation than expected."

To conduct the study, which was published in the Proceedings of the National Academy of Sciences, the research team used genetic, linguistic, and ethnographic data from 130 populations around the world to explore whether language is preferentially transmitted in parallel with maternally or paternally inherited genes.

"As people move around the globe, they take their genes and languages with them, and both the genes and the languages slowly change," Creanza said. "Thus, when two populations are further apart, they tend to be more genetically different and have more different sounds in their languages. However, males and females do not always follow the same movement patterns—for example, in some populations, wives might move to live near their husband's family, and in others, husbands might move near their wife's family."

Creanza said this study built upon her previous work, which showed that the sounds in languages followed similar geographic patterns as genes did.

"I hope that it inspires future genetic researchers to more closely consider the cultural, ethnographic, and linguistic features of the populations they study," she said. "Genes do not tell the full story of human evolution, and incorporating these cultural considerations is crucial for understanding humans and their history."

The paper appears in a special edition of *PNAS* that highlights 50 years of the quantitative study of cultural evolution, or how learned behaviors change over time, such as human cultural practices and languages.

Creanza co-edited the special edition, which features a collection of articles on the field of cultural evolution.

Creanza lab photo from Dr. Kate Snyder's Ph.D. defense celebration (submitted photo).

City Lights Are Rewriting the Calendar: Artificial Light Extends Urban Growing Seasons

City lights are rewriting the calendar. A new global study from Vanderbilt researchers Lin Meng and Huidong Li shows that artificial light at night is more powerful than temperature in extending urban growing seasons — keeping trees greener longer, with consequences for carbon cycling, frost risk, and even pollen season.

The study, "Artificial light at night outweighs temperature in lengthening urban growing seasons," published in *Nature Cities*, analyzed satellite data from 428 cities across the Northern Hemisphere, combining nighttime light measurements, air temperature, and plant greenness to uncover how urban environments shift plant phenology.

"Phenology — the timing of events like spring leaf-out and autumn color change — is widely recognized as a sensitive indicator of climate change," said Meng, assistant professor in the Department of Earth and Environmental Sciences. "But our research shows that local urban conditions, like urban heat island effect and artificial light at night, also substantially reshape these responses. Our earlier work has shown how urban warming advances spring phenology and reduces its sensitivity to temperature, and now we've demonstrated that city lights can be even more influential than temperature in shifting these seasonal patterns. These shifts affect whether, and to what extent, vegetation cools or warms the climate, as highlighted in another of our recent studies."

Global Data, Local Impact

According to the study, urban vegetation leafs out about twelve days earlier in the spring and holds onto their leaves about eleven days later in the autumn than vegetation in nearby rural areas. This means city vegetation stays green for nearly three extra weeks each year — a shift that can increase carbon sequestration and help cool cities by mitigating the urban heat island effect.

However, longer growing seasons can have downsides: extended greenery increases the likelihood of late-season frost damage, can disrupt plant–pollinator interactions, and may prolong pollen season — an unwelcome change for allergy sufferers.

Artificial Light: A Key Player

The researchers found that artificial light at night is the strongest driver of these changes, often outweighing temperature — a surprising finding given the long-standing assumption that warmer air temperatures are the primary factor behind earlier springs and delayed autumns. The study highlights the importance of considering light pollution alongside climate change when predicting how ecosystems will respond to a warming planet.

An International Effort

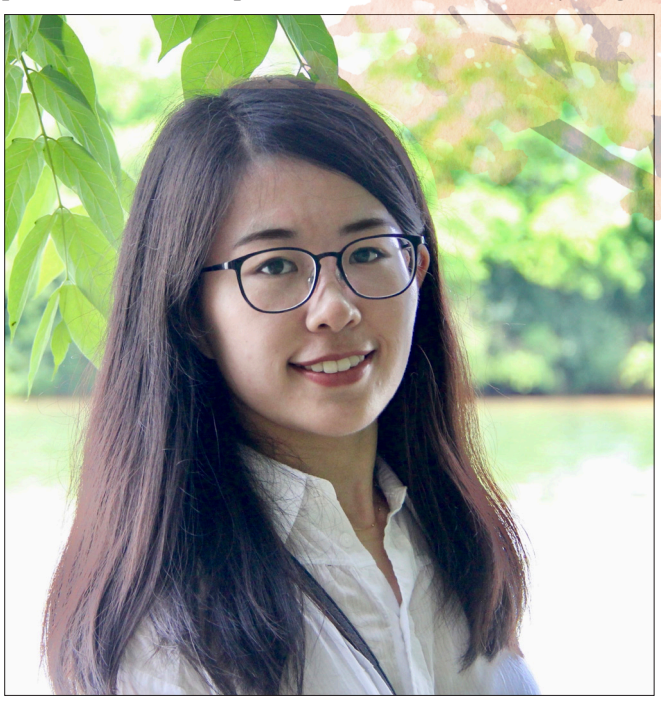
This research represents one of the most comprehensive global studies of urban plant phenology and its drivers, combining satellites, big data, and a global perspective. It is the result of a collaboration between Vanderbilt University, Oak Ridge National Laboratory, Northern Arizona University, UCLA, and international partners in Germany and China. The project has received support through Vanderbilt's Evolutionary Studies Initiative pilot grants, which Meng credits for helping launch this line of research.

Why It Matters For Nashville

Although the dataset spanned hundreds of cities, the study reports that this phenomenon is visible right here in Nashville. Vanderbilt's PhenoCam — a ground-based camera that is part of the global PhenoCam Network — monitoring tree canopy changes on campus, captures earlier leaf-out and delayed fall color year after year — a trend mirrored across the globe.

Looking Ahead

The authors conclude that with global urbanization and the rapid transition to bright, energy-efficient LEDs, nighttime light levels are expected to continue increasing. Their findings underscore the need for city planners and researchers to work together on sustainable lighting solutions that balance human needs with the health of urban ecosystems.



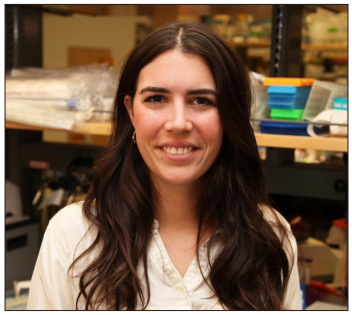
Lin Meng (submitted photo)

Hodges Lab

Gene expression and the timing of epigenetic changes

By: Lorena Infante Lara, VU Basic Sciences science writer

A person's full genetic code has the instructions to create every protein needed for every cell in the body, but somehow, these instructions are selectively applied to create unique cell types. Multicellular organisms use epigenetic modifications to ensure that each cell type only expresses genes that generate proteins relevant to its function.



Through DNA modifications such as methylation, stem cells, when differentiating into specialized cell types, make portions of the genome more or less permissive to RNA transcription, which limits the types of proteins that cell can make. DNA methylation was thought to repress transcription and removing it was required for changes in gene expression.

Emily Hodges, associate professor of biochemistry, and Ph.D. student Lindsey Guerin have robust experience in epigenetics and chromatin accessibility. A paper in *Cell Reports* led by Guerin looks at the timing of chromatin accessibility and DNA methylation changes during the process of cell differentiation and how they affect gene expression. They found that DNA methylation doesn't always limit gene transcription, especially early in differentiation. In fact, both modifications collaborate on different timescales to shape the short- and long-term regulation of enhancers during cell fate specification. Enhancers are short regions in the DNA to which certain proteins can bind to regulate how much a particular gene is expressed.

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Cell Subtypes that Increase the Risk of Diabetes

By: Lorena Infante Lara, VU Basic Sciences science writer

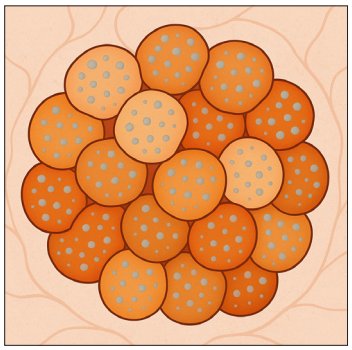
According to the American Diabetes Association, more than 10 percent of the U.S. population—approximately 38.4 million people—had diabetes in 2021, and 1.2 million more people get diagnosed each year.

Type 2 diabetes occurs when the body develops resistance to insulin, the hormone that helps regulate glucose levels in the blood. Insulin is secreted by pancreatic cells called β-cells, and in T2D, they ramp up insulin production until the β-cells eventually become exhausted. Thanks to their importance, the functional β-cell mass, or the total number of β-cells and their function, determines a person's risk of diabetes.

B-cells are not homogeneous even within a single individual and consist of different "subtypes," each with their own secretory function, viability, and ability to divide. In other words, each β-cell subtype has a different level of fitness, and the higher, the better. When diabetes develops, the proportions of some β-cell subtypes are changed. But a key question remains: Are the proportion and fitness of different β-cell subtypes altered by diabetes or are the changes responsible for the disease?

Cue Guoqiang Gu, Hodges, and Ken Lau, Vanderbilt faculty who set out to answer these questions and more. Their recent work, published in *Nature Communications*, is a step toward determining whether it is possible to enhance functional β-cell mass to reduce the risk of T2D. Studying β-cell subtypes is challenging. The most common method of studying them is called "terminal examination of samples at single-cell levels," which means that scientists can only study particular β-cell subtypes once, and only when they are fully developed, which precludes them from examining a specific cell subtype at distinct stages in differentiation, maturation, proliferation, senescence, death, and more. If they could monitor β-cells at multiple stages, researchers could better understand how cells' states drift over time or under different physiological conditions.

Top: Emily Hodges (VUMC). Middle: Lindsey Guerin (submitted photo). Bottom: Cartoon of β-cells generated in DALL-E.



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Other Work from VUMC

Genetic analysis reveals lung cancer susceptibility

Associate Professor of Medicine **Eric Gamazon** contributed his expertise in statistical genetics and computational modeling to a new study published in *The American Journal of Human Genetics*.

In "Genetic Analysis in African Ancestry Populations Reveals Genetic Contributors to Lung Cancer Susceptibility," Michael Betti, now a postdoctoral researcher at St. Jude Children's Research Hospital in Memphis, led a genome-wide association study of lung cancer in 6,490 individuals of African ancestry.

Submitted photo

Betti, Ph.D. alumnus (2025) of Aldrich & Gamazon labs.

The team identified ten risk loci and used advanced genomic methods to prioritize likely causal genes such as CHRNA3, EML4, PSMA4, and SNRNP200.

The study also introduced several methodological innovations, which allowed the team to model population substructure and detect associations that would have been missed using standard approaches. Fine-mapping pinpointed variants with high posterior probability of being causal, many of which were present in African ancestry populations but absent in European cohorts.

Follow-up TWAS and causal inference analyses further highlighted biologically relevant genes and pathways, shedding light on mechanisms of disease susceptibility and emphasizing the importance of studying underrepresented populations in genomic research.

This work highlights how genetic and evolutionary perspectives can reveal hidden contributors to disease and inform strategies for improving human health.

Read More >>

Genetic analysis reveals lung cancer susceptibility

A new study from the **Georgiev Lab** at the Vanderbilt Vaccine Center and the **Bonami Lab** in the Division of Rheumatology and Immunology uncovered a remarkable class of antibodies that may help pave the way for next-generation antivirals and vaccines. The study was led by Matthew Vukovich and senior author Ivelin Georgiev. The paper, "Isolation and characterization of IgG3 glycan-targeting antibodies with exceptional cross-reactivity for diverse viral families" was published in *PLOS Pathogens*.

The Georgiev team, including Andrea Shiakolas, Alexandra Abu-Shmais, Kathryn Gripenstraw, Sabina Leonard, Ian Setliff, and Vukovich used single-cell sequencing and immune-profiling technology to screen thousands of B cells and identify rare antibodies targeting the sugar molecules that coat viral proteins. Among their discoveries was antibody 2526, which showed an extraordinary ability to recognize glycans across a wide range of viruses, including HIV-1, influenza, coronaviruses, hepatitis C, and others.

Rachel Bonami and her trainee, Lindsay Bass, also supported this work. Bonami's lab specializes in studying B cell biology, immune tolerance, and autoimmune disease.

This is exactly the kind of interdisciplinary research that evolutionary studies strives to promote, bringing together diverse expertise to reveal how evolutionary principles shape immunity and can guide the development of therapies.

Read More >>

Left half: Georgiev lab. Right half: Bonami Lab (all in white coats or gray vests). Photos from lab websites.

The Scopes "Monkey" Trial Centennial Symposium

On July 12–13, 2025, the Evolutionary Studies Initiative hosted the Scopes "Monkey" Trial Centennial Symposium to commemorate 100 years since the landmark Tennessee trial. The event brought together nearly two dozen leading scholars in history, science, education, and philosophy to reflect on the trial's legacy, its impact on evolution education, and its ongoing relevance in today's public discourse.

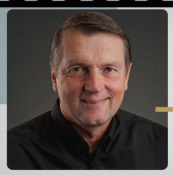
The program covered six major themes: The History of the Scopes Trial; Modern Challenges to Teaching Evolution; Evolution Today; Applications of Evolutionary Concepts; Teaching Evolution; and The Relationship between Evolution and Religion. Each session featured rigorous scholarship and lively discussion.

An integral component of the symposium was the recording and sharing of talks, making the content accessible to audiences beyond Nashville. Topics included reflections on how science and religion interact, debates over how evolution is taught in schools, and explorations of evolutionary theory's broader resonance in public life.

The symposium fostered deeper connections among researchers, educators, and the public, all focused on ensuring that evidence-based evolution education is understood, defended, and advanced.

See the recordings here >>

Above, Amanda Townely presents Antonis Rokas with the Friend of Darwin award (Wesley Elsberry). After lunch on day two, Brynn Wooten, Neil Kelley, and Andy Flick led a tour of the ESI History of Evolution at Vanderbilt exhibit in the central library. Here, Wooten shows off a hands-on fossil activity.



Ed Larson

History of the Scopes Trial: Facts and Folklore

Randy Moore

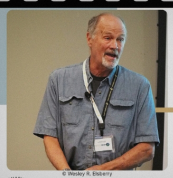
The Legacy of John T. Scopes

Adam Laats

Fundamentalism at the Time of the Scopes Trial

Barbara Forrest

Creationism's Trojan Horse: The Wedge of Intelligent Design

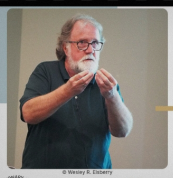


Ken Miller

The *Kitzmiller v. Dover* Trial

Amanda Townley

Modern Challenges to Teaching Evolution in Public Schools



Sean Carroll

Chance in Evolution

Jonathan Losos

Natural Selection and Design

Marlene Zuk

How Behavior Evolves and why it Matters

Steve Brusatte

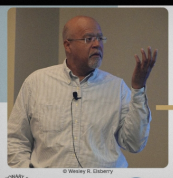
Evolution: The Fossil Record

Briana Pobiner

Human Evolution

Owen Jones

Force of Nature: Applications of Natural Selection to Other Fields

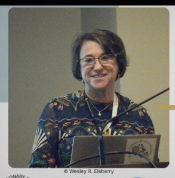


Paul Turner

Evolutionary Medicine

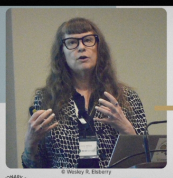
Sophien Kamoun

The Evolution of Plant Disease



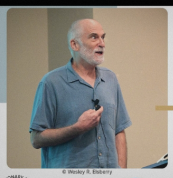
Gale Sinatra

Science Denial and Teaching Evolution



Corrie Moreau

Teaching Evolution through Museum Exhibits



Wesley Roberts

Teaching Evolution in the Bible Belt

Jamie Jensen

Reconciling Evolution and Belief

Katy Hinman

Science and (*not versus*) Religion

Liz Barnes

Promoting Harmony between Religion and Evolution

Lee Meadows

Inclusive Approaches to Teaching Evolution

"I am really impressed with how well everything went."
-Marlene Zuk

"Keep Evolving"
-Ed Larson

"It was probably the best symposium I have ever had the pleasure of attending."
-Ken Miller

PILOT

Global Change and Extinct Animals

Rayshaun Pettit

Brynn Wooten

Ph.D. candidate **Brynn Wooten** received a Pilot Grant to explore the paleoecology of *Archaeotherium*, a pig-like animal that survived for more than 14 million years despite dramatic global climate shifts. These mammals lived through the Eocene-Oligocene extinction, a cooling Earth, and the transition from dense forests to more open habitats. Wooten's work seeks to understand how *Archaeotherium* adapted to these changes, revealing insights into a group whose ecological role is poorly understood.

She will apply dental microwear texture analysis to *Archaeotherium* teeth, providing a microscopic view of what these animals were eating in the final weeks and months of life. Paired with stable isotope analyses of carbon and oxygen from tooth enamel, the research reconstructs climate conditions, vegetation cover, and dietary preferences across time and space. Sampling trips to major fossil collections at Yale's Peabody Museum, the Denver Museum of Nature & Science, and the University of Nebraska State Museum ensure that Wooten's data cover the full geographic and temporal range of this genus.

Beyond the scientific findings, this project fosters collaboration between the DeSantis and Oster labs at Vanderbilt and provides training for both graduate and undergraduate researchers in cutting-edge paleoecological techniques. "Support from ESI allows me to collect data that will form the foundation of my dissertation," Wooten said. "These grants make it possible for students like me to ask big evolutionary questions using under-studied fossil collections."

Social Stress, Gene Expression and Reproduction

Rachel Petersen

Postdoctoral researcher **Rachel Petersen** received a 2025 Evolutionary Studies Initiative Pilot Research Grant to investigate how social adversity shapes reproductive biology. Her work uses rhesus macaques from the long-term Cayo Santiago field site to explore how early-life adversity and social rank influence gene regulation in ovarian tissue. Understanding these mechanisms could help reveal whether reproductive health differences arise primarily from sociocultural factors, like access to healthcare, or from evolved biological pathways that respond to adversity.

With pilot funding, Petersen is applying a cost-effective single-cell RNA sequencing (scRNA-seq) technique to ovarian tissue samples from eight macaque females—half low-ranking, who experience greater social stress and limited access to resources, and half high-ranking, who hold dominant positions in the group. This approach will allow her to identify gene expression patterns across thousands of individual cells, as well as the cell types most affected by social status. These data will serve as the first single-cell atlas of ovarian gene expression from free-ranging non-human primates and provide a critical proof-of-concept for expanding to additional reproductive tissues in future projects.

Beyond advancing primate biology, this project is a training platform for collaboration and mentorship. Petersen is working closely with the Bick Lab and mentoring a high school student who will assist with data analysis pipelines, gaining experience with cutting-edge genomics tools. "These data will help us uncover the cellular processes that adversity disrupts," Petersen said, "bringing us closer to understanding the biological roots of resilience and vulnerability."

GRANTS

A Beetle Model for Fungal Infection Research

Thomas Sauters

Postdoctoral researchers **Allyson Ray** and **Thomas Sauters** received a Pilot Grant to establish the red flour beetle (*Tribolium castaneum*) as a robust, ecologically relevant model for studying fungal virulence. Opportunistic fungal infections cause more than three million deaths annually, and many of the pathogens responsible live harmlessly in the environment until they encounter a susceptible host. The project seeks to understand how environmental interactions—especially with arthropods like beetles—shape fungal pathogenicity over evolutionary time.

Their approach uses *T. castaneum* to test virulence across multiple strains of *Aspergillus fumigatus* and *A. flavus*, two major pathogens of humans and crops. Flour beetles offer high-throughput experimental potential, a well-annotated genome, and advanced functional genomics tools. By combining survival assays, fungal load measurements, and RNA sequencing, the team will identify immune pathways activated in response to low- and high-virulence strains, comparing them with responses in mammalian model.


Allyson Ray

The project will also provide research opportunities for undergraduate students giving them hands-on experience in pathogen-host ecology and molecular analysis.

Predicting Health Outcomes with Computational Models

Associate professor **Nicole Creanza** and assistant professor **Amanda Lea** received a Pilot Grant to explore how rapid lifestyle change impacts women's health worldwide. In many human populations, transitions from subsistence farming and foraging to urban living have happened in just the last two centuries—an evolutionary blink of an eye. Creanza and Lea's collaboration examines how market integration, urban infrastructure, and other environmental factors affect cardiometabolic and reproductive health, with a focus on the unique challenges faced by women during these transitions.

Preliminary analyses of more than 4,000 individuals from the Turkana of northwest Kenya and the Orang Asli of Malaysia revealed two striking findings: first, local infrastructure and market-derived material wealth predicted cardiometabolic health better than diet or physical activity. Second, urbanization had a disproportionately negative effect on women, who showed greater increases in body fat and other health risk factors. These results suggest that interventions to improve health outcomes during urban transitions should prioritize women and their access to care.

With this funding, the team will build a novel agent-based computational model using directed acyclic graphs to integrate health data, reproductive outcomes, and lifestyle measures across populations. "Our goal is to predict which relatively easy-to-obtain measurements will offer the greatest insight into women's health across different populations," the team wrote. The resulting framework will help guide cost-effective, scalable health monitoring strategies and inform future interventions designed to mitigate the health costs of urbanization.


Rayshaun Pettit

Rayshaun Pettit

Amanda Lea (top) and Nicole Creanza

PILOT

Evolutionary Links to Vision Loss in Diabetes

Submitted photo

Christopher Otieno

Another graduate student, **Christopher Otieno** (Edwards Lab) will lead a project investigating how evolutionary history shapes the risk of Diabetic Macular Edema (DME), a vision-threatening complication of diabetic retinopathy. This research builds on a recent *Nature Medicine* study that identified a strong association between the glucose-6-phosphate dehydrogenase (G6PD) locus and DME.

He will focus on genetic trade-offs that link past evolutionary pressures to modern disease. Gene variants, which evolved under malaria selection, protect carriers from infection but also cause G6PD deficiency. This condition distorts red blood cell turnover and complicates the use of HbA1c for diabetes diagnosis. Risk variants at the APOL1 gene, which rose in frequency under selective pressure from trypanosomiasis, are associated with kidney disease and may contribute to DME susceptibility, particularly in individuals of African ancestry.

To investigate these connections, Otieno will use large biobank datasets with more than 15,000 DME cases, making this the largest and most ancestrally diverse genetic study of DME to date. By comparing risk across populations, the project aims to identify both shared and ancestry-specific genetic loci that influence disease progression and diagnostic accuracy.

Goals and Hypotheses

First, Otieno will fine-map and evaluate genetic variation at the G6PD and APOL1 loci, assessing how differences across populations contribute to DME risk. Second, he will test whether genetic risk for DME has been shaped by evolutionary pressures using selection analyses such as iHS and polygenic adaptation tests.

Cultural Flourishing Shapes Biological Stress Responses

Submitted photo

Rosseirys De La Rosa (center)

Graduate student **Rosseirys De La Rosa** (Benn Torres Lab) will collect biomarker data to build individualized allostatic load profiles with community partners in Piñones, Puerto Rico. The project will explore how chronic stress accumulates in the body — a concept known as allostatic load — and how cultural and social factors may protect against its effects.

De La Rosa's work centers on the concept of flourishing, defined within Piñones as "survival with meaning." Rather than treating flourishing as a universal, fixed state, the project considers it a dynamic, culturally grounded experience tied to land, community belonging, and placemaking. From an evolutionary perspective, aspects of flourishing such as social cohesion may function as adaptive mechanisms that reduce biological stress and support long-term health.

Fieldwork will include minimally invasive collection of dried blood spot samples, as well as on-site measures for cholesterol, glucose, triglycerides, blood pressure, and other cardiometabolic indicators. Participants will receive immediate health feedback using a CardioCheck Plus machine, linking community engagement with actionable health information. These data will be processed and integrated with statistical modeling and mentoring support from Monica Keith's Lab.

Goals and Hypotheses

This project hypothesizes that flourishing, as locally defined, is associated with lower allostatic load. By connecting cultural experiences of belonging and well-being with physiological measures of stress, De La Rosa aims to test whether flourishing acts as a biological buffer against adversity. Results will guide future research on stress and health in racialized populations and generate preliminary data for dissertation funding proposals, including the Wenner-Gren Dissertation Fieldwork Grants.

GRANTS

Honorable Mention: From Cells to Humans to Forests

Six trainees recieved honorable mention this year.

Evolution of Virulence Under Variable Immune Responses: Rayshaun Pettit is experimentally evolving the insect pathogen *Bacillus thuringiensis* through genetically modified *Drosophila* lines with deficiencies in specific immune pathways. By tracking host mortality, pathogen load, and genomic changes across serial passages, this project will determine how different arms of host immunity select for changes in pathogen growth rate and virulence.

Lifestyle Effects on Immune Response at the Single-Cell Level: Layla Brassington is testing how urbanization and other lifestyle factors influence immune cell gene expression during infection. Using cryopreserved blood samples from Orang Asli, Turkana, and U.S. populations, she will generate single-cell RNA-seq data from stimulated and control immune cells to map cell type–specific transcriptional responses.

Climate-Driven Autumn Phenology and Carbon Uptake: Xingyi Huang is investigating how climate change is shifting the end of the growing season (EOS) in deciduous and mixed forests and how those shifts impact global carbon uptake. Using satellite-derived phenology data, ERA5-Land climate records, and advanced causal forest modeling, Huang aims to detect a potential EOS tipping point where warming could reverse current trends toward longer growing seasons. The project integrates modeling with validation from experimental and observational datasets to improve predictions of autumn phenology and enhance Earth system models used to forecast carbon cycle feedbacks.

Evolutionary Genomics of Blood Pressure Regulation: Human blood pressure regulation reflects deep evolutionary history, yet current genetic studies remain Eurocentric. Hannah Seagle's project uses data from 2.5 million individuals across diverse ancestries to fine-map causal variants, explore evidence for polygenic selection, and uncover population-specific drug targets for treatment-resistant hypertension. By integrating GWAS, TWAS, and ancestry-stratified Mendelian randomization with massive electronic health record datasets, Seagle's work will inform precision medicine approaches to cardiovascular disease that better serve underrepresented populations.

Clonal Hematopoiesis and Cardiometabolic Disease: Marina Watowich is examining how clonal hematopoiesis of indeterminate potential (CHIP) — a mutation-driven expansion of blood stem cell lineages — varies across subsistence and urbanizing populations. With new sequencing of Tsimane, Turkana, Orang Asli, and U.S. samples, this work will clarify how environment, aging, and genetic background shape CHIP dynamics and methylation profiles. The project will provide unprecedented insight into how industrialization may amplify age-related disease risks through hematopoietic mechanisms.

Forest Edge Age and Carbon Resilience: Xiuyi Wu's project explores how forest edge age influences carbon storage and recovery in the Amazon rainforest, where edge effects contribute up to one-third of annual carbon loss. By combining GEDI and ICESat-2 LiDAR data with ecosystem models, Wu will map edge age, quantify its effects on aboveground biomass, and project future carbon dynamics under climate and disturbance scenarios. This work will improve predictions of Amazon carbon resilience and inform conservation strategies aimed at mitigating edge-driven carbon loss.

Submitted photos

From left: Pettit, Brassington Huang, Seagle, Watowich, Wu

Bringing Evolution Education to TN

From rural high schools to elementary classrooms, trainees of the Evolutionary Studies Initiative (ESI) are bringing evolutionary science directly to the next generation.

A team of ESI trainees visited **McGavock Elementary School** in Nashville to lead a series of hands-on science activities with students from kindergarten through fifth grade. They ran short, rotating lessons in a festival-style format, including a dice-based phylogeny game and a paleontology-themed activity developed in collaboration with Dr. Neil Kelley. Each session invited students to engage directly with the concepts of evolution, biodiversity, and extinction in age-appropriate, accessible ways.

"The vibes were definitely chaotic, but so much fun!" said graduate student Brynn Wooten. "There were so many moments that stood out—one student kept asking how I became a paleontologist, and another asked, 'If we evolved from monkeys, why are they still here?' I explained it, and I could see in her eyes the moment it clicked."

Wooten emphasized how early access to scientific role models can make a lasting impression. "I personally was bitten by the evolution and paleontology bug at around eight years old, so I know how it feels to be that inspired. I hope to instill that spark in these kids—whether or not they pursue science, a passion for learning is just as important."

This elementary outreach builds on ESI's growing commitment to science education and engagement across Tennessee.

The **Computational Biology Rural High School Research Program** was launched by Vanderbilt graduate students Ximena Leon and Olivia Riedling to bridge the opportunity gap for rural students interested in STEM. The pair mentored six students from Marshall County High, guiding them through professional development and original research in evolutionary biology. Projects included computational analyses of birdsong evolution and comparative fungal genomics. Each student presented their findings at a public showcase and will be named co-authors on a forthcoming peer-reviewed publication—an extraordinary milestone for high school students.

"Seeing the students' confidence grow throughout the program was the most rewarding part of mentoring," said Leon. "They became more independent, found excitement in presenting their findings, and realized their contributions to science truly matter."

Riedling echoed that sentiment: "They really tackled a lot—computational skills, writing, presenting. Watching them step out of their comfort zones and take charge of their projects was incredible. Some even continued their work outside the program and are now volunteering in our lab."

The impact of this program has already rippled into students' future plans. "One of my students told me, 'I didn't think I would ever like biology,' and now wants to minor in it alongside pre-med," Riedling said. "These

experiences can completely change a student's outlook."

"These programs aren't just about science content," said Antonis Rokas, director of the ESI. "They're about building scientific identity and making sure students, especially in rural and underserved communities, see themselves as part of the future of science."

For the graduate students and postdocs involved, the experience has been equally transformative. "My view of mentorship has shifted," said Riedling. "We tailored the program to fit students' needs, and that required learning how each student absorbs information and how best to support them. It's something I'll carry forward."

Leon agreed, adding, "This experience significantly changed how I think about mentorship in scientific research. We had to be flexible, resourceful, and inclusive in how we structured our support—and the results were more than worth it."

ESI also went to the **Adventure Science Center** for the Way Late Play Date, Jurassic Camp where hundreds of Nashvillians got to take home fossils and learn evolution.

Finally, in July, ESI helped run an evolution-themed Scopes Trial Day with the local **Girl Scouts of America**. Sophia Rokas coordinated the event as part of her Gold Award. Dozens of girls learned about the Scopes "Monkey" Trial and participated in an interactive evolution simulator run by postdoctoral researcher, Kyle David.

Opposite: from right, Kelley, Larisa DeSantis, and Wooten teach visitors at the Adventure Science Center about paleontology and evolution. This page top: Leon (left) and Riedling (right) present their students with achievement certificates (submitted photo). This page bottom: the Girl Scouts of America Scopes trial day scenes and badge (Tracy Rokas).

‘24/‘25 Undergraduate Research Fairs

Mentor: Megan Behringer, Biological Sciences

Doris Jiang	Distribution of fitness effects of *Lactobacillus acidophilus*
Yenchan Kim	Role of Loss-of-Function Mutations in *E. coli* Resistance Against *L. crispatus*

Mentor: Alexander Bick, Medicine

Ketan Hoey	Do SLAMF1 Mutant Cells Display Decreased Sensitivity to IL-6?

Mentor: Rachel Bonami, Medicine

Hannah Bhattacharya	Key B lymphocyte subsets undergo gene expression changes following immune checkpoint inhibitor-induced autoimmune sicca in melanoma participants

Mentor: Kendall Broadie, Biological Sciences

Yewon Ahn	The Elusive Pathomechanisms of Kohlshütter-Tönz syndrome and its Associated Rogdi Gene
Yuchen Du	Investigating the Role of Serotonin in Learning and Memory Using Fragile X Syndrome Model
Valeria Toscano Pasos	Palmitoyl protein thioesterase-1 (Ppt1) Regulates Presynaptic Neurotransmission at a Glutamatergic Synapse

Mentor: Gianni Castiglione, Biological Sciences

Isabella Bautista	Rhodopsin-mediated penguin vision adaptation to extreme conditions

Mentor: Walter Chazin, Biochemistry

Tammy Le	Developing Inhibitors for Receptor for Advanced Glycation End-products (RAGE) Using a Virtual Fragment Based Discovery Approach
Melumo Togashi	Characterization of ZigA, a Predicted Zn-Dependent Metallochaperone from *S. aureus*

Mentor: Tim Cover, Medicine

Lauren Solecki	Identification of Protein-Protein Interactions in the *Helicobacter pylori* Cag Type IV Secretion System

Lauren Solecki, now at Epic, worked with ESI mentors Cover and Tung. (LinkedIn)

Mentor: Larisa DeSantis, Biological Sciences

Aditya Kurre	A Multi-Proxy Approach to Pleistocene Ground Sloth Paleoecology

Mentor: Emily Hodges, Biochemisry

Jacqueline Yap	Understanding the Time-Dependent Role of TET Activity During NPC Differentiation

Mentor: Eric Gamazon, Genetic Medicine

Namju Kim	Modeling protein expression for proteome-wide association studies

Mentor: Carl Johnson, Biological Sciences

Margaret Jones	Circadian Regulation of Cyanobacterial Responses to Amoebal Predation

Mentor: Amanda Lea, Biological Sciences

Selina Wang	Effects of Early Life Adversity on Cardiometabolic Health in Turkana

Mentor: Huidong Li, Earth and Environmental Sciences

Andre Mendoza	Analyzing the Effects of a Large Extensive Green Roof on Storm Water Runoff in Nashville, TN

Mentor: Lin Meng, Earth and Environmental Sciences

Xiyu Wang	Understanding the roles of green roofs in mitigating urban heat island in the U.S

Mentor: David Rinker, Biological Sciences

Corey Wiseman	*Purpureocillium lilacinum*: Genomic and Growth Comparison of Clinical and Environmental Samples

Mentor: Antonis Rokas, Biological Sciences

Rene Huerta	Diversity in colony morphology across Saccharomycotina yeast species

Mentor: Eric Skaar, Pathology, Microbiology and Immunology

Karen Nie	Characterizing the Function of Putative Iron-Sulfur Cluster Protein A1S_0780 in *Acinetobacter baumannii*

Mentor: Ann Tate, Biological Sciences

Phoebe Lin	Investigating Fitness Costs to Two Pesticide Classes and *Pseudomonas entomophila* across Five Beetle Species
Sowmya Senthilkumar	Evolutionary Dynamics of Pleiotropy in *Drosophila* Neuronal and Immune Genes

Mentor: Tiffiny Tung, Anthropology

Tierney Cunningham	Llama and Alpaca Husbandry in the Ancient Andes: Reconstructing Diet and Migration with Stable Isotope Analysis of Camelid Teeth from the site of Chavín de Huántar, Peru
Lauren Solecki	Analyzing Diet at Nuestra Señora de Belén through Stable Carbon and Nitrogen Isotopes

Mentor: Allison Walker, Chemistry

Michelle Bramlett	Using Computational Methods to Design and Optimize Monobody Inhibitors of the Glucagon Receptor
Navin Vazrala	Experimental Validation and Characterization of Bioactive Compounds Produced by *Actinoplanes teichomyceticus*

Mentor: Larry Zwiebel, Biological Sciences

Leon Li	Investigating the role of IR25a in *Anopheles coluzzii*

Mentor: Wenhan Zhu, Pathology, Microbiology and Immunology

Muen Shen	Rational engineering of an obligate anaerobe to survive oxygen

Awards

Initiative-wide

- Friend of Darwin - National Center for Science Education
- T32 Training Grant - Naitonal Institutes of Health

Faculty

- Alex Bick - VU Chancellor's Faculty Fellow
- Gianni Castiglione - Keck Foundation Research Award
- Julián Hillyer - VU Centennial Professor
- Emily Hodges - VU Chancellor's Faculty Fellow
- Ivelin Georgiev - VU Endowed Chair
- Eric Skaar - Innovation Catalyst Fund award, Elected Fellow of the National Academy of Science and 2025 NAS Award in Molecular Biology
- Keivan Stassun - Innovation Catalyst Fund award, US National Medal of Science
- Digna Velez Edwards - VU Endowed Chair
- Allison Walker - 2025 Cottrell Scholar

Postdoctoral Researchers

- Juan Carvajal-Garcia - VUSM Destination Biochemistry Advanced Postdoctoral Scholar

Graduate Students

- Audrey Arner - Leakey Foundation and Wenner Gren Foundation Dissertation Grants. SSE Rosemary Grant Advanced Award
- Anamika Bose - NSF GRFP Honorable Mention
- Darra Boyer - VU Dissertation Enhancement Grant
- Rosseirys De La Rosa - Meharry-Vanderbilt Community Engaged Research Core Community Scholars Award
- Owen Hale - Danone Corporation Annual Gut Microbiome, Yogurt, and Probiotic Fellowship
- Chloe Hecht - NSF GRFP Honorable Mention
- Kylie Jozwick - NSF GRFP Honorable Mention
- Amy Longtin - James P. Taylor Foundation Biology of Genomes Scholarship, NSF GRFP
- Katharine Walls - NSF GRFP Honorable Mention
- Brynn Wooten - Paleontological Society President's Student Research Award

Undergraduate Students

- Karen Nie - VURF Poster Runner-Up
- Andrei Olaru ('24) - NSF GRFP
- Joyce Sanks ('24) - NSF GRFP Honorable Mention

Carvajal-García named Destination Biochemistry Advanced Postdoc Scholar

By: Lorena Infante Lara, VU Basic Sciences science writer with edits from Andy Flick

Submitted photo

Carvajal-García, has been working with his advisor, Professor of Biochemistry Houra Merrikh, since 2021 to understand spontaneous mutagenesis and the evolution of antimicrobial resistance.

"It is through mutations that bacteria evolve antibiotic resistance and cancer cells become resistant to chemotherapy," he said. "However, the processes that promote spontaneous mutagenesis, and therefore drive evolution and disease, remain incompletely understood."

The research program that Carvajal-García will establish combines genetics and genomics techniques that he learned during his postdoc with molecular biology and biochemistry-based assays that he learned during his Ph.D. at the University of North Carolina at Chapel Hill. His goal will be to understand the mechanisms behind mutagenesis-driven evolution and will seek to determine the evolution of evolvability, an extension of the work he did in his first paper in the Merrikh lab showing that error-prone DNA polymerases are critical for evolution.

"Juan is a true scientist who is in science due to his passion to discover the unknown," Merrikh said.

"He is a model trainee when it comes to evolution at Vanderbilt," praised ESI director, Antonis Rokas.

ESI Quick Facts

The Evolutionary Studies Initiative was founded in 2019 by Antonis Rokas with the help of the Advisory Board (Jada Benn Torres, Larisa DeSantis, Suzanna Herculano-Houzel, Owen Jones, Houra Merrikh, and Betsey Robinson).

In 2021, ESI began a Pilot Grant Program with the aim of funding collaborative research projects across not just labs, but also departments. To date, we have given out 45 grants to fund research in Biological Sciences (BSCI), Earth and Environmental Science (EES), Anthropology, Medicine, and Communication of Science and Technology. These grants have started new collaborations between BSCI and EES as well as BSCI and Medicine.

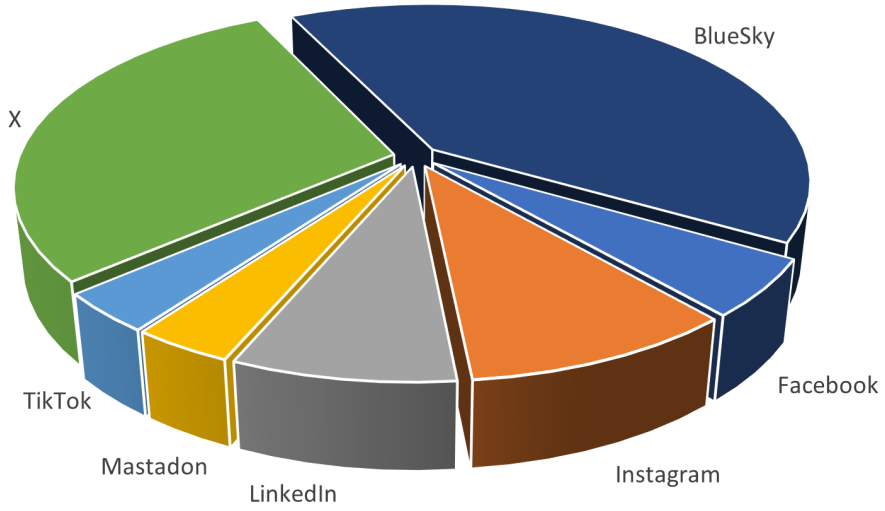
Projects led by graduate students have already had a massive return on investment. Of the 45 grants given out, 26 have been to graduate students. Those students have received seven NSF GRFPs, two NSF DDIGs, one DoD NDSEG, two Wenner Gren fellowships, and two SSE Rosemary Grant Graduate Research Excellence Awards.

We engage in several outreach activities, with our two major projects consisting of teaching high school students about evolution while digging for fossils at Coon Creek Science Center and working with local high schools to run research projects in the biological sciences.

We also engage with the community on many social media platforms. We have more than 2,700 followers across all platforms. Our pie chart below breaks down our followers by social media type. BlueSky has surpassed X as our largest platform with significant growth on LinkedIn in the past year as well. Find us on most platforms as EvolutionVU.

On TikTok and Instagram, we have gained many new followers this year thanks to the Scopes "Monkey" Trial Centennial Symposium. We post short clips daily featuring three roughly one-minute long sections of each talk.

On Instagram, short clips on Fossil Fridays of Steve Brusatte's talks have gotten nearly ten-fold more views and likes than our previous content. While on TikTok, about one short video from the symposium per week garners more than one thousand views. The top video to date is Amanda Townley, executive director of NCSE, talking about why she doesn't believe in evolution - she accepts it based on the facts. The video has more than 1,800 views, 166 likes, 17 comments, and 16 saves!



ESI Awarded NIH / NIGMS T32 Program

We are excited to report that the long wait from our initial application in September 2023 is finally over! We have received funding from the National Institutes of Health, National Institute for General Medical Sciences to fund two students in a new program on Compuational Evolutionary Approaches to Disease (CoEvoD).

The first two students in the program are second year student Joshua Eis of the Castiglione Lab and third year student Layla Brassington of the Lea Lab.

Eis uses machine learning and other computational tools to reverse-engineer the molecular mechanisms by which birds evolved their long lifespans. Preliminary data shows extensive variations in metabolic genes that are unique to the avian clade. Eis will infer the evolutionary timing of avian-specific mutations at key phylogenetic nodes (e.g. the evolution of flight), searching for coevolving mutations in deep time that may be compensatory, followed by 'fine-tuned' adaptive variation in derived lineages hypothesized to diverge between clades due to ecological and physiological variables.

Brassington will look to answer a central question in evolutionary medicine: why do humans remain vulnerable to chronic disease, despite strong selective pressures on survival and reproduction? A leading explanation is the evolutionary mismatch hypothesis—the idea that rapid lifestyle change has created a gap between the environments our genomes evolved in and the ones we inhabit today.

Two additional students, Ashlynn Bruder of the Behringer Lab and Abigail Rose of the Zhu Lab will join the program with funding provided by ESI. Bruder studies long term evolution of *E. coli* while Rose focuses on metabolic pathways of the gut symbiont *Bacteroides thetaiotaomicron*.

RECRUITING NOW

Brian O. Bachmann (Biochem)
Biosynthesis, Secondary Metabolites, Directed Evolution, Drug Discovery

Megan Behringer (BSCI)
Population genetics, genomics, microbiology, *E. coli*

Rachel Bonami (PMI)
B cell evolution, *T* cell, autoimmunity, type 1 diabetes, arthritis, microbiome

Benjamin Bratton (PMI)
Bacterial evolution, microscopy, cell shape, quantitative biology

Gianni Castiglione (BSCI)
Molecular evolution, vision, oxidative stress, evolutionary medicine

Larisa DeSantis (BSCI)
Vertebrate paleontology, paleoecology, paleoclimates

Ivelin Georgiev (PMI)
Immunology, virology, vaccines, antibodies, computational, disease

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

Antonis Rokas (BSCI)
Evolutionary genomics, molecular evolution, phylogenomics, fungi, mammals, fungal diversity

Eric Skaar (PMI)
Bacteria, host-pathogen interactions, biochemistry, molecular biology, cell biology

Ann Tate (BSCI)
Immune system, virulence, systems biology, coinfection, host-parasite coevolution, life history evolution

UNIVERSITY POSITIONS

Professor of the Practice:
Climate and Environmental Policy
Environmental Engineering

Senior Lecturer:
Anatomy and Physiology
Biological Sciences
Chemical Biology
Neuroscience
Psychology

Assistant Professor:
Biomedical Engineering
Cell & Developmental Biology
Computational Systems Biology
Medical Anthropology

Current Job Postings

Support our mission to **create a world-class center for evolutionary studies** at Vanderbilt! Our researchers conduct groundbreaking evolutionary research across the disciplines, while offering the highest quality education to our trainees. Your donation supports cross-disciplinary research, student travel grants, and helps us bring in the world's best speakers to our seminar series.

Donate today at tinyurl.com/29tycx3p or

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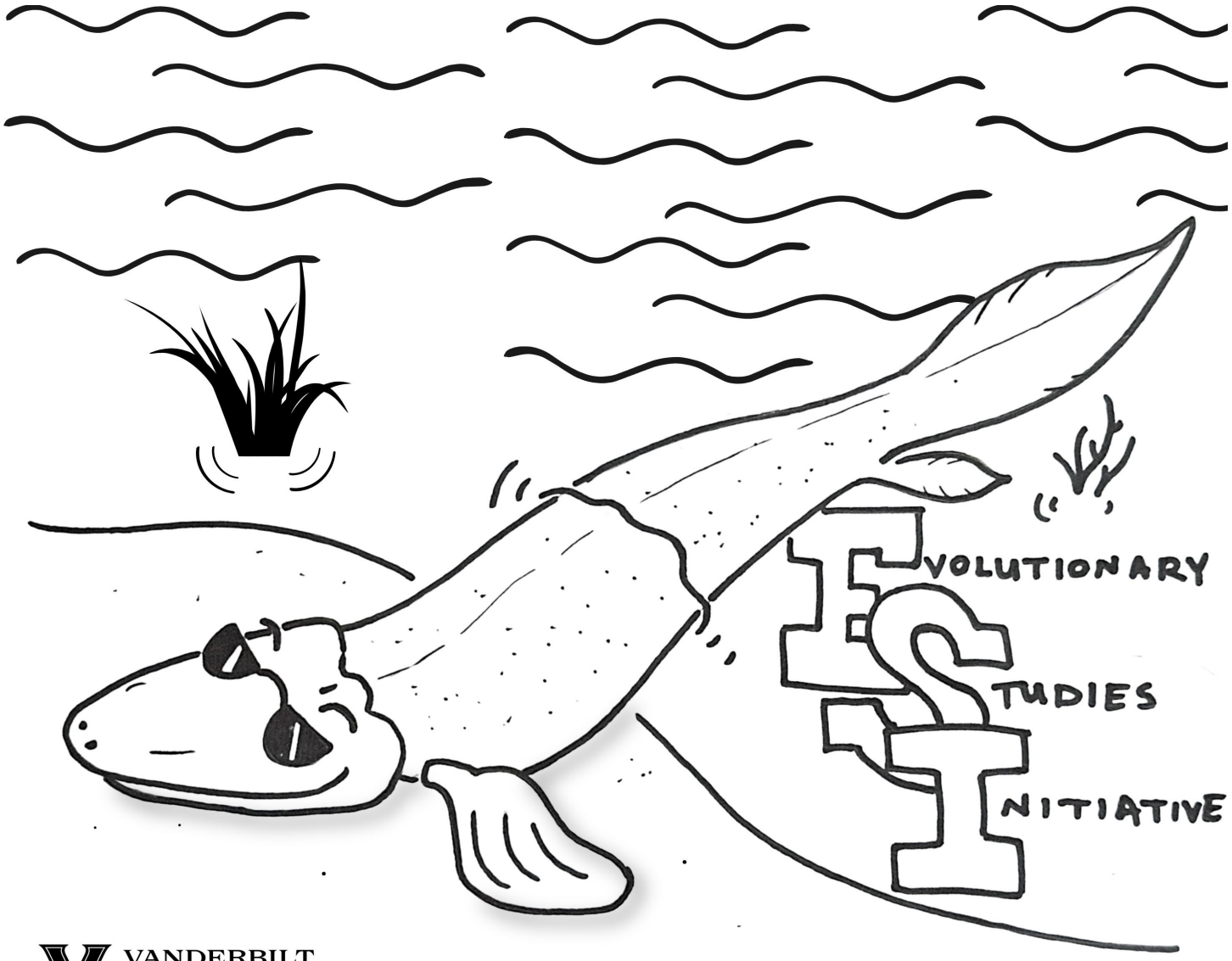
Wesley Elsberry

Matthew David



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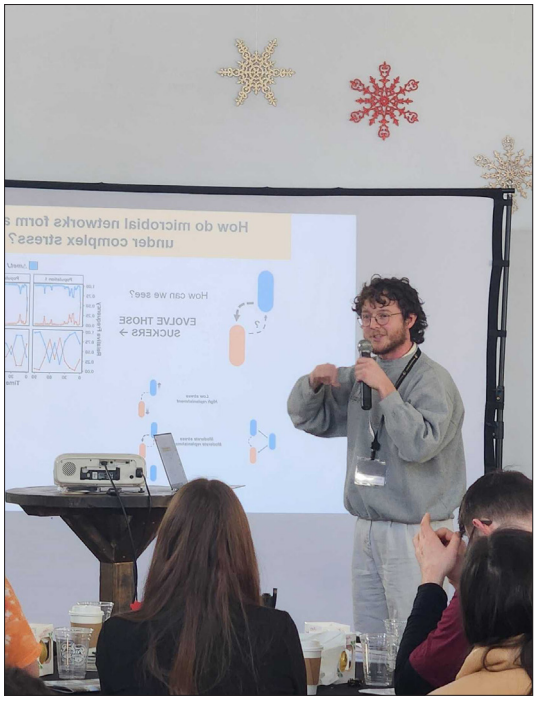

About the artist:

William McLaughlin joined Megan Behringer's Lab in 2023 and is studying the evolution of metabolic cooperation in populations of *E. coli*. He is also looking for causal agents to the persistence of cheater phenotypes in these bacteria by investigating resource limitation.

William has a BS in Cell and Molecular Biology from Auburn University where he served as a learning assistant mentor and a research assistant in the Rashotte Lab.

This work is titled: Life on land is for cool folks only!