

**EVENT
PROGRAM**

LIFE ON A SUSTAINABLE PLANET: EXPLORING AND UNDERSTANDING OUR NATURAL WORLD

NATURAL SCIENCE SYMPOSIUM

April 18, 2024, 10:30 AM – 5:00 PM

Smithsonian National Museum of Natural History,
Washington, D.C.



NATIONAL
MUSEUM *of*
**NATURAL
HISTORY**

* Smithsonian



Natural Science Symposium: Agenda

April 18, 2024, 10:30 AM – 5:00PM

Welcome and Opening Remarks		
Time	Speaker Name and Affiliation	Talk Title
10:30am–10:45am	Rebecca Johnson, <i>Smithsonian National Museum of Natural History</i>	<i>Welcoming Remarks and Introduction</i>
10:45am–10:55am	Ellen Stofan, <i>Smithsonian Institution</i>	<i>Opening Remarks – Life on a Sustainable Planet</i>

Theme 1: Assessing Global Change: Past, Present, and Future		
Time	Speaker Name and Affiliation	Talk Title
11:00am–11:20am	Meghan Balk, <i>Natural History Museum of Oslo</i>	<i>How do animals respond to a changing planet? Linking micro to macro processes to assess species' ability to persist</i>
11:20am–11:40am	Bastian Bentlage, <i>University of Guam</i>	<i>Sedimentation impacts on corals in Guam's nearshore reefs</i>

Theme 2: Exploring and Understanding Biodiversity		
Time	Speaker Name and Affiliation	Talk Title
11:40am–12:00pm	Sahas Barve, <i>Archbold Biological Station</i>	<i>Colorful puffy jackets: bird feathers on the world's highest mountains</i>
12:00pm–1:30pm	Lunch Break	
1:30pm–1:50pm	Kayce Bell, <i>Natural History Museum of Los Angeles County</i>	<i>Charismatic microfauna: biodiversity exploration in chipmunk lice and their bacteria</i>

Theme 2: Exploring and Understanding Biodiversity

Time	Speaker Name and Affiliation	Talk Title
1:50pm–2:10pm	Richie Hodel, <i>Smithsonian National Museum of Natural History</i>	<i>Machine learning applications with digitized herbarium specimens reveal the hybrid origin of the cherry/plum genu</i>
2:10pm–2:30pm	Ricardo Betancur, <i>Scripps Institution of Oceanography UC San Diego</i>	<i>Ecological transitions along the water column in marine fishes over deep time</i>
2:30pm–2:50pm	Manuela Dal Forno, <i>Botanical Research Institute of Texas</i>	<i>Preserving the Past, Exploring the Future: Insights from Historical Lichen Collections</i>
2:50pm–3:10pm	Maureen Turcatel, <i>Field Museum</i>	<i>Diversity and Evolutionary History of Horse Flies</i>
3:10pm–3:40pm	Afternoon Break	

Theme 3: Understanding Earth's Origin and Evolution

Time	Speaker Name and Affiliation	Talk Title
3:40pm–4:00pm	Laura Waters, <i>New Mexico Institute of Mining and Technology</i>	<i>Why are Earth's continents missing a layer? A perspective from obsidians</i>

Theme 4: Humans in the 21st Century

Time	Speaker Name and Affiliation	Talk Title
4:00pm–4:20pm	Audrey Lin, <i>American Museum of Natural History</i>	<i>The History of Coast Salish 'Woolly Dogs' Revealed by Ancient Genomics and Indigenous Knowledge</i>
4:20pm–4:50pm	Rebecca Johnson, <i>Smithsonian National Museum of Natural History</i>	<i>Q/A with students and speakers</i>
4:50pm–5:00pm	Carla Easter, <i>Smithsonian National Museum of Natural History</i>	<i>Closing Remarks</i>

Natural Science Symposium: Biographies

Meghan Balk, Ph.D.

Natural History Museum at the University of Oslo, Norway

Dr. Meghan A. Balk is a postdoctoral fellow in the Evolution and Paleobiology group at the Naturhistorisk museum in Oslo, Norway. Her research interests are in exploring how abiotic (i.e., climatic) and biotic (i.e., predation, competition) drives trait evolution within lineages and across communities. She uses museum collections and AI-driven techniques to extract trait data from fossil and modern specimens. From 2017-19, she was a Peter Buck Postdoctoral Fellow at the Smithsonian's National Museum of Natural History (NMNH) exploring trait changes across communities dominated by megafauna.

Mentored by Matthew T. Carrano during their fellowship.



Sahas Barve, Ph.D.

Archbold Biological Station, US

Dr. Sahas Barve is the Program Director of Avian Ecology at Archbold Biological Station. There, he oversees a 55 year-long study of threatened Florida Scrub-Jays. Previously, Sahas has worked on a wide range of taxa and systems including tracking king cobras in south India, avian field work in the Himalayas, acorn woodpeckers in California, and museum research at the Smithsonian's National Museum of Natural History (NMNH) on Himalayan and Andean birds. Sahas is broadly interested in life-history evolution of birds and enjoys communicating research with the public in new and innovative ways. He is an avid birder, and has also won awards in multiple grilled cheese making competitions.

Mentored by Carla Dove during their fellowship.



Kayce C. Bell, Ph.D.

Natural History Museum of Los Angeles County, US

Museum collections form a vital component of Dr. Kayce C. Bell's research on mammal and parasite diversity and distribution. Her research has largely centered on the processes that shape squirrel species diversity and the interaction of factors impacting parasite diversity. Kayce completed a B.S. and M.S. in Biology at Idaho State University and Ph.D. in Biology at the



University of New Mexico. Between her M.S. and Ph.D., Kayce worked at the Denver Museum of Nature and Science studying the relationships among chipmunk species and hybridization between species. For her dissertation work she used genetic data to compare genetic relationships and distributions of chipmunks and their parasitic lice and roundworms. Kayce completed a Peter Buck Postdoctoral Fellowship at the Smithsonian's National Museum of Natural History (NMNH), where she worked on the genomic diversity of the sucking lice and roundworms that infect chipmunks. Kayce became the curator of terrestrial mammals at the Natural History Museum of Los Angeles County in 2019. In that position, she continues investigating mammal and parasite diversity, with an additional focus on urban species. She is currently leading a project studying the evolutionary history and adaptations of all mammalian sucking lice and projects on the distribution and diversity of native rodents in urbanized areas of Southern California.

Mentored by Anna Phillips and Kristofer Helgen during their fellowship.

Bastian Bentlage, Ph.D.

University of Guam, US

Dr. Bastian Bentlage is Associate Professor of Bioinformatics at the University of Guam (UOG) in the western tropical Pacific. After an undergraduate education in zoology, ecology and aquatic biology in Germany, Bastian earned a Ph.D. in Ecology and Evolutionary Biology from the University of Kansas, with a thesis that focused on the biogeography and evolutionary relationships of jellyfish and their kin. He spent two years during this time at the Smithsonian's National Museum of Natural History (NMNH), studying specimens in the collections and publishing taxonomic revisions, including new species descriptions, of venomous box jellyfish. During a postdoctoral appointment at the University of Maryland, College Park, Bastian conducted research on gene expression signatures of species interactions in algae competing for resources. Here, he built his skill-set in bioinformatic data analysis. Following this appointment at the University of Maryland, Bastian returned to the Smithsonian Institution under a Peter Buck Postdoctoral Fellowship to leverage the NMNH collections to investigate the evolution of open ocean and deep sea jellyfish. In 2016, Bastian took a tenure track appointment at UOG, leading efforts to increase research capacity in the US territory of Guam. Since arriving at UOG, he has served as co-PI and research coordinator for NSF-funded programs totaling more than \$20 million in funding to facilitate upgrades of laboratories, cyberinfrastructure (networking and high throughput computing), and hires of personnel. At UOG, Bastian's research focuses on the impacts of environmental degradation and climate change on corals and their symbiotic algae and bacteria.



Mentored by Allen Collins during their fellowship.

Ricardo Betancur, Ph.D.

Scripps Institution of Oceanography at University of California San Diego, US

Originally from Colombia, Dr. Ricardo Betancur-R. embarked on his academic journey in 1994, earning his B.Sc. in Marine Biology from Universidad Jorge Tadeo Lozano. He then pursued his M.Sc. in Marine Biology from 2001 to 2004 at Universidad Nacional de Colombia, graduating *magna cum laude*. In 2004, Ricardo moved to the U.S. to continue his academic education, completing his Ph.D. in Biological Sciences in 2009 at Auburn University. Following his doctoral studies, Ricardo commenced his postdoctoral research at The George Washington University, where he remained until 2013. Notably, from 2013 to 2014, Ricardo was awarded a Peter Buck Postdoctoral Fellowship at the Smithsonian's National Museum of Natural History (NMNH).



From 2014 to 2018, Ricardo served as an Assistant Professor at the Department of Biology, University of Puerto Rico, Rio Piedras campus. He then continued his academic journey as an Assistant Professor at the Department of Biology, University of Oklahoma from 2019 to 2023, where he was later promoted to Associate Professor in 2023. Currently, Ricardo serves as an Associate Professor at the Marine Biology Research Division of Scripps Institution of Oceanography, UC San Diego, a position he has held since last year. His research interests lie in organismal marine biology, with a major focus on phylogenetic inference and comparative analysis using fishes as study systems. This research approach prioritizes the implementation of genome-scale approaches for robust inferences in macroevolutionary research. Fieldwork is an important component of his research, and he has participated in multiple expeditions across four continents.

Mentored by Richard Vari and Lynne Parenti during their fellowship.

Manuela Dal Forno, Ph.D.

Botanical Research Institute of Texas, US

Dr. Manuela Dal Forno is a lichenologist at the Botanical Research Institute of Texas (BRIT) and her work focuses on multiple aspects of the lichen symbioses. She is originally from Brazil, where she received a B.S. in Biology and a M.Sc. in Botany. She obtained her Ph.D. in Environmental Sciences and Public Policy from George Mason University in Virginia, with her doctoral research focusing on the evolution and diversity of the subtribe *Dictyonematinae*, the most species-rich clade of basidiolichens.



Following the completion of her doctoral studies, Manuela served as a National Science Foundation Postdoctoral Research Fellow, conducting collaborative research at the Smithsonian's National Museum of Natural History (NMNH) and the University of Graz in Austria. Subsequently, she was awarded the esteemed Peter Buck Postdoctoral Fellowship at the NMNH, where she furthered her investigations into collections-based research with lichens.

Mentored by Eric Schuettpelz during their fellowship.

Richie Hodel, Ph.D.

National Museum of Natural History, US

Dr. Richie Hodel received his Ph.D. in Botany, with a focus on the comparative phylogeography of Caribbean mangroves, from the University of Florida in December 2017. He then worked as a postdoctoral research associate at the University of Michigan, where he studied the processed driving recent (i.e., Pleistocene) diversification in montane sedges (genus *Carex*, Cyperaceae).



His Peter Buck Postdoctoral Fellowship project (2020-2022) focused on identifying and characterizing the processes that generate biodiversity in the cherry/plum genus (*Prunus*, Rosaceae), which includes economically important species such as almonds, apricots, cherries, peaches, and plums. Richie used genomic DNA evidence extracted from hundreds of the Smithsonian's National Museum of Natural History (NMNH) herbarium specimens to infer the phylogeny and evolutionary history of the genus. He also used machine learning approaches, which leverage computer vision algorithms to identify morphological characters in digitized herbarium sheets, to identify vegetative and reproductive features associated with hybridization.

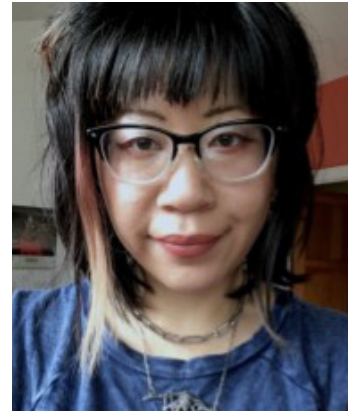
To date, he has published 27 papers in peer-reviewed scientific journals, with 7 published during his Peter Buck Postdoctoral Fellowship. Currently, Richie is the Biodiversity Genomics Postdoctoral Fellow at the Smithsonian Institution. His current fellowship aims to improve our understanding of the relative roles of the genome and the environment on shaping phenotypic variation on recent and ancient evolutionary scales. This project uses the widespread tree species, black cherry (*Prunus serotina*), as a model species for comparative analysis of genomic, phenomic, and environmental variation in herbarium specimens. In Fall 2024, Richie will start a Research Scientist position at the University of Michigan.

Mentored by Jun Wen during their fellowship.

Audrey Lin, Ph.D.

American Museum of Natural History, US

Dr. Audrey T. Lin (pronouns: she/they) is a paleogeneticist and a Gerstner Bioinformatics and Computational Biology Postdoctoral Scholar at the American Museum of Natural History in New York City. She received her Ph.D. from the Department of Zoology, University of Oxford (2020) where she used bioinformatic methods to investigate the consequences of genome evolution and its impact on molecular rate, demographic spread, and its physiological and functional changes over time. Between 2020-2023, she was based in the Anthropology Department at the Smithsonian's National Museum of Natural History (NMNH) where she held the Peter Buck Postdoctoral Fellowship and the George Burch Postdoctoral Fellowship in Theoretical Medicine and Affiliated Theoretical Science. While at NMNH, she led several collections-based projects, including two fully-funded projects with the aim of recovering viral RNA from museum specimens to better understand the molecular evolution of zoonotic viruses of biomedical interest—particularly the 1918 pandemic influenza virus and bat coronaviruses. The last project she led was in collaboration with Coast Salish weavers, Knowledge Keepers, Elders, and artists, utilizing “Two-Eyed Seeing” to view the world through the combined strengths of Indigenous knowledge and western science. This holistic approach revealed the deep history and recent decline of the Coast Salish woolly dog due to colonialism.



Mentored by Logan Kistler during their fellowship.

Maureen Turcatel, Ph.D.

Field Museum, US

Dr. Maureen Turcatel is an insect taxonomist and systematist, especially interested in the diversity and phylogeny of horse flies (Diptera: Tabanidae). Her research focuses on using museum specimens to perform revisionary work on horse flies, potentially finding and describing new species. She is also interested in using Next-generation sequencing data for phylogenetic analyses, which allow us to better understand the evolutionary history of horse flies and the relationships within them.

Maureen frequently conducts domestic and international fieldwork to obtain genome-quality samples for her phylogenomics research, and some of her recent expeditions included Brazil and Madagascar. In addition to research, she currently manages the Insects, Arachnids and Myriapods collection at the Field Museum of Natural History in Chicago, supervising staff on day-to-day curatorial activities,



and collaborating with other researchers to promote digitization efforts, collections access and growth.

Mentored by Torsten Dikow during their fellowship.

Laura Waters, Ph.D.

New Mexico Institute of Mining and Technology, US

Dr. Laura Waters is interested in understanding the processes that govern the evolution, differentiation and stratification of Earth's continents through petrographic (studying mineral compositions and textures), geochemical and experimental studies of volcanics erupted in subduction zones and rifts. Laura uses results from experiments and thermodynamics to develop models to decode the record of temperature, pressure and H₂O contents recorded by minerals in natural samples and understand the conditions that lead to the formation and eruption of a magma. Laura received a Peter Buck Postdoctoral Fellowship from the Smithsonian's National Museum of Natural History (NMNH) in 2015 that provided her with stability and funds to support her research. The Peter Buck Postdoctoral Fellowship and mentorship she received in the Department of Mineral Sciences provided her with an excellent foundation for her career today. Laura is currently an assistant professor at New Mexico Institute of Mining and Technology, where she has a group of four graduate students, working on projects related to crystallization kinetics in rhyolites, understanding the impact of changes to ice sheet thickness on volcanic eruptions in Antarctica, determining the role of fluid salinity in mobilizing rare earth elements from monazite (which are required for renewable energy), and characterizing rock formations and to understand their potential to become CO₂ sequestration sites.



Mentored by Benjamin Andrews during their fellowship.

Ellen R. Stofan, Ph.D.

Smithsonian Institution, US, Under Secretary for Science and Research

Dr. Ellen Stofan is the Under Secretary for Science and Research at the Smithsonian Institution. She oversees the science museums and science research centers as well as the Smithsonian Libraries and Archives, Smithsonian Scholarly Press, and Scientific Diving Program. Her focus is on the Smithsonian's Our Shared Future: Life on a Sustainable Planet



initiative and collective research, especially in areas of biodiversity, climate change, global health, sustainable communities, and environmental justice.

Stofan previously was the John and Adrienne Mars Director of the Smithsonian's National Air and Space Museum. She came to the Museum with more than 25 years of experience in space administration and planetary science.

As the former Chief Scientist of NASA, Stofan served as the principal advisor to the Administrator on science programs and strategic planning. She helped guide the development of a long-range plan to send humans to Mars, and on strategies for NASA to support commercial activity in low Earth orbit.

She held senior scientist positions at NASA's Jet Propulsion Laboratory, including work on missions to Venus, Earth, Mars, and Saturn. She is currently on the science team of the NASA Dragonfly mission to Titan.

Stofan holds master's and doctorate degrees in geological sciences from Brown University, and a bachelor's degree from the College of William & Mary. Awards received include the Presidential Early Career Award for Scientists and Engineers, the NASA Distinguished Service Medal and the Explorers Club Lowell Thomas Award. She serves on National Geographic Society's Board of Trustees and the Presidential Committee on the National Medal of Science.

Rebecca Johnson AM, Ph.D.

**Smithsonian's National Museum of Natural History, US,
Chief Scientist and Associate Director for Science**

Dr. Rebecca Johnson is the Chief Scientist and Associate Director for Science at the Smithsonian's National Museum of Natural History (NMNH). She is responsible for overall science leadership and administration of the museum's research and collections activities. Rebecca oversees seven scientific departments comprising over 300 staff; the Laboratory of Analytical Biology; the Collections Program (care, registration, digitization); Academic Services to interns, graduate students, fellows, research associates and collaborators, and emeritus scientists; high-level liaison and hosting of resident Federal Agencies (USDA, Commerce, Interior, Defense); numerous cross-cutting strategic science initiatives; field stations (Smithsonian Marine Station at Fort Pierce Florida and Carrie Bow Cay, Belize) at a variety of locations including Anchorage, Alaska, Florida, Washington, D.C. and Suitland, Maryland.

Dr. Johnson is a wildlife forensic scientist and conservation geneticist. As chief investigator of the Koala Genome Consortium she contributed to significantly advancing scientific knowledge and improved on the ground management



recommendations for this iconic Australian species. She previously held the role of Australian Museum Chief Scientist and Director of the Australian Museum Research Institute where she established wildlife forensic science as a specialty discipline and worked with government agencies and law enforcement. She also developed translational research through applied conservation genomics developing strong direct links to the aviation industry. Rebecca has a Bachelor of Science with honours from the University of Sydney, and a PhD from La Trobe University in Melbourne Australia. She is a graduate of the INSEAD (Singapore) program and spent four months at Kyoto University in 2019 as a visiting Professor.

Rebecca is most passionate about the importance of museum science and how it can improve our daily lives by “using the past to see the future” through enhanced understanding of our connection with nature, our ability to critically think and important applications such as conservation.

Carla Easter, Ph.D.

Smithsonian’s National Museum of Natural History, US, Broh-Kahn Weil Director of Education

Dr. Carla Easter is the Smithsonian’s National Museum of Natural History’s (NMNH) first Broh-Kahn Weil Director of Education, the leader of our Department of Education, Outreach and Visitor Experience. She leads the teams responsible for developing and deploying the museum’s digital and on-site educational and community programming, welcoming and engaging our visitors, and the operations of the live Insect Zoo, Butterfly Pavilion, and Q?rius, the Coralyn W. Whitney Science Education Center.



Carla has been a community advocate with more than 15 years of experience establishing and maintaining partnerships with local and national organizations and leading initiatives that promote the engagement of diverse communities in understanding science and its translation to health and society.

Prior to joining the museum, Carla served as chief of the Education and Community Involvement Branch of the National Human Genome Research Institute (NHGRI) at the National Institutes of Health. She previously also served as director of outreach for Washington University School of Medicine’s Genome Sequencing Center and as a research instructor in genetics and research associate in the department of Education where she explored the notions of science among secondary students.

Carla earned her bachelor’s degree in microbiology from the University of California, Los Angeles, her doctorate in biology with an emphasis on molecular genetics from the University of California, San Diego, and conducted post-doctoral research at Washington University School of Medicine in the department of Molecular Microbiology.

Speaker Talk Titles and Abstracts

Meghan Balk

Title: How do animals respond to a changing planet? Linking micro to macro processes to assess species' ability to persist.

Abstract: We live in a rapidly changing world; however, global change is not a new phenomena. Past global change has led to changes in species richness, biodiversity, and species distributions. During periods of environmental upheaval, species have essentially three options: to go extinct, move, or adapt. We can use the past as a series of natural experiments to understand how species have responded to past global change. A lot of research has focused on large-scale (macro) processes, such as the extinction of species and reorganization of communities in response to past climate change. Less is known about how species are able to persist despite environmental change. One way may be through phenotypic change. Species interact with and respond to their environment from the time they originate in a place until they go extinct. Natural variation in species' traits that may allow them to adapt - and persist - in situ during periods of change. Taking a within-lineage (micro) approach is useful to assess how species have - and can - respond to global change. Here, I will give three examples of the ways in which species have persisted during periods of change: how a small mammal responds to temperature change across 40,000 years; how a colonial invertebrate responds to changing habitats across 2.3 million years; and how a large shark responded to changes in prey resources across 11 million years. I will show that linking micro- and macro- processes can inform how species may respond to a changing world.

Sahas Barve

Title: Colorful puffy jackets: bird feathers on the world's highest mountains

Abstract: In the frigid Himalayas, feathers form an important insulating barrier against the cold for birds. Using a comparative study utilizing over 1700 specimens of 250 species at the NMNH, Sahas will explore the various plumage adaptations Himalayan birds have to stay warm. Feathers also play a role in mate attraction and camouflage. Sahas will further explore if highland birds show any tradeoffs between having bright colors that may make them attractive, versus those that keep warm.

Kayce Bell

Title: Charismatic microfauna: biodiversity exploration in chipmunk lice and their bacteria

Abstract: Natural history collections serve as vast troves of data for biodiversity research across spatial, temporal, and interaction scales. Coupling historic specimens with new specimens can leverage advances in genomic methods and lead to new insights about biodiversity. The 23 species of western North American chipmunks collectively host one species of *Hoplopleura* sucking louse and the single species of eastern chipmunk hosts a different species of *Hoplopleura*. However, an evolutionary tree generated using genomic data from recent and historic collections suggests that the two species are really a single species of *Hoplopleura* louse parasitizing both western and eastern chipmunks. Additionally, louse evolutionary relationships suggest that western and eastern chipmunks have interacted and shared parasites in the past, providing a new perspective on chipmunk biogeographic history. Similar to how parasites add perspective to chipmunk interactions, we can also learn about species associations by zooming in on louse endosymbiotic bacteria. While all sucking lice likely have endosymbiotic bacteria, the history of these associations is complex and suggests multiple losses and acquisitions throughout evolutionary time. Whole genome sequence data from chipmunk sucking lice included bacterial sequences and examination of those data led to the description of a new genus of endosymbiotic bacteria. These studies demonstrate that there are still many unexplored components of biodiversity and emphasize that natural history collections have an important role to play in these discoveries.

Bastian Bentlage

Title: Sedimentation impacts on corals in Guam's nearshore reefs

Abstract: Coastal development and poor land-use practices are a major cause of erosion and terrestrial runoff, leading to sedimentation that caused declines of near-shore coral reefs along Guam's southern shores. Species of *Porites* are among the few corals able to tolerate turbid waters and sedimentation. My lab employed a combination of in situ transcriptomics, symbiont metabarcoding, and microbiome genomics, with the aim of elucidating mechanisms that *Porites* and its symbionts employ when dealing with sedimentation stress. Our data suggest that *Porites* switch between energy generation pathways to facilitate survival when faced with sedimentation. For example, reduction of aerobic respiration-associated gene expression at sites with high chronic sedimentation suggests acclimation to hypoxic conditions. We further found that chronic sedimentation stress is linked to upregulation of genes with immune and cell-cell signaling functions, suggesting shifts in immune metabolism for survival. Algal (Symbiodiniaceae) endosymbiont community compositions remained relatively stable across a

sedimentation gradient, with *Caldocopium* C15 dominating across sites and seasons. Bacterial microbiome communities were dominated by coral-endosymbiotic species of *Parendozaicomonas*; increased runoff during the wet-season was associated with increased microbiome diversity. Interestingly, relative abundance of actinomycetes increased in *Porites* microbiomes during the wet-season. Actinomycetes are ubiquitous and a source of antimicrobial compounds. Our working hypothesis is that some actinomycetes are transported from degraded upstream soils to Guam's near-shore reefs, as a result of erosion. Degraded soils may promote the proliferation of antimicrobial resistance genes, which could negatively impact Guam's near-shore coral reef ecosystems exposed to such bacteria via runoff.

Ricardo Betancur

Title: Ecological transitions along the water column in marine fishes over deep time

Abstract: Macroevolution has traditionally been studied from the viewpoint of paleontology and paleobiology. However, the increasing availability of time-calibrated molecular trees has more recently fueled the development of novel approaches to studying diversification dynamics and morphological evolution over deep time. My presentation will cover research conducted in my lab, focusing on the implementation of robust phylogenetic trees and their subsequent use in phylogenetic comparative analyses. More specifically, this research focuses on how habitat transitions along the water column have shaped the macroevolutionary trajectory of multiple marine fish groups. Studies covered on these topics include examining how historical mass extinction events, such as the Cretaceous–Paleogene extinction (66 million years ago), have promoted lineage, ecological, and morphological diversification in association with newly released niches along the benthic-pelagic ecological axis. Additionally, they investigate how the repeated origin of water column forms in time and space has led to convergent evolution in body shapes, an outcome driven by deterministic factors. Lastly, while the more uniform water column theoretically provides fewer opportunities for diversification compared to the ecologically and structurally complex bottom habitats, I will present exceptions to this hypothesis, highlighting extraordinary radiations in pelagic habitats. All in all, this research underscores the importance of making robust phylogenetic inferences to address broader questions about macroevolutionary processes.

Manuela Dal Forno

Title: Preserving the Past, Exploring the Future: Insights from Historical Lichen Collections

Abstract: The global biodiversity crisis, stemming from climate change and the rapid loss of habitats, stands as one of our most pressing and immediate threats. Ecosystems at risk contain thousands of species, many of which have yet to

be discovered or fully characterized. Lichens, while ubiquitous, are among the traditionally understudied groups for which basic biodiversity knowledge is lacking. These complex symbiotic units are formed by a main fungal partner (mycobiont), a green algal and/or a cyanobacterial partner (photobiont), along with a diverse community of microorganisms. Lichens form an important and diverse biological assemblage that is present in most terrestrial ecosystems and represent a main nutritional strategy within Fungi. It is thus urgent to gain a broader understanding of how diverse lichens are and where most of their diversity might still be discovered. Fortunately, lichen specimens collected worldwide for centuries have been amassed by the millions in herbaria and are available for assessing species boundaries, geographical distributions, and phenotypic variation. These extensive collections not only serve as essential resources for traditional taxonomic studies but also hold immense potential for genetic research and as a roadmap to where future efforts should be concentrated. Utilizing basidiolichens as models, this presentation will focus on examples of how current methodologies can unlock additional data layers from historical specimens, enhancing the value of existing natural history collections.

Richie Hodel

Title: Machine learning applications with digitized herbarium specimens reveal the hybrid origin of the cherry/plum genus

Abstract: Understanding the responses of species to past environmental changes can help us infer how species' will respond to future climatic changes—which are now occurring at an unprecedented rate in Earth's history. Synthesis of biogeographic patterns across the Tree of Life has revealed that the vast majority of species and lineages are unable to develop the genomic and/or phenotypic traits necessary to move between radically different environments (e.g., transitioning between tropical and temperate biomes). It is imperative that we study the rare lineages that have been able to adapt to novel environments. One such group is the cherry/plum genus, *Prunus* (Rosaceae). This genus contains approximately 250-400 evergreen and deciduous species occurring in temperate and tropical regions. Recent phylogenetic analyses have identified three major groups within the genus, characterized by different inflorescence types.

Here, I present results from my Buck Fellowship project. We used 610 nuclear loci and plastid genomes generated via Hyb-Seq to resolve the phylogeny of *Prunus* using over 80 species representing all major clades and geographic regions of the genus. Analyses of discordance between gene trees and species trees, and comparisons of phylogenetic networks, provided several lines of evidence of a history of hybridization in *Prunus*. Using a novel machine learning approach that extracts morphological characters from digitized museum specimens, we detected

morphological evidence associated with a hybridization event that occurred over 50 million years ago. I discuss the implications of our phylogenetic and morphological results on the biogeographic diversification of this group.

Audrey Lin

Title: The History of Coast Salish ‘Woolly Dogs’ Revealed by Ancient Genomics and Indigenous Knowledge

Abstract: Prior to European colonization, Indigenous Coast Salish peoples in the Pacific Northwest traditionally raised a long-haired domestic dog breed to harvest its hair for weaving. The woolly dogs were a form of wealth and status, and blankets woven with dog hair were items of prestige. The decline of dog-hair weaving has been attributed to the introduction of machine-made blankets by British and American trading companies in the early 19th century, and these “woolly dogs” disappeared by the late 19th century. Coast Salish Elders and Knowledge Keepers reject the narrative that woolly dogs disappeared due to the introduction of cheap, machine-woven textiles. We analyzed the genome, isotopic signatures, and archival records of “Mutton,” the only known woolly dog pelt—collected in 1859—and contextualize these analytical approaches using ethnographic interviews to better understand the history, importance, and decline of these dogs. Genomic analyses reinforce the Indigenous North American origins of woolly dogs, demonstrate the careful reproductive isolation needed for the woolly phenotype, and provide insights to the genetic underpinnings of woolliness. Isotopic and archival evidence illustrates the final months of Mutton’s life with colonial naturalists. Traditional knowledge and family memories shared through ethnographic interviews underscore that deliberate persecution of Coast Salish people and culture through colonial government policies, and not simple economic forces, was largely responsible for the loss of woolly dogs. Altogether, we demonstrate how community-led research questions coupled with quantitative scientific methods contribute to reviving and reclaiming Coast Salish cultural traditions.

Maureen Turcatel

Title: Diversity and Evolutionary History of Horse Flies

Abstract: The family Tabanidae, commonly known as horse flies or deer flies, represents the largest group of bloodsucking insects, comprising approximately 4,400 species worldwide. The majority of adult females are blood-feeders, and some can be responsible for the mechanical transmission of parasites. While most species target large mammals for blood meals, a minority feed on reptiles or birds. Notably, horse flies also play a significant role as pollinators, with all males and some females exclusively feeding on nectar and pollen. Molecular evidence

strongly supports the monophyly of Tabanidae. However, traditional multi-locus methodologies proved largely inconclusive to reconstruct the relationships within certain major lineages of horse flies. Emerging next-generation sequencing techniques and phylogenomic methodologies, such as Ultraconserved Elements (UCE), hold promise for providing a more refined understanding of the evolutionary history of these flies. Preliminary findings from the assembly of the first high-quality genome of a horse fly are presented, alongside a brief overview of the largest collection of the Field Museum's largest collection: the Insects, Arachnids, and Myriapods collection.

Laura Waters

Title: Why are Earth's continents missing a layer?: A perspective from obsidians

Abstract: Earth's continents are stratified in SiO₂, where the lower portion of the crust has low-SiO₂ contents and the upper crust has intermediate-SiO₂ contents. The compositions of rocks formed in the crust resemble those erupted on Earth's surface, with the exception that high-SiO₂ rocks (i.e., rhyolites) are not commonly observed in the crust at subduction zones, despite their occurrence in large erupted volumes (i.e., 2,000 km³) in other tectonic settings. To understand why Earth's continents are missing a high-SiO₂ layer, we examine the solidification behavior (i.e., crystallization kinetics) of obsidians from Glass Mountain, CA. Obsidians are ideal samples to investigate the missing layer in Earth's crust, as they are compositional analogues for the missing crust and, yet, they were able to efficiently segregate from their crustal sources and slowly erupt (with abundant time to crystallize). We find that obsidians can erupt because they initiate ascent from fluid-undersaturated conditions and undergo a period of time during ascent above their liquidus (where no crystals exist). Super-liquidus conditions destroy nucleation sites, which inhibits crystal growth, facilitates eruption and the formation of glass. In contrast, high-SiO₂ melts in subduction zones form in fluid-saturated conditions. If the high-SiO₂ melts segregate and ascend in Earth's crust, they immediately and efficiently crystallize, owing to abundant nucleation sites. Hence, Earth is missing a high-SiO₂ layer in its continents because high-SiO₂ melts form in the presence of a fluid, which stabilizes nucleation sites and facilitates abundant crystal growth, preventing melts from efficiently segregating and forming high-SiO₂ batholiths at subduction zones.