

AMERICAN SOCIETY OF MAMMALOGISTS

93rd ANNUAL MEETING

Philadelphia Marriott Downtown • Philadelphia, Pennsylvania



ASM★2013
PHILADELPHIA

PROGRAM & ABSTRACTS

The 2013 American Society of Mammalogists Annual Meeting logo features a pronghorn, and the city of Philadelphia skyline with the Liberty Bell in the background. The logo was designed by Hadley Jerman, Graphic Designer at the Sam Noble Museum in Norman, Oklahoma.

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AMERICAN SOCIETY OF MAMMALOGISTS (ASM)

The American Society of Mammalogists (ASM) was established in 1919 for the purpose of promoting interest in the study of mammals.

An Overview—In addition to being among the most charismatic of animals, mammals are important in many disciplines from paleontology to ecology and evolution. We, of course, are mammals and thus are in the interesting position of studying ourselves in quest of a greater understanding of the role of mammals in the natural world.

The ASM is currently composed of thousands of members, many of who are professional scientists. Members of the Society have always had a strong interest in the public good, and this is reflected in their involvement in providing information for public policy, resources management, conservation, and education.

The Society hosts annual meetings and maintains several publications. The flagship publication is the *Journal of Mammalogy*, a journal produced 6 times per year that accepts submissions on all aspects of mammalogy. The ASM also publishes *Mammalian Species* (accounts of individual species) and *Special Publications* (books that pertain to specific taxa or topics), and we maintain a mammal images library that contains many exceptional photographs of mammals.

We encourage you to peruse the ASM web site for information about mammals and the American Society of Mammalogists. Check out our interesting history by clicking on the Our History tab on the Archives Committee page. We hope it will stimulate your interest in mammals and further your appreciation of their importance.

ASM Leadership—The ASM is led by a group of scientists who are elected by the membership.

ASM Committees—Much of the work that the ASM does is accomplished through a large number of volunteer committees. These committees work to further the aims of the Society and the science of mammalogy as a whole.

ASM Endorses Human Diversity—The ASM is dedicated to ensuring the opportunity for active, equal participation in all ASM functions by all members, regardless of gender, race, ethnic background, age, physical disabilities, or sexual orientation.

<http://www.mammalsociety.org/>

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WELCOME

Welcome to the 93rd annual meeting of the American Society of Mammalogists.

We have an exciting meeting planned for this year. The conference will feature a stimulating array of high-quality contributed papers and posters, as well as diverse symposia and special sessions. This year, we are pleased to present symposia on White-nose Syndrome in Bats, Ecological Niche Modeling, and Advances in Ungulate Biology, plus a special session on Mammalian Predator Control. Plenary sessions will feature student Honoraria and Fellowship recipients and the 2012 recipients of the ASM Grinnell, Merriam, and Leopold Awards. This year's distinguished assemblage of plenary speakers will include Dr. James H. Brown, Dr. James Estes, and Dr. Dean Biggins. We are honored to include featured presentations on climate change by Dr. James E. Hansen of the NASA Goddard Institute for Space Studies and ungulate biology by Professor Colin Groves of the Australian National University.

Workshops offer hands-on training useful in your research and career development. This year's meeting offers workshops on Geometric Morphometrics, High-throughput Sequencing, Ecological Niche Modeling, and How to Write a Successful NSF DDIG. We plan to make workshops a regular feature of future ASM meetings.

Opening night festivities will begin with mixers for students and new ASM members or first-time meeting attendees. Mentors will be available to provide an overview of the annual meeting and facilitate introductions between students and more senior ASM members throughout the meeting. Everyone attending an annual meeting should feel a welcome part of the ASM family.

This year, we will introduce prizes for the posters in each session voted as favorites. We hope you will enjoy the Gordon Kirkland Run for Research, which will follow the route run by Rocky Balboa, and a "picnic" at the Reading Terminal Market—a century-old public farmers' market with an old world, historic setting. Finally, we will honor and celebrate the achievements of our members, colleagues, and students at the banquet on the final night of the meeting, following the capstone symposium.

Help the ASM be all it can be! While you are here, volunteer to serve on a committee that interests you and attend a committee meeting. Offer to organize a symposium, special session, workshop or even host a future meeting. Offer ideas to officers or committee chairs on things we can do better. Participate in the post-conference survey. Or just enjoy great interactions with fellow mammalogists.

I hope that you enjoy all that Philadelphia—the City of Brotherly Love—has to offer and I look forward to seeing you at the 94th annual meeting in Oklahoma City.

Happy trails,

Edward J. Heske, President, American Society of Mammalogists

ACKNOWLEDGEMENTS

Program Committee:

Janet Braun (Chair)

Kaycee Bell

Brad Blood

Brandi Coyner

Meredith Hamilton

Lauren Helgen

David Leslie

Susan Loeb

Karen Mabry

Daniel Odell

Marcia Revelez

Margaret Schadler

Cody Thompson

Patrick A. Zollner

Hadley Jerman — Sam Noble Museum (2013 and 2014 logo designs)

Tony Ballard — Kansas State University Conference Planning Services

Following the conclusion of the meeting, be sure to stop by ASM's Registration Desk to drop off your badge and lanyard—ASM is striving to recycle as many meeting materials as possible.

SPONSOR LIST

DIAMOND SPONSOR — PRONGHORN



SILVER SPONSORS — SILVER-HAIRED BAT



Oklahoma Cooperative Fish and Wildlife Research Unit
Department of Natural Resource Ecology and Management
Oklahoma State University

BRONZE SPONSORS — KANGAROO RAT



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Oklahoma City
Convention & Visitors Bureau



H. Steven Logsdon — Wildlife Artist



Wildlife Materials, Inc.
1202 Walnut Street
Murphysboro, IL 62966 USA



Women of the Cloud Forest

CONTRIBUTORS

Anonymous



Tomahawk Live Traps^{llc}

LITERATURE



Royal Society **Publishing**
Biological Sciences

GENERAL MEETING INFORMATION

Meeting Room Information

Please turn off all beepers and cell phones or set them to manner mode (vibrate) during presentations,

Auction and Raffle — Franklin B
Banquet — Salon E
Board of Directors Meeting (Friday) — Salon AB
Board of Directors Meeting (Sunday) — Salon D
Capstone Symposium and Book Signing— Salon E
Committee Meetings — Conference Rooms 406-410, 411, 413
Donor Reception — Salon F
Exhibit Area — Franklin B
Featured Speaker — Salon E
Members Meetings — Salon E
New Members/Attendees Reception — Salon E
Officers and Plenary I Speakers Lunch — JW's
Opening Reception — Salon E
Oral Presentations — Salons A, B, C, E, F, IJ
Picnic — Reading Terminal Market
Plenary I — Salon E
Plenary II — Salon E
Poster Presentations — Franklin B
Refreshment Breaks — Franklin B
Registration — Franklin B Foyer
Run for Research —start from the Philadelphia Marriott Downtown, running the *Rocky* route
Poster Social — Franklin B
Pre-banquet Social — Salon F
Saturday Evening Social — The Field House (located at 1150 Filbert Street)
Student Mixer — JW's
Symposium I — Salon E
Symposium II — Salon E
Thematic Sessions I and II — Salon E
Workshop I — 410
Workshop II — 413
Workshop III — 411/412
Workshop IV — 411/412

Internet Access

Internet access is free to all ASM participants in public areas of the hotel, but not available in the conference area.

Registration Desk

The ASM Registration Desk, located at the Franklin B Foyer of the Philadelphia Marriott Downtown, will be open for registration from 7:00 a.m. – 11:00 p.m. Friday, 14 June, 7:00 a.m. – 5:00 p.m. Saturday, 15 June, and 7:00 a.m. – 5:00 p.m. Sunday, Monday, and Tuesday.

Business Center

The Business Center is open 24 hours for all hotel guests. The Philadelphia Marriott Downtown Business Center Desk can assist you with all your copying, shipping, and faxing needs.

Messages and Job Announcements

Message boards are located near the Registration Desk. Participants may post messages for friends and colleagues. The registration staff will also post telephone and other messages on these boards. Urgent messages should be directed to the Philadelphia Marriott Downtown (215) 625-2900. These will be relayed to meeting coordinators and posted for participants as soon as possible.

Job announcements or information about employment opportunities may be posted on the message boards as well.

Food and Beverage

Morning and afternoon refreshment breaks will be served in Franklin B.

Cash bars will be available during:

- Student Mixer, 5:00 – 6:00 p.m., Friday 14 June
- New Members/Attendees Reception, 6:00 – 6:30 p.m., Friday 14 June
- Opening Reception, 6:30 – 11:00 p.m., Friday 14 June
- Saturday Evening Social, 7:30 – 10:30 p.m., Saturday 15 June at The Field House
- Picnic, 6:30 – 9:30 p.m., Sunday 16 June
- Poster Session II, 7:00 – 9:00 p.m., Monday 17 June
- Auction, 9:00 – 11:00 p.m., Monday 17 June
- Donor Reception, 5:30 – 6:00 p.m., Tuesday 18 June
- Pre-banquet Social, 6:00 – 7:00 p.m., Tuesday 18 June
- Banquet, 7:00 – 9:00 p.m., Tuesday 18 June

Lunch is on your own each day. A number of restaurants, from casual to fine dining, are available on-site or nearby. A list of local restaurants is listed on page 141.

Name Badge Color Scheme

- Award Recipient – White
- Board of Directors – Emerald Green
- Committee Chair – Royal Blue
- Editor – Royal Blue
- Honorary Member – Emerald Green
- Past President – Black
- President – Emerald Green
- President Elect – Emerald Green
- Program Committee – Red
- Recording Secretary – Emerald Green
- Secretary Treasurer – Emerald Green
- Sponsors – Turquoise
- Trustee – Emerald Green
- Vice President – Emerald Green

15th Annual Gordon L. Kirkland Memorial Run/Walk for Research

Monday, 17 June

Race Starts: 6:00 a.m.

Start Location: Philadelphia Marriott Downtown

Race Course: Rocky Balboa's famous route

Length: 5K run or 2K run/walk—Maps will be provided

Sign-up: Register on-line or during Registration hours at the Registration Desk

Entry Fee: \$20 (no t-shirt); \$35 (includes t-shirt)

All proceeds go to the American Society of Mammalogists (ASM) – Future Mammalogists Fund, which provides research grants to undergraduate and graduate student members.

PRESENTATION INFORMATION

Oral Presenters

Oral presentations will be allotted 12 min for the talk and 3 min for questions. Please bring your presentation to the assigned session at least 15 min prior to the start of your session on a USB Flash “thumb” drive or a CD. The computers used for presentations will *not* have internet access. Laser pointers will be available.

Your presentation must be created in, or converted to, Microsoft’s PowerPoint program. The computers in the session rooms will be Windows based PCs (Windows 7) with Microsoft Office 2010. It is recommended that all image and video files be saved into a folder with your PowerPoint file on a USB Flash “thumb” drive or a CD in the event that there are problems when you review your presentation. PowerPoint files created on Macintosh computers should be previewed on a PC to ensure cross-platform compatibility.

Session moderators have been designated to facilitate each session. The names of the moderators are noted in the session schedule. Moderators will be provided a packet of instructions when checking in at the Registration Desk.

Poster Presenters

Poster session dates and times are as follows:

Poster Session I: Sunday, 16 June 4:00 – 5:30 p.m.
Poster Session II: Monday, 17 June 7:00 – 9:00 p.m.

At least one author must be present during the entire poster session time period.

Poster Size—Poster boards (4' high and 4' long) [1.2 m high by 1.2 m wide] and pushpin or Velcro attachments will be provided.

Poster Board Assignments—All poster boards will be numbered. Because some posters are being evaluated, please make sure that you place your poster in the correct location.

Poster Board Set-up and Take-down—Posters will be available for viewing during the entire meeting. You can place your poster on your assigned board beginning 8:00 a.m. Saturday, 15 June; all posters must be in place by the 3:30 p.m., Sunday 16 June. Your poster must be removed by the end of the conference. If your poster is not removed or claimed by 5:00 p.m. on Tuesday, 18 June, it will be discarded.

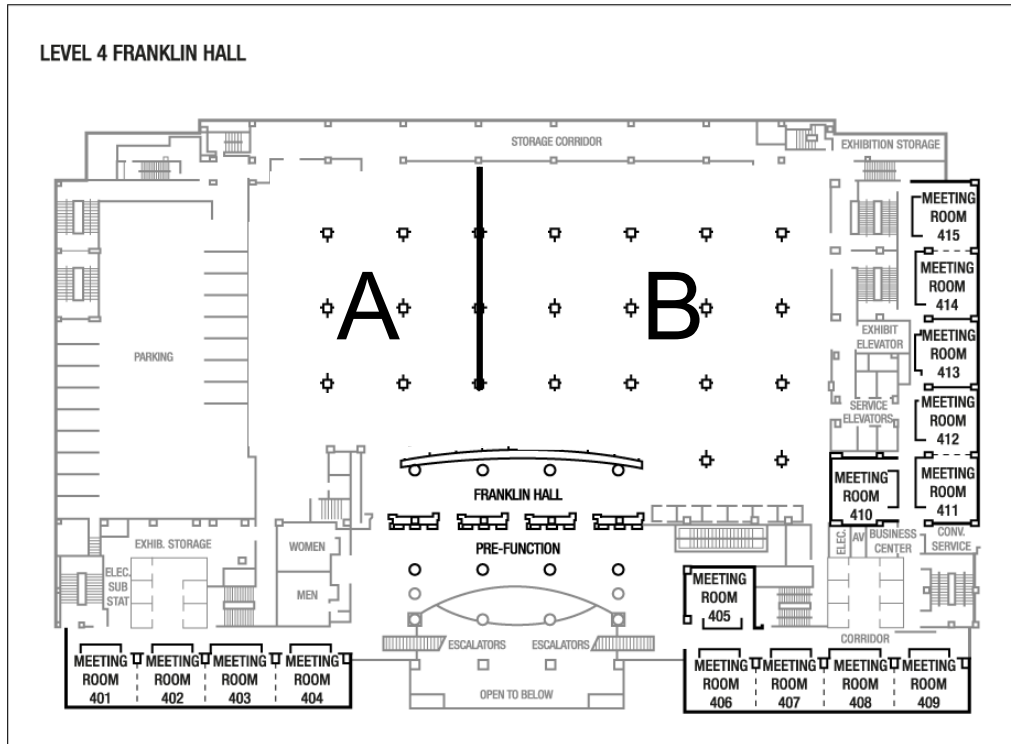
F1000 Posters!

Consider extending the life of your presentation by depositing it in the open access repository—F1000 Posters! Go to <http://f1000.com/posters/fordepositors> for information. Upload your file and maximize the value of your conference presentations.

EXHIBITORS

Exhibitors are located in Franklin B of the Philadelphia Marriott Downtown during following hours:

Saturday, 15 June	8:00 a.m. – 5:30 p.m.
Sunday, 16 June	8:00 a.m. – 5:30 p.m.
Monday, 17 June	8:00 a.m. – 5:00 p.m., and 6:30 – 9:00 p.m.
Tuesday, 18 June	8:00 a.m. – 1:30 p.m.



Allen Press provides the most comprehensive offering of integrated services for scholarly journal and special interest publication production.

Northeast Natural History & Supply Co. is a provider of new, used, and antiquarian books, monographs, and journals on all disciplines of natural history, as well as a distributor of archival museum specimen trays designed for museum, institution, or personal collections.

North Star Science and Technology provides tracking, two-way monitoring, and messaging/data collection services via satellite and GSM.

Oklahoma City Convention & Visitors Bureau is the official Tourism Promotion Agency for Oklahoma City.

Reconyx is known worldwide as the industry leader in digital infrared game cameras.

Research and Testing Laboratory offers services in the evaluation of microbial diversity, sequencing, bioinformatics, and biostatistics.

Steve Logsdon/Wildlife Artist specializes in quality wildlife jewelry and t-shirts.

The Johns Hopkins University Press publishes books, journals, and online collections for students, professionals, and general readers.

Wildlife Materials, Inc. manufactures radio telemetry equipment that has benefited wildlife and fishery researchers, helped recover valuable hunting dogs and falcons, assisted 911 rescue teams, and assisted numerous professional care facilities around the world.

Women of the Cloud Forest, a Fair Trade project, supplies rainforest seed jewelry from Costa Rica and hand-embroidered bags from Costa Rica with color reproductions of North and Central American species.

Literature Only—Advanced Telemetry Systems provides researchers with animal tracking and monitoring products of the highest quality and reliability. **Royal Society Publishing**, the publishing division of the Royal Society, informs the science of the future via its 9 journals. **Tomahawk Live Trap** offers hundreds of animal and pest control products used by professionals,

SOCIAL EVENTS

Thursday, 13 June – 6:00 p.m.
Board of Directors Dinner

Friday, 14 June – 5:00 – 6:00 p.m.
Student Mixer – JW's

All student members of the ASM are welcome to come and socialize with your friends and colleagues, and meet new student members. Enjoy a great selection of complimentary light hors d'oeuvres and a cash bar. The Student Mixer is hosted by the Education and Graduate Students Committee.

Friday, 14 June – 6:00 – 6:30 p.m.
New Members/Attendees Reception – Salon E

Members who have recently joined the ASM or are attending their first meeting are invited to this New Member/Attendees Reception to meet ASM members and other new members. Even if this isn't your first time to an ASM Annual Meeting or you are not a new member, feel free to stop by and welcome new members and new meeting attendees. Enjoy a great selection of complimentary light hors d'oeuvres and a cash bar. The New Member/Attendee Reception is hosted by the Membership Committee.

Friday, 14 June – 6:30 – 11:00 p.m.
Opening Reception – Salon E

Attendees will kick off the conference with an opening night reception. Enjoy the opportunity to socialize with friends, colleagues, and other conference attendees, and meet our 2013 exhibitors. Enjoy a great selection of complimentary light hors d'oeuvres and a cash bar.

Saturday, 15 June – 12:30 – 2:00 p.m.
ASM Officers and Plenary Session I Speakers Lunch – JW's

The ASM officers invite the speakers from Plenary Session I to an informal lunch in honor of their awards.

Saturday, 15 June – 7:30 – 10:30 p.m.
Saturday Evening Social – The Field House (located at 1150 Filbert Street)

Socialize with other conference attendees at The Field House, one of Philadelphia's largest sports bars. Enjoy complimentary light hors d'oeuvres and drinks; a cash bar also will be available.

Sunday, 16 June – 6:30 – 9:30 p.m.
Picnic – Reading Terminal Market

Join your friends and colleagues at the picnic at the Reading Terminal Market—a century-old public farmers' market with an old world, historic setting. The Market and its merchants are not only committed to deliciously prepared foods, but to local farming communities, a healthy environment, and sustainable agriculture. A cash bar will be available.

Monday, 17 June – 7:00-9:00 p.m.
Poster Session Social – Franklin B

The Monday night poster session will include an evening social, poster awards, and raffle. What a great opportunity to discuss research with poster presenters and socialize with your colleagues. The social will offer a great selection of complimentary light hors d'oeuvres and a cash bar.

Monday, 17 June – 9:00-11:00 p.m.
Auction and Raffle – Franklin B

Continue your socializing and support the ASM's Future Mammalogists Fund through donating to and purchasing from the auction! The Auction will follow the Poster Session Social.

Tuesday, 18 June – 5:30 – 6:00 p.m.

Donor Reception – Salon F

In appreciation and recognition of the generosity of those who donated to the ASM in 2012, the society invites all 2012 donors to a reception hosted by the Development Committee. Donor contribution(s) enhance the vitality of the society and support the careers of the next generation of mammalogists—our students and young professionals. We thank you for your generosity and hope to see you at the reception. Complimentary light hors d'oeuvres and a cash bar will be provided.

Tuesday, 18 June – 6:00 – 7:00 p.m.

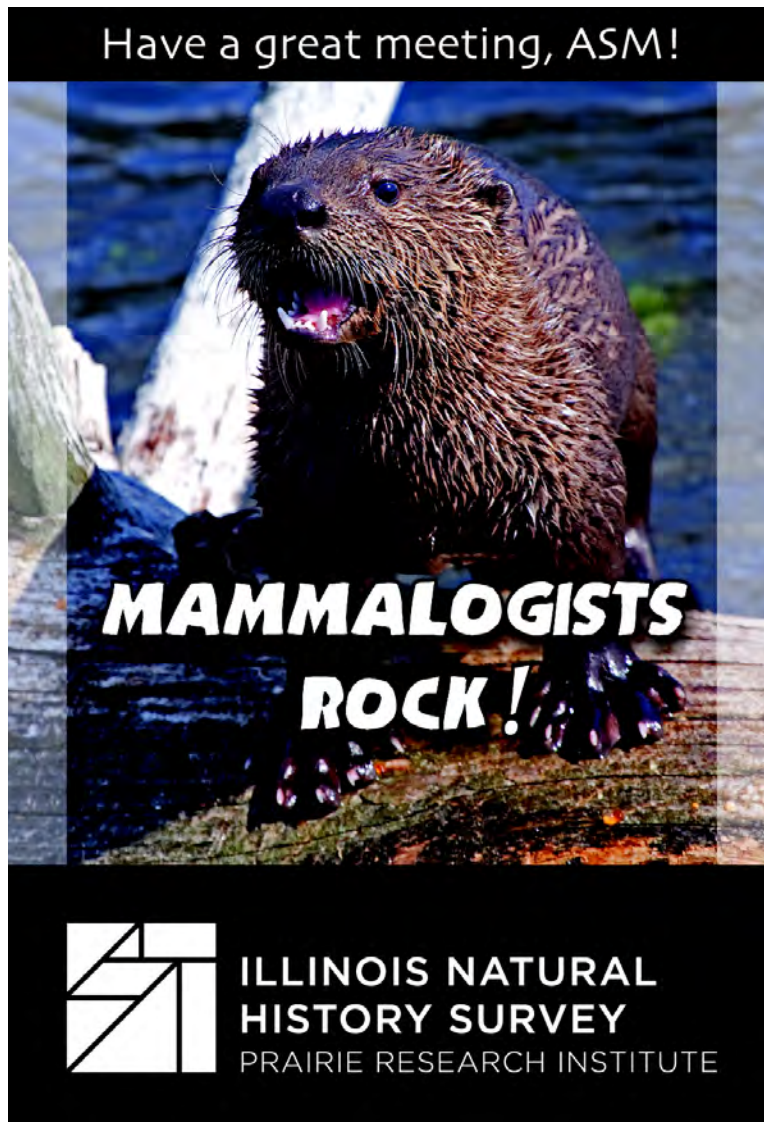
Pre-Banquet Social - Salon F

This is your invitation to meet and socialize with colleagues with complimentary light hors d'oeuvres and a cash bar at the Pre-Banquet Social Hour.

Tuesday, 18 June – 7:00 – 9:00 p.m.

Banquet – Salon E

Join us at the Annual Banquet where ASM members and friends recognize and honor a few of their own during this awards presentation. Unwind, socialize, and say good-byes at this conclusion to a great week. Dinner and a cash bar will be provided.



FEATURED SPEAKER

Dr. James Hansen

Monday, 17 June — 8:30 – 9:30 a.m., Salon E

A special presentation by, featured speaker Dr. James Hansen, NASA Goddard Institute for Space Studies and Adjunct Professor of Earth and Environmental Sciences at Columbia University, will highlight the annual meeting. Dr. Hansen's research interests are broad and include radiative transfer in planetary atmospheres, especially interpreting remote sounding of the earth's atmosphere and surface from satellites. His development and use of global climate models has contributed to the further understanding of the Earth's climate. Dr. Hansen is well known for his research in the field of climatology, his testimony on climate change to congressional committees in 1988 that helped raise awareness of global warming, and his advocacy of action to avoid dangerous climate change. In recent years, Dr. Hansen has become an activist for action to mitigate the effects of climate change.

CAPSTONE SYMPOSIUM: UNGULATES TODAY

Professor Colin Peter Groves, Keynote Speaker

Tuesday, 18 June — 1:30 – 3:30 p.m., Salon E

The keynote speaker for the capstone symposium, *Ungulates Today*, is Professor Colin P. Groves with the Bioanthropology Program at the Australian National University, who is the author of our new worldview of the taxonomy of ungulates and primates. Professor Groves' application of the phylogenetic species concept to these groups has greatly expanded the number of known species and the challenges facing their conservation. Four other invited speakers will lead up to Professor Groves' capstone talk and explore contemporary topics such as ecological determinants of ungulate breeding strategies, conservation genetics, recovery strategies and captive breeding of the most imperiled ungulates, and impacts of climate change on ungulates past and present.

A book signing will immediately follow the symposium. Copies of *Ungulate Taxonomy* may be purchased at The Johns Hopkins University Press sponsor table.

PLENARY II

Sunday, 16 June — 8:00 – 10:30 a.m., Salon E

Dr. James H. Brown, Joseph Grinnell Awardee

The 2012 recipient of the Joseph Grinnell Award is Dr. James H. Brown, Distinguished Professor of Biology at the University of New Mexico, Albuquerque. During his long and productive career, he has mentored over 50 PhD students and 20 Postdoctoral Fellows. He has helped establish and promote the careers of numerous women in science as well as those of many international scholars. At the core of his success in mentoring and many of his scientific accomplishments is his continued demonstration that mammals are model organisms in the study of community ecology, biogeography and macroecology. His boundless enthusiasm for science and the study of mammals has inspired countless undergraduate and graduate students who, themselves, are now inspiring the next generation of mammalogists.

Dr. Dean E. Biggins, Aldo Leopold Awardee

The 2012 recipient of the Aldo Leopold Award is Dr. Dean Biggins, of the US Geological Service in Colorado. The black-footed ferret would likely be extinct or in a few zoos if it were not for Dr. Biggins, but today black-footed ferrets have been reintroduced into 8 US states, Mexico and Canada. He pioneered new methods in captive breeding, mitigating pathogens, measuring prairie dog populations, and determining suitable habitat for reintroduction in the wild. Although best known for his 30 years of conservation research on this secretive mustelid, his contributions to conservation also extend across the North American prairie ecosystem to Asia and include a wide range of species.

Dr. James A. Estes, C. Hart Merriam Awardee

The 2012 recipient of the Merriam award is Dr. James Estes from the University of California, Santa Cruz and USGS. A pioneer in the study of marine communities, his insights have strongly influenced theories of community functioning, predator-prey relationships, the role of apex predators, and the evolution of food webs. He is the leading expert in the biology of sea otters and impacts of apex predators on ecosystems. His research on trophic cascades has been a driving force for 30 years in the field of community ecology. His work on sea otters and kelp forest systems provides evidence for the importance of top predators in healthy ecosystems. He has been the leading scientific voice in promoting the recovery of the southern sea otter from near extinction.

SYMPOSIA

White-nose Syndrome: A Deadly Disease of North American Hibernating Bats

Organizer: Dr. DeeAnn Reeder

Saturday, 15 June — 2:00 – 4:00 p.m., Salon E

This symposium will review the current state of knowledge regarding WNS in a way that is informative to professional mammalogists. The symposium will advance research and management of this devastating disease in bats through communication, facilitated discussion, and collaboration.

Ecological Niche Modeling: Concepts, Applications, Challenges, and Solutions

Organizers: Drs. Mariano Soley-G. and Robert Anderson

Sunday, 16 June — 1:30 – 3:30 p.m., Salon E

The field of ecological niche modeling (ENM, and associated species distributional modeling) has undergone a remarkable advance during the last decade. Indeed, these techniques have been applied to a diverse set of fields and research agendas, ranging from biological inventories, biogeography, and conservation, to assessments of invasion risk and diseases. This symposium will present a broad overview of ecological niche modeling and its wide range of exciting applications, highlighting along the way its assumptions, challenges, potential pitfalls and ways to overcome them.

WORKSHOPS

Geometric Morphometrics

Presenter: David Sheets

Friday, 14 June — 9:00 a.m. – 5:00 p.m., 410

A desire to quantify long term evolutionary trends in fossil lineages led presenter Dr. David Sheets to learn and contribute to the rapidly growing set of statistical techniques for addressing hypotheses about the shapes of organisms known as Geometric Morphometrics. These approaches allow us to address a wide range of questions about the morphology of a wide range of organisms and structures, leading to applications in biology, anthropology, paleobiology and forensics. The workshop will be an introduction to these methods, with an emphasis on hands-on experience with the software and methods used.

How to Write a Successful DDIG NSF Proposal

Presenter: Michael R. Willig

Friday, 14 June — 1:00 – 3:00 p. m., 413 (Part I), 3:30 – 5:00 p. m., 413 (Part II)

ASM is excited to offer 2 workshops on writing successful grant proposals. While the workshops will focus on NSF's Doctoral Dissertation Improvement Grants (DDIG), you can pick up useful tips for writing any scientific grant proposal. Dr. Michael Willig spent 6 years at the National Science Foundation, first as Program Director for the Ecological Studies Cluster, then as Director of the Division of Environmental Biology. Part I will address topics such as the purpose of the DDIGs, tips for writing successful proposals, and the review process for submitted proposals. Part II will be a hands-on intensive writing workshop using excerpts from attendees' DDIG proposals (new or declined) to demonstrate how text can be improved based on tips given in Part I of the workshop.

High-throughput Sequencing (HTS)

Presenter: Sonal Singhal

Sunday, 16 June — 1:00 – 4:00 p.m., 411/ 412

High-throughput sequencing (HTS) is transforming the way that genetic data are collected and analyzed. Like allozymes and polymerase chain reaction (PCR) before it, HTS has revolutionized the biomedical sciences; with ever-decreasing prices and ever-increasing read lengths, HTS is now poised to do the same for those working with non-model organisms. HTS will become the new standard for collecting sequencing data; as such, it is important that researchers understand the power and limitations of this technology. In this workshop, the basics of this technology will be outlined through general information sharing and hands-on tutorials. The workshop will end with group discussions on how this technology can be used to facilitate the research programs of attendees.

Ecological Niche Modeling

Presenters: Robert P. Anderson, Mariano Soley-G., and Robert Boria

Sunday, 16 June — 4:30 – 5:30 p.m., 411/412

The techniques of ecological niche modeling (ENM, and associated species distributional modeling) have been applied to a diverse set of fields and research agendas, ranging from biological inventories, biogeography, and conservation, to assessments of invasion risk and diseases. This workshop will provide an opportunity to learn basic procedures of data management, analysis, and interpretation.

BOARD OF DIRECTORS, MEMBERS, AND COMMITTEE MEETINGS

All meeting rooms listed below are located in the Philadelphia Marriott Downtown.

Friday, 14 June

8:00 a.m. – 5:00 p.m. Board of Directors Meeting – Salon AB (refreshments and lunch provided)

Saturday, 15 June

11:15 a.m. – 12:30 p.m. Members Meeting – Salon E
Noon Mammal Images Library Committee – 407
Noon Honorary and Travel Awards Committee – 408
Noon Public Education Committee – 409
12:30 – 2:00 p.m. Publications Committee – 406
12:30 – 2:00 p.m. Conservation Committee – 413
1:30 – 2:00 p.m. Conservation Awards Committee – 410
4:00 p.m. Development Committee – 406
4:00 p.m. Program Committee – 407
7:00 p.m. Human Diversity Committee – Salon E

Sunday, 16 June

11:00 a.m. – 12:30 p.m. Members Meeting – Salon E
12:30 – 1:30 p.m. Education and Graduate Students Committee – 407
Noon Systematic Collections Committee – 408
Noon Animal Care and Use Committee – 409
1:30 – 3:00 p.m. Board of Directors Meeting – Salon D (lunch not provided)
2:00 p.m. Grants-in-Aid Committee – 406

Monday, 17 June

9:30 – 10:30 a.m. Nomenclature Committee – 407
10:00 a.m. Informatics Committee – 408
Noon Public Education Committee – 408
Noon Membership Committee – 409
12:30 – 1:30 p.m. Publications Committee – 407
4:00 p.m. International Relations Committee – 407
4:00 p.m. Development Committee – 408

Committees Not Scheduled to Meet

Archives Committee
Grinnell Award Committee
Jackson Award Committee
Latin American Fellowship Committee
Legislation and Regulations Committee
Marine Mammals
Office of Ombudsperson

PROGRAM AT-A-GLANCE

	Room	Saturday 15 June	Sunday 16 June	Monday 17 June	Tuesday 18 June
AM	Salon A			TS3 Evolutionary Biology	
	Salon B			TS4 Population Ecology	
	Salon C			TS5 Behavior	
	Salon E	Plenary I Members Meeting	Plenary II Members Meeting	Featured Speaker TS6 Biogeography, Community Ecology, and Conservation	Thematic Session II TS15 Systematics and Biogeography: Old World Mammals
	Salon F				TS16 White-nose Syndrome and Wildlife Disease
	Salon IJ				TS17 Community Ecology
PM	Salon A		TS1 Natural History, Outreach, and Education	TS7 Systematics and Biogeography: New World Mammals TS11 (TS7 cont.)	
	Salon B		TS2 Morphology	TS8 Disturbance Ecology TS12 Urban and Disturbance Ecology	
	Salon C			TS9 Physiology and Community Ecology TS13 Population Ecology	
	Salon D		Board of Directors Meeting		
	Salon E	Symposium I Thematic Session I	Symposium II	TS10 Conservation Genetics: Carnivores TS14 Conservation Genetics	Capstone Symposium and Book Signing
	Franklin B		Poster Session I		
	411/412		Workshop III Workshop IV		
EVE	Salon E				Banquet
	Salon F				Donor Reception Pre-Banquet Social
	Franklin B			Poster Session II Raffle Auction	
	Reading Terminal Market		Picnic		
	The Field House	Saturday Evening Social			

American Society of Mammalogists 93rd Annual Meeting—Philadelphia, Pennsylvania

SATURDAY, 15 JUNE, MORNING SESSION

Plenary I - Salon E

- 8:00 AM** **Welcome and Announcements**
President Edward J Heske
- 8:15 AM** **Annie M. Alexander Award**
1^E Phylogeography of a Holarctic Rodent (*Clethrionomys rutilus*): Testing High-latitude Biogeographic Hypotheses and the Dynamics of Range Shifts
B A Kohli, V B Fedorov, E Waltari, J A Cook
- 8:30 AM** **Anna M. Jackson Award**
2^{E**} Range-wide Phylogeography of a Widespread, Specialist Carnivore, the American Badger
E M Kierepka, E K Latch
- 8:50 AM** **Elmer C. Birney Award**
3^{E**} Plant Defenses and Prey Behavior Mediate a Trophic Cascade in East Africa
A T Ford, J R Goheen
- 9:10 AM** **A. Brazier Howell Award**
4^E Using Biogeographic History to Inform Conservation: The Case of Preble's Meadow Jumping Mouse
J L Malaney
- 9:30 AM** **Albert R. and Alma Shadle Award**
5^{E**} Mammals from Andean Cloud Forest: Studies on Diversity, New Species and Biogeographic Origins
C Miguel Pinto
- 10:00 AM** **ASM Fellowship**
6^{E**} Linking Climate to Behavior and Fitness of Endotherms: A Bioenergetic Approach
Ryan A Long, R Terry Bowyer, John G Kie, Warren P Porter
- 10:30 AM** **Closing and Announcements**
President Edward J Heske

10:45 AM	BREAK – Franklin B
11:15 AM	MEMBERS MEETING – Salon E
12:30 PM	OFFICERS AND PLENARY I SPEAKERS LUNCH – JW's
12:30 PM	LUNCH

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American Society of Mammalogists 93rd Annual Meeting—Philadelphia, Pennsylvania

SATURDAY, 15 JUNE, AFTERNOON SESSIONS

Symposium I - Salon E

White-nose Syndrome: A Deadly Disease of North American Hibernating Bats - Moderator: D M Reeder

- 2:00 PM Welcome and Introduction
D M Reeder
- 2:05 PM 7 Status of the Response to White-nose Syndrome
J T H Coleman, J S Johnson
- 2:25 PM 8 Chilled Chiropterans as Fungal Fodder: Why *Geomyces destructans* is Killing North American Bats
J Lorch, D Lindner, C Meteyer, L Muller, M Verant, D Blehert
- 2:45 PM 9 Immune Responses to Infection By *Geomyces destructans* Vary Between Species Exhibiting Differential White-nose Syndrome Population Declines
M S Moore, K A Field, G G Turner, M E Furze, D W F Stern, P R Allegra, S A Brownlee, C D Musante, M E Vodzak, M E Biron, M B Meierhofer, D M Reeder
- 3:05 PM 10 Patterns of *Geomyces destructans* Infection Across North America
W F Frick, T Cheng, K Langwig, K Drees, A Janicki, G McCracken, J Foster, A M Kilpatrick
- 3:25 AM Discussion and Concluding Remarks
D M Reeder, W F Frick, J S Johnson, J Lorch, M S Moore

4:00 PM	BREAK – Fanklin B
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Thematic Session I -Salon E

Recent Advances in Mammalogy - Moderator: Ryan Long

- 4:30 PM 11 Evolution in the Anthropocene: Landscape Genomics of White-footed Mice Along an Urban-to-Rural Gradient
J Munshi-South
- 5:00 PM 12^T Trophic Cascades and Infectious Disease
T Levi, F Keesing, A M Kilpatrick, M Mangel, C C Wilmers, R S Ostfeld
- 5:30 PM 13 Ecological Effects of the Loss of Large Mammals in African Savanna Ecosystems
F Keesing

6:00 PM	DINNER
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7:30 PM	SOCIAL – The Field House – 1150- Filbert Street
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American Society of Mammalogists 93rd Annual Meeting—Philadelphia, Pennsylvania

SUNDAY, 16 JUNE, MORNING SESSION

Plenary II - Salon E

- 8:00 AM** **Welcome and Announcements**
President-Elect Eileen Lacey
- 8:00 AM** **Joseph Grinnell Award**
14 How to Train a Scientist?
J H Brown
- 8:45 AM** **Aldo Leopold Award**
15 Black-footed Ferret Conservation: A Mix of Scientific Investigation and Operational Tasks
D E Biggins
- 9:30 AM** **C Hart Merriam Award**
16 Sea Otters and Kelp Forests: An Ecological History of the North Pacific Ocean
J A Estes
- 10:15 AM** **Closing and Announcements**
President-Elect Eileen Lacey

10:30 PM	BREAK – Fanklin B
11:00 AM	MEMBERS MEETING – Salon E
12:30 PM	LUNCH
1:00 PM	WORKSHOP: HIGH-THROUGHPUT SEQUENCING (HTS) – 411/412
1:30 PM	BOARD OF DIRECTORS MEETINGS – Salon D
1:30 PM	TECHNICAL SESSIONS 1 and 2 – Salon A and Salon B
1:30 PM	SYMPOSIUM II – ECOLOGICAL NICHE MODELING: CONCEPTS, APPLICATIONS, CHALLENGES, AND SOLUTIONS

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SUNDAY, 16 JUNE, AFTERNOON SESSION

Symposium II - Salon E

Ecological Niche Modeling: Concepts, Applications, Challenges, and Solutions - Moderator: M Soley-Guardia

- 1:30 PM** Welcome and Introduction
M Soley-Guardia
- 1:35 PM** 17 Ecological Niche Modeling: Theory, Reality, and Room for Improvement
R P Anderson
- 2:05 PM** 18 Determining Whether Peninsular Populations of Rodents Inhabit Novel Climatic Conditions in Northern South America, by Using Optimally Complex and Habitat-informed Ecological Niche Models
M Soley-Guardia
- 2:25 PM** 19 Testing the Predicted Geographic Pattern of Competitive Exclusion in Two Species of the Marsupial Genus *Marmosa*
E E Gutiérrez
- 2:45 PM** 20** Using Phylogeographic Data to Test Biological Hypotheses Generated by ENMs
T Jezkova
- 3:05 AM** 21 Incorporating Model Uncertainty in Ecological Niche Models to Predict Future Species Distribution and Contact Dynamics: A Case Study Using *Sorex cinereus* and *S. ugyunak* In Alaska
E Waltari
- 3:25 AM** Discussion and Concluding Remarks
R Anderson, E Gutiérrez, T Jezkova, M Soley-Guardia, E Waltari

3:30 PM	BREAK – Fanklin B
4:00 PM	POSTER SESSION I – Franklin B
4:30 PM	WORKSHOP: ECOLOGICAL NICHE MODELING – 411/412
6:30 PM	PICNIC – Reading Terminal Market

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American Society of Mammalogists 93rd Annual Meeting—Philadelphia, Pennsylvania

SUNDAY, 16 JUNE, AFTERNOON SESSIONS

ROOM		Salon A		Salon B
SESSION/SYMPOSIUM		Technical Session 1: Natural History, Outreach, and Education		Technical Session 2: Morphology
MODERATOR		Rodrigo Medellin		Frank Fish
1:30 PM	22	<u>D Schmidly</u>	29 ^E	<u>H Ahrens</u>
		The Life and Career of Vernon Bailey: America's Greatest Field Naturalist-Mammalogist		Quantification of Olfactory Bulb Shape and Patterns of Brain Shape Variation in Procyonidae
1:45 PM	23	<u>N Woodman</u>	30	<u>F Fish, P Weber, L Howle, M Murray, J Reidenberg</u>
		Rafinesque's Apocryphal Western Mammals: Why the Type Localities of the Mule Deer (<i>Odocoileus hemionus</i>) and the Long tailed Deer (<i>Odocoileus virginianus macrotus</i>) Are Not Where We Thought They Were		Association of Flipper Morphology and Hydrodynamics with the Maneuvering Ecology of Large Whales
2:00 PM	24	<u>J Ososky</u>	31 ^{E,T}	<u>K Jones, A Goswami, C Ruff</u>
		True Stories from the Archives: The Emergence of Modern Marine Mammal Science During the Era of Smithsonian Curator Frederick W. True		Seals, Skulls, and Sexual Dimorphism
2:15 PM	25	<u>R Hoyt, J Hart</u>	32	<u>B Alhajeri, J Schenk, S Steppan</u>
		Mammal Technical Committee of the Pennsylvania Biological Survey: Triumphs and Challenges		Ecological Correlates of Morphological Variation in the Tympanic Bulla of Gerbils (Rodentia, Gerbillinae): Testing the Influence of Phylogeny, Adaptation, and Drift
2:30 PM	26	<u>R Medellin, L Aguirre, B Rodriguez</u>	33 ^E	<u>S Rhodig, L Ruedas</u>
		The Latin American Network for Bat Conservation		Functional Anatomy of Mammalian Carnivores: Ecological Role of the Sagittal Crest in Mastication and Bite Force
2:45 PM	27	<u>R Kays, R Costello, W McShea, T Forrester, M Baker, A Parsons, R Montgomery, J Millspaugh</u>	34 ^E	<u>B McLean, J Cook</u>
		eMammal - Citizen Science Camera Trapping as a Solution For Broad-scale, Long-term Monitoring of Wildlife Populations		New Geometric Morphometric Methods for Taxonomic Identification of Fossil Ground Squirrels (Rodentia: Marmotini)
3:00 PM	28	<u>M Grigione, D Farkas</u>	35C	<u>K Monteith, R Long, V Bleich, J Heffelfinger, P Krausman, T Bowyer²</u>
		Integrating Carnivore Research, Technology, Field Experience and Collaboration in the Undergraduate Biology Curriculum		Effects of Harvest, Culture, and Climate on Trends in Size of Horn-like Structures in Trophy Ungulates

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SUNDAY, 16 JUNE, AFTERNOON SESSIONS

ROOM		Salon A		Salon B
SESSION/SYMPOSIUM		Technical Session 1: Natural History, Outreach, and Education		Technical Session 2: Morphology
MODERATOR		Rodrigo Medellin		Frank Fish
3:15 PM	28/257	<u>D Garneau</u> , E Settevendemio, K Juneau, K Podwirny	35/255 ^E	<u>W Ary</u> , T Cranford, P Krysl, A Berta
		Monitoring Wildlife Using Smartphones: The Role of Mobile Devices in Research and the Classroom		Structure and Function of the Tympanoperiotic Complex in Odontocete Cetaceans
3:30 PM		BREAK – Franklin B		
4:00 PM		POSTER SESSION I – Franklin B		
4:30 PM		WORKSHOP: ECOLOGICAL NICHE MODELING – 411/412		
6:30 PM		PICNIC – Reading Terminal Market		

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SUNDAY, 16 JUNE, POSTER SESSION I

	PRESENTER (S)	TITLE
36 ^E	<u>McGinnis</u> , Sewall	Fungal Diseases of Mammals and Other Wildlife Species: Factors Influencing Disease Dynamics and Host Mortality
37C	<u>Soria</u>	Role of Mammalian Species as Hosts for <i>Trypanosoma cruzi</i>
38	<u>Stamper</u> , <u>Dick</u>	Evaluating Host Specificity Assessments of Bat Flies (Diptera: Streblidae) from Ecuador
39	<u>Morano</u> , <u>Stewart</u> , <u>Wolff</u> , <u>Wasley</u>	Habitat Use of Mule Deer on Agricultural Lands: Implications for Survival and Reproduction
40 ^E	<u>Hodge</u> , <u>Arbogast</u>	Biogeographic Patterns, Life-history Trends and Conservation Status of Wild Canids
41	<u>Nolder</u> , <u>Duchamp</u> , <u>D'Acunto</u>	Bat Response to Oak Regeneration Silviculture
42	<u>Johnston</u> , <u>Yunger</u> , <u>D'Arcy</u>	Heavy Metal Contamination and Accumulation at Abandoned and Untreated Copper Mines In Keweenaw, Michigan
43 ^E	<u>Blum</u> , <u>Stewart</u> , <u>Schroeder</u> , <u>Wasley</u>	Impacts of Mining on Mule Deer Migrations in Nevada
44 ^E	<u>Day</u> , <u>Westover</u> , <u>McMillan</u>	Factors Influencing Mortality of Translocated Northern River Otters (<i>Lontra canadensis</i>) in Utah
45 ^E	<u>Prout</u> , <u>Hayssen</u> , <u>Noonan</u>	Hind Foot and Tail Length in Mustelid Climbers and Diggers
46	<u>Noonan</u>	Taking Measure of Mustelids: Morphological Diversity
47 ^E	<u>Wells</u> , <u>Wilson</u> , <u>Van Vuren</u> , <u>Kelt</u>	Body Mass as an Estimate of Body Condition in a Hibernating Small Mammal, the Golden-mantled Ground Squirrel (<i>Callospermophilus lateralis</i>)
48	<u>Bresnahan</u> , <u>Kwiecinski</u>	Immunohistochemical Study of Merkel Cells in Verrucae of <i>Artibeus jamaicensis</i>
49	<u>Flaherty</u> , <u>Ben-David</u> , <u>Pauli</u>	Locomotor Performance in the Pacific Marten: Are Semi-arboreal Mustelids More Efficient Runners than Semi-aquatic Ones?
50 ^E	<u>Munster</u> , <u>Brown</u> , <u>Utzurum</u> , <u>Brooke</u> , <u>McCracken</u> , <u>Russell</u>	Differential Dispersal of Two Codistributed Species of <i>Pteropus</i> in the South Pacific
51	<u>Murphy</u> , <u>Matocq</u>	Experimental Tests of Interactions Between Woodrats Across a Zone of Secondary Contact: Asymmetry in Body Size and Aggression Limit Interspecific Mating
52	<u>Solomon</u> , <u>Willen</u> , <u>Keane</u>	Reproductive Success of Male Prairie Voles (<i>Microtus ochrogaster</i>) Displaying Alternative Reproductive Tactics
53	<u>Naples</u>	A New Model of Ricochetral Locomotion in Mammals
54 ^E C	<u>Krause</u> , <u>Lambert</u> , <u>Adler</u>	Influence of Resource Abundance on Two Echimyid Rodents in Central Panama

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SUNDAY, 16 JUNE, POSTER SESSION I

	PRESENTER (S)	TITLE
55	Ober, DeGroot, McDonough, Mizell III, Mankin	The Importance of Sensory Information in the Foraging of Wild Nine-banded Armadillos
56	Wolff, Heske, Schooley	Influence of Crayfish on Diet and Summer Habitat Selection by American Mink
57 ^E	Webb, Day, Westover, McMillan, Zollner	Preliminary Analysis of Niche Partitioning Among Mammals of Riparian Corridor
58 ^E	Howe, Yungler	Foraging Behaviors of Field Mice Under Direct Cues of Predation Risk
59	Steele, Stratford, Rompré, Zhang, Lello, Dudeck	The Influence of Habitat Structure and Predation Risks on Seed Dispersal by Scatter Hoarding Rodents
60	Browning	Whistling Land Mammals: Groundhogs, Tapirs, and Dholes
61	Barry	Vigilance Strategies of Bush (<i>Heterohyrax brucei</i>) and Rock (<i>Procavia capensis</i>) Hyraxes While Basking
62 ^E	Holdman, Bienz, Zollner	Using Cameras to Estimate <i>Peromyscus</i> Activity Levels Relative to Predator Risk
63	Keane, Castelli, Davis, Solomon	Influence of Male avpr1a Genotype on Social and Reproductive Behavior in Prairie Voles (<i>Microtus ochrogaster</i>)
64 ^E	Rogers, Eggleston, Crawford, Rose	Variations of a Small Mammal Community in a Changing Landscape in Southeastern Virginia
65	Zahn, Shaughnessy Jr.	The Impact of Precipitation on Insectivore and Arthropod Abundance in Prairie Dog <i>Cynomys ludovicianus</i> Towns in Southwest North Dakota
66	LaBarron, Gillie	Small Mammal Diversity in Edge Versus Forest Interior Habitats
67 ^E	Zaharick Jr., Beck, Beauchamp	An Experimental Test of Small Mammal Dispersal of Arbuscular Mycorrhizal Fungi Spores
68	Aliperti, Kelt, Meserve, Gutiérrez, Milstead, Previtali	Biogeographical Patterns of Energetic Compensation in Desert Small Mammal Assemblages
69 ^{E,T}	Fender, Kelly, Schnell, Kennedy, Wooten, Sánchez-Hernández, Romero-Almaraz, Best	Resource Partitioning Among Sympatric Congeners of <i>Reithrodontomys</i>
70	Kaufman, Kaufman, Kaufman	Expansion of the Semi-arboreal White-footed Mouse in Tallgrass Prairie: Three Decades of Fire, Woody Invasion and Land-cover Change
71 ^E	Stuhler, Orrock	Fire and Land Use Interact to Affect Patterns of Rodent Granivory
72	Thibault	A Standardized Design for Small Mammal Sampling Across Habitats, Decades, and Spatial Scales for the National Ecological Observatory Network
73	Bell, Rickart, Rowe	The Expansion of Pinyon-juniper Woodland and the Appearance of <i>Peromyscus truei</i> in the Toiyabe Range of Central Nevada
74	Kingston, Sagot, Gopal	Detection and Characterization of Bat Hotspots

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American Society of Mammalogists 93rd Annual Meeting—Philadelphia, Pennsylvania

MONDAY, 17 JUNE, MORNING SESSION

6:00 AM

RUN FOR RESEARCH – Rocky Balboa Route – Starts from the Philadelphia Marriott

Featured Speaker – Salon E

8:30 AM J Hansen

Dr. James Hansen, NASA Goddard Institute for Space Studies and Adjunct Professor of Earth and Environmental Sciences at Columbia University, is the featured speaker at this year's annual meeting. Dr. Hansen's research interests are broad and include radiative transfer in planetary atmospheres, especially interpreting remote sounding of the earth's atmosphere and surface from satellites. His development and use of global climate models has contributed to the further understanding of the Earth's climate. Dr. Hansen is well known for his research in the field of climatology, his testimony on climate change to congressional committees in 1988 that helped raise awareness of global warming, and his advocacy of action to avoid dangerous climate change. In recent years, Dr. Hansen has become an activist for action to mitigate the effects of climate change.



9:30 AM

BREAK – Franklin B

American Society of Mammalogists 93rd Annual Meeting—Philadelphia, Pennsylvania

MONDAY, 17 JUNE, MORNING SESSIONS

ROOM		Salon A		Salon B
SESSION/SYMPOSIUM		Technical Session 3: Evolutionary Biology		Technical Session 4: Population Ecology
MODERATOR		Brandi Coyner		Aaron Reed
10:00 AM	75	A Russell, L Dávalos	83	C Downs, K Stewart, B Dick, M Wisdom
		Sex-biased Dispersal Drives High Error Rates In Mitochondrial Tree-based and Distance-based Species Delimitation		Effects of Elk Population Density on Immune Function Mediated by Body Condition
10:15 AM	76	J Esselstyn, K Rowe, A Achmadi, B Evans	84 ^E	S Gilbert, D Person, K Hundertmark
		The Influence of Reproductive Ecology on Genome Evolution in Rodents		Population Dynamics of a Forest Ungulate Respond to Winter Severity and Habitat Alteration
10:30 AM	77 ^T	B Coyner, M Matocq	85	S Morano, K Stewart, A Ellsworth, T Dilts
		Genetic Analysis of a Hybrid Zone Between Two Species of Woodrats (<i>Neotoma</i>)		Pinyon-juniper Expansion in the White Mountains: Implications for Mule Deer Demographics and Habitat Use
10:45 AM	78	M Matocq, B Coyner, P Murphy	86 ^{E,T}	C Schroeder, K Stewart, T Wasley
		Reproductive Success Across a Hybrid Zone in <i>Neotoma</i> : Differential Fitness Effects Among Pure and Hybrid Genotypic Classes		Migration Behavior, Body Condition, and Sex Differences in Survival of Mule Deer
11:00 AM	79	M Davis	87 ^E	J Oyster, E Finck, M Peek
		Some Animals are More Equal Than Others: Functional Diversity vs. Functional Group Richness in Large Quaternary North American Mammals		Distance Sampling as a Technique to Monitor Pronghorn in Kansas
11:15 AM	80 ^{E,T}	J Burger, A Davidson, M Hamilton, J Brown	88 ^{E,**}	R Green, K Purcell, C Thompson, D Kelt, H Wittmer
		Multiple Trait Combinations Predict Brain Size in Mammals		Insights into the Reproductive Ecology of Fishers (<i>Martes pennanti</i>) at the Southernmost Extent of the Range in California
11:30 AM	81 ^E	P Durst, V Roth	89	A Facka, J Lewis, R Powell
		Defining Extreme: A New Perspective on Insular Mammalian Body Size Change		The Effects of Translocation on Reproductive Success in Newly Released Fishers
11:45 AM	82	L Olson	90	H Bryan, M Musiani, L Koren, K Wynne-Edwards, P Paquet, J Smits
		Climate Change and Body Size: A Review and Plea for Standards		Hormonal Patterns Reflect Social Instability in a Heavily Hunted Wolf Population
12:00 PM		LUNCH		

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MONDAY, 17 JUNE, MORNING SESSIONS

ROOM		Salon C		Salon E
SESSION/SYMPOSIUM		Technical Session 5: Behavior		Technical Session 6: Biogeography, Community Ecology, and Conservation
MODERATOR		Nancy Solomon		Eric Rickart
10:00 AM	91	B Pasch, M Abbasi, S Phelps, P Wilson, M Ryan	99^E	K Preston, N Dochtermann
		Steering Sound Beams: The Influence of Social Context on Acoustic Radiation Patterns in Neotropical Singing Mice		Are There Taxonomic Patterns of Population Variability, Density Dependence, and Conservation Status?
10:15 AM	92	L Hayes, L Ebensperger	100	S Maher, T Morelli, M Hershey, A Flint, L Flint, C Moritz, S Beissinger
		Mammalian Plural Breeding: Why Bother?		Analyzing the Geography of Extinctions and Climate Change in the Sierra Nevada
10:30 AM	93^{E,T}	B Roberts, D Rubenstein	101	Z Luo, Z Jiang
		The Effects of Perinatal Behavior and Maternal Decisions on Neonate Survival in a Hiding Ungulate		Impacts of Climate Change on the Distributions and Diversity Patterns of Ungulates on the Tibetan Plateau
10:45 AM	94^{**T}	G Carter	102	N Harris
		A Positive Interaction Between Reciprocal Help and Relatedness Predicts Cooperative Food Sharing in Common Vampire Bats		Small Mammal Distribution and Diversity Throughout Ghana, West Africa
11:00 AM	95^{E,T}	J Nations, L Olson	103^{E,**T}	L Patrick, R Stevens
		Scansorial and Arboreal Behavior in Northern Red-backed Voles in Alaska		Morphological and Phylogenetic Community Structure of North American Desert Bats
11:15 AM	96	A Sullivan	104^{E,**T}	L Cisneros, M Willig
		Stem diameter and Toughness Affect Vole (<i>Microtus</i> spp.) Foraging Patterns in Tallgrass Vegetation		Identifying Landscape Characteristics that Promote Taxonomic, Functional and Phylogenetic Dimensions of Bat Biodiversity
11:30 AM	97^E	M van de Kerk, D Onorato, S McKinley, M Criffield, M Oli	105	M Willig, K Burgio, L Cisneros, L Dreiss, B Klingbeil, B Patterson, S Presley
		Multiphasic Movement Patterns of Florida Panthers		Comparative Biodiversity of Bats and Rodents Along an Extensive Tropical Elevational Gradient: Taxonomic, Functional, and Phylogenetic Dimensions
11:45 AM	98	T Stankowich, P Haverkamp, T Caro	106^E	P Galante, R Boria, R Anderson
		Ecological Drivers of Antipredator Defenses in Carnivores		Comparing Species-specific Tuning Versus AIC _c to Select Optimally Complex Ecological Niche Models
12:00 PM		LUNCH		

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MONDAY, 17 JUNE, AFTERNOON SESSIONS

ROOM		Salon A		Salon B
SESSION/SYMPOSIUM		Technical Session 7: Systematics and Biogeography: New World Mammals		Technical Session 8: Disturbance Ecology
MODERATOR		Ryan Norris		Karen McBea
1:00 PM	107	<u>P Velazco</u> , H O'Neill, G Gunnell, R Rimoli, A Rosenberger, N Simmons	114	<u>C Hood</u> , L Nolfo-Clements
		Quaternary Bat Diversity in the Dominican Republic		Large Mammal Diversity, Abundance, and Activity Patterns at Jean Lafitte National Park, Louisiana: Pre- and Post-Katrina
1:15 PM	108	<u>B Patterson</u> , <u>P Velazco</u>	115 ^{E,T}	<u>M Buchalski</u> , <u>J Fontaine</u> , <u>P Heady III</u> , <u>J Hayes</u> , <u>W Frick</u>
		Diversification of the Yellow-shouldered Bats, Genus <i>Sturnira</i> (Chiroptera, Phyllostomidae), in the New World Tropics		Bat Response to Differing Fire Severity in Mixed-conifer Forest California, USA
1:30 PM	109 ^E	<u>R Platt II</u> , <u>Y Zhang</u> , <u>D Witherspoon</u> , <u>J Xing</u> , <u>R Stevens</u> , <u>L Jorde</u> , <u>D Ray</u>	116	<u>J Duggan</u> , <u>J Diffendorfer</u> , <u>D Morin</u> , <u>S Tremor</u> , <u>L Hargrove</u> , <u>P Unitt</u>
		BAT-Scan: Phylogenomics of <i>Myotis</i> Using Retrotransposon Capture		The Role of Life History Traits in Post-fire Recovery of Small Mammals in the Chaparral Shrublands of Southern California, USA
1:45 PM	110	<u>A Baird</u> , <u>C Tran</u> , <u>J Patton</u> , <u>J Bickham</u>	117 ^E	<u>A Ahlers</u> , <u>P Wolff</u> , <u>E Heske</u> , <u>R Schooley</u>
		Phylogeography of the Hoary Bats (<i>Lasiurus</i>): Molecular Evidence for Species Diversity and Multiple Invasions of the Hawaiian Islands		Environmental Change and Habitat Occupancy of Semiaquatic Mammals: Insights from the Midwest Drought of 2012
2:00 PM	111 ^{E,**}	<u>T Giarla</u> , <u>S Jansa</u>	118 ^{E,C}	<u>A Ricketts</u> , <u>B Sandercock</u>
		Multilocus Phylogeography and Phylogenetics of <i>Thylamys</i> Mouse Opossums: The Impact of Pleistocene Glacial Cycles on Andean Taxa		Small Mammal Community Responses to a Severe Drought in Tallgrass Prairie Managed with Fire and Grazing
2:15 PM	112 ^{**}	<u>M Pérez</u> , <u>N Basso</u> , <u>A Holley</u> , <u>B Patterson</u> , <u>M Weksler</u>	119 ^E	<u>B Zinke</u> , <u>E Finck</u>
		Phylogeny and Evolution of Body Size in Caviidae (Rodentia, Hystricognathi, Caviioidea): Approach of a Combined Analysis with Morphology and Molecular Data		Small Mammal Community Structure at a Dried Wetland Site
2:30 PM	113	<u>E Gutiérrez</u> , <u>K Helgen</u> , <u>R Dikow</u> , <u>F Bauer</u> , <u>M Roberts</u> , <u>B Patterson</u> , <u>J Maldonado</u>	120 ^E	<u>S Garza</u> , <u>K Wilson</u> , <u>G Bowser</u>
		A Preliminary Test of the Traditional Taxonomy of New World Deer (Cervidae: Rangiferini) and its Implications for Conservation		Changes in Small Mammal Populations Following Capping of Artesian Wells in Great Sand Dunes National Park and Preserve
2:45 PM			121 ^E	<u>G Savory</u> , <u>C Hunter</u> , <u>B Person</u> , <u>N Lehner</u> , <u>N Pamperin</u>
				The Effect of Resource Development on Arctic Fox Survival on the Arctic Coastal Plain of Alaska
3:00 PM		BREAK – Franklin B		

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American Society of Mammalogists 93rd Annual Meeting—Philadelphia, Pennsylvania

MONDAY, 17 JUNE, AFTERNOON SESSIONS

ROOM		Salon C		Salon E
SESSION/SYMPOSIUM		Technical Session 9: Physiology and Community Ecology		Technical Session 10: Conservation Genetics: Carnivores
MODERATOR		Leslie Carraway		Brock McMillan
1:00 PM	122 ^{E,**,T}	D Tufts, J Storz	129 ^T	S Sharma, T Dutta, J Maldonado, T Wood, H Panwar, J Seidensticker
		Genetic Differences in Hemoglobin Function Between High and Low Altitude Pika Species		Are Corridors Important for Tigers?
1:15 PM	123	M Yamato, H Koopman, G Feijoo, D Ketten, M Niemeyer	130 ^{E,T}	T Wilbert, D (Smith) Woollett, M Westphal, A Whitelaw, K Ralls, J Maldonado
		Aquatic Sound Reception in Cetaceans		Distribution and Population Connectivity of San Joaquin Kit Foxes in the Panoche Valley, California: The Power of Non-Invasive Surveys
1:30 PM	124 ^{E,**}	C Bauer, L Hayes, L Ebensperger, L Romero	131	K Aubry, K McKelvey, N Anderson, A Clevenger, J Copeland, K Heinemeyer, R Inman, J Squires, J Waller, K Pilgrim, M Schwartz
		Seasonal Variation in the Degu (<i>Octodon degus</i>) Endocrine Stress Response		Recovery of Wolverines in the Western United States: Recent Extirpation and Re-colonization or Range Retraction and Expansion?
1:45 PM	125	T Orr, P Brennan	132	J Bohling, L Waits, J Dellinger, J McVey, D Cobb, C Moorman
		Female Sperm Storage: How Can We Distinguish Sperm Storage from Simple Sperm Longevity in Mammals?		Estimating the Extent of Interspecific Hybridization Across the Range of the Endangered Red Wolf (<i>Canis rufus</i>)
2:00 PM	126 ^E	B Pauli, P Zollner, S Haulton	133 ^T	A Caragiulo, I Dias-Freedman, S Rabinowitz, J. A Clark
		Using Multi-species Occupancy Modeling to Identify Suitable Habitat for Bats in Indiana with Focus on the Endangered Indiana Bat		Genetic Population Structure of Neotropical Cougars (<i>Puma concolor</i>)
2:15 PM	127 ^{E,C}	T Jessen, J Koprowski	134	A Silva-Caballero, J Ortega, D Valenzuela-Galván, G León-Avila
		Testing Efficacy of Hairtube Sampling at Detecting Presence of Small Mammals		Variability and Population Genetic Structure of the White-nosed Coati (<i>Nasua narica</i>) in Mexico
2:30 PM	128	K Curry-Lindahl, B Arbogast, T Knowles, S Burneo	135 ^E	T Dutta, S Sharma, J Maldonado, T Wood, H Panwar, J Seidensticker
		Using Camera Trap Surveys to Address Terrestrial Mammal Biodiversity and Conservation in Sumaco National Park, Ecuador		Genetic Connectivity in Sloth Bear (<i>Melursus ursinus</i>) metapopulation in the Central Indian Highlands
2:45 PM			136	D Diefenbach, L Hansen, J Bohling, C Miller-Butterworth, G Veron
				Impact of Genetic Drift on Island Populations of Mesocarnivores Established on Cumberland Island, Georgia
3:00 PM		BREAK – Franklin B		

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MONDAY, 17 JUNE, AFTERNOON SESSIONS

ROOM		Salon A		Salon B
SESSION/SYMPOSIUM		Technical Session 11: Systematics and Biogeography: New World Mammals		Technical Session 12: Urban and Disturbance Ecology
MODERATOR		Neal Woodman		Helen Pigage
3:30 PM	137	J Hanson, E Rees	145 ^E	C Graff, H Beck, A O'Connell Jr.
		Evaluation of NexGen Sequence Technology for Mammalian Genomes		Surrogate Habitats for Urban Mammals: Quantifying Survival and Occupancy in Constructed Wetlands
3:45 PM	138	J Kenagy, A Chavez, J Whorley, B Arbogast	146	N de la Sancha, T McGreevy, Jr., S Musila, B Agwanda, D Abedon, T Husband
		A Tale of Three Squirrels: Comparative Mitochondrial and Nuclear DNA Data Highlight Disparate Phylogeographic and Evolutionary Histories		Mammals in a Coffee-dominated Landscape in the Highlands of Central Kenya: Implications for Conservation
4:00 PM	139**	A Chavez, B Arbogast, S Maher, J Kenagy	147C	E Unangst Jr., J Sleeter
		Diversification and Gene Flow in Island and Mainland <i>Tamiasciurus</i> spp. – Unraveling the Mystery of Vancouver Island's Squirrels		A Risk Assessment of Road Proximity and Road Crossings of Radio-collared Mule Deer (<i>Odocoileus hemionus</i>) on the US Air Force Academy
4:15 PM	140	B Arbogast, K Schumacher, A Bidlack, J Cook, J Kenagy	148 ^E	H Chen, J Koprowski
		Analysis of Nuclear and Mitochondrial DNA Reveals Cryptic Speciation in North American Flying Squirrels (<i>Glaucomys</i>)		Barrier Effects of Roads on an Endangered Forest Obligate: Role of Forest Structure
4:30 PM	141	R Norris, T Fulton, R Graham, H Semken Jr., B Shapiro	149 ^E	L Dorough, P Stapp Undergraduate Research Award
		Ancient DNA Supports Southern Survival of Richardson's Collared Lemming (<i>Dicrostonyx richardsoni</i>) During the Last Glacial Maximum		Patterns of Activity and Diversity of Bats at the Urban-wildland Interface in Southern California
4:45 PM	142	N Adams, D Berg, B Keane, N Solomon	150	C Lowrey, K Longshore
		Molecular Analysis of Current Subspecies Classification of the Prairie Vole (<i>Microtus ochrogaster</i>)		Life at the Urban Interface: Potential Effects of Parks, Golf Courses, and Bicycles on Desert Bighorn Sheep
5:00 PM	143	B Riddle, T Jezkova, D Schield, D Card, T Castoe	151	B Klatt, T Boezaart, J Gehring
		Genetic Consequences of a Range Expansion in Two Congeneric Rodents (Genus <i>Dipodomys</i>)		Bat Activity in Offshore Areas of Lake Michigan in the Context of Wind Energy Development

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ROOM		Salon A		Salon B
SESSION/SYMPOSIUM		Technical Session 11: Systematics and Biogeography: New World Mammals		Technical Session 12: Urban and Disturbance Ecology
MODERATOR		Neal Woodman		Helen Pigage
5:15 PM	144 ^E	<u>M Cason</u> , T Booms, L Olson	152 ^{E,**}	<u>B Tanis</u> , E Finck
		Distribution and Phylogeography of an Alaskan Endemic: The Alaskan Hare		Influence of Wind Turbines on Mammalian Mesocarnivore Occupancy Patterns
5:30 PM	144/256 ^E	<u>K May</u> , A Gunderson, L Olson	153 ^E	<u>D Kelt</u> , <u>D Van Vuren</u> , <u>M Johnson</u> , <u>J Wilson</u> , <u>R Innes</u> , <u>B Jesmer</u> , <u>K Ingram</u> , <u>J Smith</u> , <u>S Bigelow</u> , <u>R Burnett</u> , <u>P Stine</u>
		The Effects of Climate Change on Body Size in the Masked Shrew in Alaska Revisited		Small Mammals Exhibit Limited Spatiotemporal Structure in Sierra Nevadan Forests
6:00 PM	DINNER			
7:00 PM	POSTER SESSION II – Franklin B			
9:00 PM	AUCTION AND RAFFLE – Franklin B			

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MONDAY, 17 JUNE, AFTERNOON SESSIONS

ROOM		Salon C		Salon E
SESSION/SYMPOSIUM		Technical Session 13: Population Ecology		Technical Session 14: Conservation Genetics
MODERATOR		Matt Hopton		Peter Larsen
3:30 PM	154 ^E	<u>A Gooley</u> , E Schaubert, G Feldhamer	164 ^{E,T}	<u>K Cleary</u> , L Waits, B Finegan
		Abundance and Distribution of Eastern Woodrats (<i>Neotoma floridana</i>) in Southern Illinois Following Genetic Augmentation and Reintroduction		Agricultural Intensification in a Neotropical Biological Corridor: Can Functional Connectivity for Frugivorous Bats Be Maintained?
3:45 PM	155 ^E	<u>R Blythe</u> , T Smyser, S Johnson, R Swihart	165 ^{E,T}	<u>R Pigg</u> , S Wisely, C Lee, J Cully, Jr.
		Post-release Survival of Captive-reared Allegheny Woodrats		Broad-scale Patterns of Connectivity Among Black-tailed Prairie Dog Populations in a Heavily Managed Landscape
4:00 PM	156	<u>J Duchamp</u> , J Larkin, J Hoffman, M Taddie	166	<u>B Elias</u> , <u>L Shipley</u> , S McCusker, R Saylor
		Demographic Response of Allegheny Woodrats to Habitat Conditions and Supplemental Feeding		Genetic Diversity vs. Genetic Distance: Reproduction, Growth and Survival in Captive Pygmy Rabbits
4:15 PM	157 ^{E,T}	<u>E Troyer</u> , S Devitt, M Sunquist, V Goswami, M Oli	167 ^E	<u>S DeMay</u> , P Becker, J Rachlow, L Waits
		Factors Influencing Population Growth Rate of Virginia Opossums in North-central Florida		Comparing Telemetry and Fecal DNA Sampling Methods to Quantify Survival and Dispersal of Juvenile Pygmy Rabbits
4:30 PM	158	<u>A Reed</u> , K Wooge, N Slade	168 ^E	<u>M Sullivan</u> , T McGreevy, Jr., B Tefft, A Gottfried, T Husband
		Environmental Effects on Population Sensitivity to Reproduction		Detection of Mitochondrial Pseudogenes in New England Cottontail (<i>Sylvilagus transitionalis</i>): Implications for Species Identification and Conservation
4:45 PM	159	<u>R Gitzen</u> , R Renken, D Fantz, R Jensen, J Favara, J Millsbaugh	169	<u>E Latch</u> , E Kierepka, J Heffelfinger, O Rhodes, Jr.
		Hierarchical Modeling of Experimental Forest Harvest Effects on <i>Peromyscus</i>		Hybrid Swarm Between Divergent Lineages of Mule Deer (<i>Odocoileus hemionus</i>)
5:00 PM	160	<u>J Crawford</u> , L Berkman, C Jordan, C Nielsen	170 ^E	<u>O Alminas</u> , E Latch
		Spatial and Food Resource Partitioning in Two Sympatric Rabbit Populations in Southern Illinois		Phylogeographic Inference of Insular Mule Deer (<i>Odocoileus hemionus</i>) Divergence in Baja California

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MONDAY, 17 JUNE, AFTERNOON SESSIONS

ROOM		Salon C		Salon E
SESSION/SYMPOSIUM		Technical Session 13: Population Ecology		Technical Session 14: Conservation Genetics
MODERATOR		Matt Hopton		Peter Larsen
5:15 PM	161 ^{**T}	<u>M Merrick, J Koprowski</u>	171 ^E	<u>R Toldness, J Ivy, L Jones, E Latch</u>
		Do Naïve Dispersers Rely on Natal Habitat Cues When Making Settlement Decisions? Evidence of Habitat Cueing and Potential Consequences in an Altered Forest Landscape		Evaluation of Alternative Culling Strategies on Maintenance of Genetic Variation in Bison
5:30 PM	162 ^E	<u>T Flick, B Danielson</u>	172	<u>D Moreno, J Ortega, D Gendron, E Lacey</u>
		The Unseen Workers of the Fields: How Prairie Deer Mice are Helping Control Agricultural Weeds from Waste Grain		Variability at MHC-DQB Gene in the Population of <i>Balaenoptera musculus</i> in the Gulf of California, Mexico
5:45 PM	163	<u>M Shaughnessy Jr., M Jakubauskas, S Soman</u>		
		Area and Distance Metrics Associated with Survival, Extinction and Re-Colonization of Black-tailed Prairie Dog Colonies (<i>Cynomys ludovicianus</i>) in Southwestern North Dakota		
6:00 PM		DINNER		
7:00 PM		POSTER SESSION II – Franklin B		
9:00 PM		AUCTION AND RAFFLE – Franklin B		

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MONDAY, 17 JUNE, POSTER SESSION II

	PRESENTER (S)	TITLE
173**	<u>McCulloch</u>	Bridging the Gap: Communication Between Scientists and Policy-Makers
174 ^E	<u>Bell, Cook, Lacey, Demboski</u>	Incorporating Natural History Collections into Undergraduate Education
175 ^E C	<u>Aven, Carmichael, Ingram</u>	Correcting Spatial Bias in Wildlife Citizen-Surveys: Integrating Manatee Sighting Reports with GPS Tag Data
176	<u>Revelez, Braun, Mares, Allen</u>	From the Retired Boomer to the Young Professional: Volunteers in Mammal Collections can be a Powerful Force
177	<u>Thorington, Varner, Shaw</u>	Citizen Mammalogy: How Should ASM be Involved in Citizen Science?
178	<u>Roze</u>	Porcupines: The Animal Answer Guide
179 ^E	<u>Sullivan, Greenberg</u>	Project Passenger Pigeon: Building Sustainable Relationships with Other Species
180 ^E	<u>Sullivan, Sullivan</u>	Habitat and Dietary Preferences in a Nocturnal Primate, The Thick-tailed Greater Galago (<i>Otolemur crassicaudatus</i>)
181 ^E	<u>Reed, Litvaitis, Broman, Tate</u>	Bobcat (<i>Lynx rufus</i>) Home Range and Habitat Selection at Multiple Spatial Scales in New Hampshire
182 ^E	<u>Green, Purcell, Thompson, Kelt, Wittmer</u>	Characteristics of Reproductive Dens Used by Fishers (<i>Martes pennanti</i>) in the Southern Sierra Nevada
183	<u>Brassington, Chacko, Jang, Kisser, Passey, Goodwin</u>	Seasonal and Spatial Variation in Diet Recorded by $\delta^{13}C$ of Incisor Enamel of Free-ranging Thirteen-lined Ground Squirrels (<i>Ictidomys tridecemlineatus</i>)
184 ^{E,**}	<u>Hall, Durant, Cisneros, Hyland, Willig</u>	Reproductive Phenologies of Phyllostomid Bats from Costa Rica
185	<u>Cohen, Pauli, Zollner, Beasley, Rhodes Jr.</u>	Modeling Raccoon Removals and Recolonization of Woodlots Using Animal Dispersal Model SEARCH
186	<u>Rose, Rice</u>	Patterns of Transience in Four Species of Oldfield Herbivorous Rodents in the US
187 ^E	<u>Eggleston, Rose</u>	Demography of the Meadow Vole, <i>Microtus pennsylvanicus</i> , in Southeastern Virginia
188 ^E	<u>Meiners, Masterson, Reed, Slade</u>	Detecting the Signal of Climate Change in Small Mammal Populations of Eastern Kansas
189	<u>Loughry, Perez-Heydrich, McDonough, Madan K. Oli</u>	Population Ecology and Dynamics of Nine-Banded Armadillos
190 ^{E,**}	<u>Rodgers, Schooley, Giacalone, Jenecka, Heske</u>	Noninvasive Genetics Versus Camera Trapping: Estimating Population Density of an Elusive Carnivore, <i>Leopardus pardalis</i>

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MONDAY, 17 JUNE, POSTER SESSION II

	PRESENTER (S)	TITLE
191 ^E	<u>Cove</u> , Vargas, de la Cruz, Spinola, Jackson, Saénz, Chassot	Factors Influencing the Occurrence of the Endangered Baird's Tapir <i>Tapirus bairdii</i> : Potential Flagship Species for a Costa Rican Biological Corridor
192	<u>Baglieri</u> , <u>Grigione</u> , Sarno, Ries	The Feeding Ecology of Non-native Red Fox (<i>Vulpes vulpes</i>) on an Atlantic Barrier Island
193	Lynch, <u>Pigage</u> , Clawges, Pigage	Using Camera Traps to Evaluate Placement of Artificial Water Sources at Fort Carson, Colorado
194	Noble, Bono, Pigage, Hale, <u>Pigage</u>	Investigating Fine-scale Genetic Structure in Female Mule Deer (<i>Odocoileus hemionus</i>) Through Spatial Analysis of Microsatellite-derived Relatedness Estimates
195 ^{E,T}	<u>Tsuchiya</u> , Koepfli, Eizirik	Phylogeography, Demographic History, and Molecular Diversity of Two Neotropical Species of Family Procyonidae (Mammalia, Carnivora): <i>Nasua nasua</i> and <i>Procyon cancrivorus</i> .
196 ^{E,C}	<u>Burns</u> , Underwood	Non-invasive Approach to River Otter (<i>Lontra canadensis</i>) Monitoring and Population Estimation in the Finger Lakes Region of New York
197	<u>Malaney</u> , Feldman, Matocq	Bighorn Sheep at the Edge of the Translocated Range: Genetic and Environmental Variation
198	<u>Baird</u> , Bickham, Patton, Stuart, George, Phillips, Suydam	Population Genetics and Transcriptomics of Bowhead Whales (<i>Balaena mysticetus</i>)
199	Pfau, Sasse, Connior, Guenther, <u>Braun</u>	Short-tailed Shrews (<i>Blarina</i>) in Arkansas and Oklahoma
200 ^E	<u>Jackson</u> , McLean, Cook	Phylogeny of Holarctic Ground Squirrel Genus <i>Urocitellus</i>
201 ^E	<u>Kirby</u> , Vonhof, Bonaccorso, Olival, Pinzari, Russell	Reconstructing the Biogeography of Hawaiian Hoary Bats (<i>Lasiurus cinereus</i>)
202	<u>Neiswenter</u>	Conservation of <i>Sigmodon</i> Along the Lower Colorado River: Past, Present, and Future
203**	<u>Hornsby</u> , Matocq	<i>Neotoma</i> Species Turn-over Identified by Ancient DNA from Paleomidden Feces
204 ^E	<u>Ferguson</u> , Guerra, Ammerman, Dragoo, Dowler	Spots on Trees: Examining the Phylogeography of the Western Spotted Skunk (<i>Spilogale gracilis</i>)
205	<u>Rengifo</u> , Pacheco	A Taxonomic Revision of <i>Phyllotis andium</i> Thomas 1912 (Rodentia: Cricetidae)
206	<u>Rengifo</u> , Pacheco	Phylogenetic Position of <i>Phyllotis definitus</i> Osgood 1915 (Rodentia: Cricetidae)
207	<u>Helgen</u> , Young, Helgen	<i>Zelotomys hildegardeae</i> (Thomas, 1902): A Detailed Record of the Elusive African Stink Rat
208	<u>Rowsey</u> , Helgen Undergraduate Research Award	Species Boundaries of Brushtail Possums in the Queensland Wet Tropics
209	<u>Mathis</u> , Hafner, Hafner, Demastes	<i>Thomomys nayarensis</i> , a New Species of Pocket Gopher from the Sierra Del Nayar, Nayarit, Mexico

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MONDAY, 17 JUNE, POSTER SESSION II

	PRESENTER (S)	TITLE
210	<u>Hurtado</u> , Pacheco	First Assessment of the Medium and Large Mammal's Diversity in the Pacific Tropical Rainforest of Peru Using Line Transect Census and Camera Traps
211	<u>Worrall</u> , Haas, Braun, Vitt, Caldwell, Mares	Natural History of Small Mammals Sampled by Pitfall Arrays in Southeastern Oklahoma
212 ^E	<u>Zawacki</u> , Iudica	Recent Holocene Paleoeecology of Terrestrial Vertebrates on Guam
213	<u>Matson</u> , Garza, Bulmer, Eckerlin, Greiman	Small Mammals from an Isolated, Remnant Cloud Forest in Guatemala
214	<u>Pounds</u> , Miller, Herauf, Shaughnessy Jr.	New Records of Small Mammals from Prairie Dog Towns (<i>Cynomys ludovicianus</i>) in Southwest North Dakota
215	<u>Thorington Jr.</u> , Sheffield, Bohaska	Paradiso Found — <i>Mammals of Maryland</i> Revised
216	<u>Edelman</u> , Smith	How Much do we Actually Know About Mammals of the Southeastern U.S.?
216/258	<u>Tietje</u> , Sinervo	Climate Warming Effects on a Keystone Vertebrate

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TUESDAY, 18 JUNE, MORNING SESSION

Thematic Session II –Salon E Mammalian Predator Control – Moderator: B J Bergstrom

- 8:00 AM** **217** Coexisting with Carnivores in the U.S.: Overcoming Prejudice and Persecution
C H Fox, D Parsons, A Treves, M Soulé
- 8:15 AM** **218** Review of Non-lethal Methods for Predator Control
S W Breck
- 8:30 AM** **219** The Intricacy of Wolf Control in Areas With Domestic and Wild Prey or With Threatened Caribou
M Musiani
- 8:45 AM** **220** The Western Wolf Conflict Deconstructed
J Bruskotter
- 9:00 AM** Discussion and Concluding Remarks
B Bergstrom, C Fox, S Breck, M Musiani, J Bruskotter

9:30 AM	BREAK – Franklin B
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ROOM		Salon E		Salon F
SESSION/SYMPOSIUM		Technical Session 15: Systematics and Biogeography: Old World Mammals		Technical Session 16: White-nose Syndrome and Wildlife Disease
MODERATOR		Link Olson		Craig Frank
10:00 AM	221	T McGreevy, Jr., L Dabek, T Husband	231	C Frank, A Michalski
		Comparative Phylogeography of Three Sympatric Macropodid from Huon Peninsula, Papua New Guinea: Implications for Conservation and Management		The Biochemistry and Physiology of the Resistance to WNS by <i>Eptesicus fuscus</i>
10:15 AM	222	A Hintz, M Blacket, M Westerman, C Krajewski	232 ^{E,T}	L D'Acunto, J Duchamp
		Phylogenetics of Tribe Planigalini (Marsupialia, Dasyuridae) Using a Multigene Approach		Potential Influence of White-nose Syndrome on Summer Bat Distribution in Pennsylvania
10:30 AM	223	K-P Koepfli, J Pollinger, J Robinson, Z Fan, A Lea, R Schweizer, O Thalmann, E Geffen, F Zachos, R Godinho, W Johnson, R Wayne	233 ^E	A Martin, M Vonhof, A Russell
		Genomic Evidence for Extensive Admixture in African Golden Jackals (<i>Canis aureus</i>) from Gray Wolves (<i>Canis lupus</i>)		Regional Extinction Risks of the Eastern Pipistrelle Bat

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TUESDAY, 18 JUNE, MORNING SESSION

ROOM		Salon E		Salon F
SESSION/SYMPOSIUM		Technical Session 15: Systematics and Biogeography: Old World Mammals		Technical Session 16: White-nose Syndrome and Wildlife Disease
MODERATOR		Link Olson		Craig Frank
10:45 AM	224 ^{E,T}	M McDonough, C Phillips, J Bryja, K Helgen, D Schlitter, V Mazoch, R Šumbera, R Baker	234 ^{E,C}	L Powers, E Pritchard, J Bailey, B Francis
		Plio-Pleistocene History of the Southern African Savanna — Diversification of Southern African Rodents of the Genus <i>Gerbilliscus</i>		Does <i>Geomyces destructans</i> Infection Impair Reproductive Capacity in the Little Brown Bat (<i>Myotis lucifugus</i>)?
11:00 AM	225 ^{E,T}	T Demos, J Peterhans, M Hickerson	235	H Young, K Dittmar de la Cruz, D McCauley, S Billeter, T Young, K Helgen
		Cryptic Species Delimitation and Long-term Persistence Among Small Mammal Lineages in the Eastern Afrotropical Biodiversity Hotspot		Large Herbivore Removal Increases Rodent-borne Disease Prevalence in East Africa
11:15 AM	226	K Everson, L Olson	236	T Smyser, L Page, S Johnson, C Hudson, K Kellner, R Swihart, O Rhodes, Jr.
		Evolutionary Relationships and Divergence Timing of Oryzoricline Tenrecs		Management of Raccoon Roundworm in Free-ranging Raccoon Populations Via Anthelmintic Baiting
11:30 AM	227 ^E	R Boria, M Shcheglovitova, A Radosavljevic, S Jansa, L Olson, R Anderson	237	T Livieri, D Biggins, R Griebel, T Rocke
		Assessing Niche Evolution and Population Connectivity Over Glacial Cycles for Two Malagasy Small Mammals		Mitigation Efforts to Conserve Black-footed Ferrets During a Plague Epizootic
11:45 AM	228	K Rowe, A Achmadi, J Esselstyn, P Smissen, J Shenck, S Stepan	238	K Helgen, S Sonsthagen, R Dikow, F Hailer, R Fleischer
		Biogeographic Transitions in Extant Murinae (Rodentia: Muridae) of the Indo-Australian Archipelago		Devil Disease Before DFTD: Museum Specimen Insight into Marsupial Carnivore Declines
12:00 PM	229 ^{E,**}	M Roberts, J Leonard, K Helgen, J Maldonado	239	C Burdett, M Farnsworth, M Lutman, T DeLiberto, K Pedersen, R Miller
		Molecular Phylogenetics of Southeast Asian Squirrels Based on Mitochondrial DNA Reveals Paraphyly in the Genus <i>Dremomys</i>		Modeling the Distribution of Feral Swine in the United States
12:15 PM	230	E Sargis, N Woodman, N Morningstar, A Reese, L Olson	240 ^E	R Nadolny, H Gaff
		Morphological Distinctiveness of Javan <i>Tupaia hypochrysa</i> (Scandentia, Tupaiidae)		Interactions Between Small Mammals and Ticks in Successional Wetlands in Virginia
12:30 PM		LUNCH		

^EOral or Poster Presentation that is being evaluated
^{**}Research funded by an award from the ASM

^TRecipient of a travel award
 C = Cancelled presentation

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TUESDAY, 18 JUNE, MORNING SESSIONS

ROOM		Salon IJ
SESSION/SYMPOSIUM		Technical Session 17: Community Ecology
MODERATOR		Diane Post
10:00 AM	241	<u>J Goheen</u>, S Newsome, D Boro, K Fox-Dobbs, A-M Hodge, T Otieno, H Young
		Pathways to Ecological Generalism in a Savanna Small-Mammal Community: An Experimental Test of a Macroecological Pattern
10:15 AM	242 ^E	<u>P Eyheralde</u>, S Fairbanks
		Bison-mediated Seed Dispersal in a Tallgrass Prairie Reconstruction
10:30 AM	243 ^E	<u>L Hall</u>, M Westover, C Day, R Knight, R Larsen, B McMillan
		Influence of an Exotic Ungulate on Community Dynamics of Wildlife at Water Sources in the Great Basin Desert
10:45 AM	244	<u>J Orrock</u>, M Witter
		Mammalian Consumers Mediate the Effect of Mycorrhizae on the Establishment and Growth of a Native Perennial Bunchgrass
11:00 AM	245**	<u>C Habeck</u>, N DeMelfy, A Classen, R Norby, R Lindroth
		Impact of Rodents on Composition and Chemistry of Transitional Plant Communities
11:15 AM	246 ^E	<u>R Stephens</u>, E Anderson
		Habitat Associations and Assemblages of Small Mammals in Natural Plant Communities of Wisconsin
11:30 AM	247	<u>J Hoffman</u>
		Habitat Characteristics Within a Zone of Separation Between the Ranges of Two Species of Pocket Gophers
11:45 AM	248 ^E	<u>D Gaydos</u>, S Scuderi, T Barrett, G Barrett
		Mesocosms Designed to Investigate Ecological Facilitation Between <i>Ochrotomys nuttalli</i> and <i>Peromyscus leucopus</i>

^EOral or Poster Presentation that is being evaluated

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American Society of Mammalogists 93rd Annual Meeting—Philadelphia, Pennsylvania

TUESDAY, 18 JUNE, MORNING SESSIONS

ROOM		Salon IJ
SESSION/SYMPOSIUM		Technical Session 17: Community Ecology
MODERATOR		Diane Post
12:00 PM	249^E	<u>R Eguren</u>, K McBee
		Community Structure, Population Demographics, and Biomarkers in Chiroptera from Tar Creek Superfund Site, Oklahoma, USA
12:15 PM	250	<u>S Sheffield</u>, J Yunger, H Lin, X Lu
		Exposure and Effects of Heavy Pesticide Application on Small Mammals Inhabiting an Arid Agroecosystem in Xinjiang Province, China
12:30 PM		LUNCH

^EOral or Poster Presentation that is being evaluated

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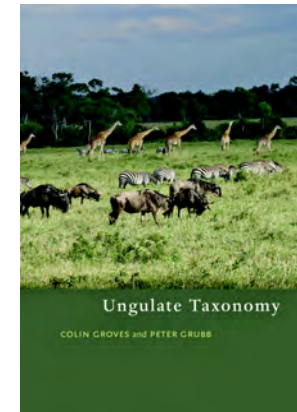
TUESDAY, 18 JUNE, AFTERNOON SESSIONS

**Capstone Symposium - Salon E
Ungulates Today - Moderator: D M Leslie, Jr**

- 1:30 PM** Introduction
D M Leslie, Jr
- 1:35 PM** **251** Evolution of Ungulate Mating Systems: Sociality, Resources, and Terrain
R T Bowyer, D R McCullough, J L Rachlow, S Ciuti, J C Whiting
- 1:55 PM** **252** Conservation Genetics of Ungulates: How Far We've Come
K J Hundertmark
- 2:15 PM** **253** From Rhetoric to Results: Making Captive Ungulate Populations Relevant to Conservation Efforts
B A Huffman
- 2:35 AM** **254** Carl Meets Karl: The Case for Testability in Ungulate Taxonomy
C Groves Keynote Speaker
- 3:20 AM** Discussion and Concluding Remarks
R T Bowyer, C Groves, B A Huffman, K J Hundertmark, D M Leslie, Jr

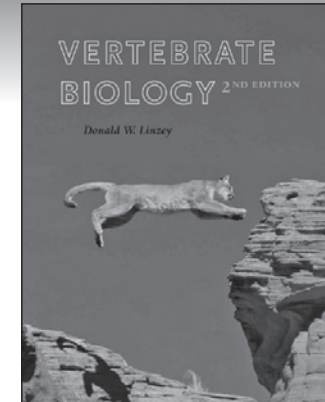
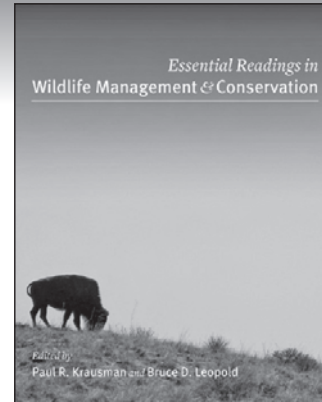
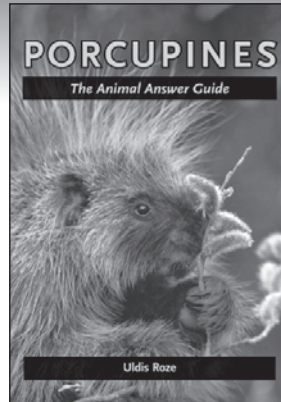
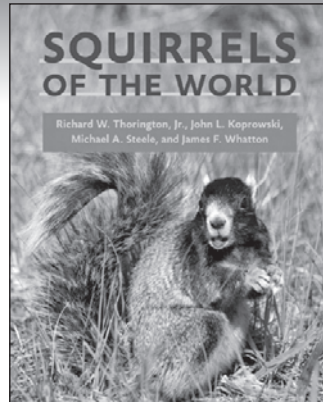
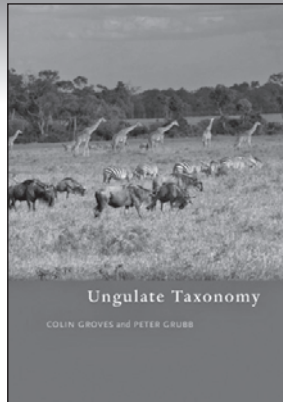
***Ungulate Taxonomy* Book Signing**

You are cordially invited to meet Professor Groves and to a book signing event at the conclusion of the *Ungulates Today* Capstone Symposium. Copies of *Ungulate Taxonomy* may be purchased in advance from The Johns Hopkins University Press sponsor table at a special price of \$60.00, tax inclusive. The special price will be good throughout the meeting.



5:30 PM	DONOR RECEPTION – Salon F
6:00 PM	PRE-BANQUET SOCIAL – Salon F
7:00 PM	BANQUET – Salon E

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ABSTRACTS

E = Evaluated Student Oral or Poster Presentation; C = Cancelled Presentation
ST = Recipient of a student travel award; ECT = Recipient of an early career travel award;
**Research funded by an award from the ASM

1 (E) ANNIE M. ALEXANDER AWARD, Plenary I, Salon E, Saturday 15 June 2013

Brooks A. Kohli¹, Vadim B. Fedorov², Eric Waltari³, Joseph A. Cook¹

¹Department of Biology and Museum of Southwestern Biology, University of New Mexico, Albuquerque NM 87131–1051 USA; ²Institute of Arctic Biology, University of Alaska Fairbanks, Fairbanks, AK 99775-7000 USA; ³City College of New York, Department of Biology, Marshak Science Building 814, 160 Convent Ave, New York, NY 10031 USA

Phylogeography of a Holarctic Rodent (*Clethrionomys rutilus*): Testing High-latitude Biogeographic Hypotheses and the Dynamics of Range Shifts

Pleistocene glacial cycles greatly influenced demography and geographic distribution of high-latitude species and played an essential role in determining how contemporary genetic diversity is partitioned. This history of change in northern ecosystems sets the stage for forecasting how species inhabiting tundra and boreal forest will respond to the ongoing alterations in climate. We use a multilocus phylogeographic approach (1 mtDNA gene, 3 nuclear genes) combined with species distribution models to investigate the response of a Holarctic mammal, the northern red-backed vole (*Clethrionomys rutilus*), to environmental change. Our assessment is based on widespread sampling, a species tree approach for integration of multiple lines of genetic evidence, and population genetic techniques to elucidate the biogeographic and demographic history of northern red-backed voles. The phylogeographic history of *C. rutilus* is characterized by isolation and subsequent expansion from multiple refugia in Asia, an uncommon history among other predominantly boreal forest-associated species. Demographic and distributional changes are dynamic and emphasize the effect pre-LGM glacial-interglacial cycles had on contemporary phylogeographic structure.

2 (E, **) ANNA M. JACKSON AWARD, Plenary I, Salon E, Saturday 15 June 2013

Elizabeth M. Kierepka, Emily K. Latch

Department of Biological Sciences, University of Wisconsin-Milwaukee, Milwaukee, WI 53211 USA

Range-wide Phylogeography of a Widespread, Specialist Carnivore, the American Badger

Genetic variation within mobile, widespread species can be difficult to predict based on the multiple potential isolating factors at large spatial scales. In North America, for example, Pleistocene glaciation events, anthropogenic landscape changes, and landscape barriers all can influence evolutionary dynamics. Most widespread species are generalists and are typically characterized by high gene flow across most barriers. In contrast, more specialized species should be sensitive to habitat heterogeneity, but few studies have tested this hypothesis. Therefore, we focused on the American badger, a grassland-associated mesocarnivore adapted for semifossoriality. Genetic data (12 microsatellites, 1,000 bp mtDNA) were collected from 1,000 harvested or road-killed badgers from 2009 to 2013 across much of their North American range. Analyses indicated the presence of 2 main lineages: east and west. While the Great Lakes were detected as a barrier within the eastern lineage, the main split between east and west did not correspond to any conspicuous barrier. Instead, east and west appear to be 2 separate refugial populations undergoing secondary contact in the midwestern United States. This area is a well-characterized suture zone, which indicates that clearing of forests within the Midwest may have facilitated gene flow between east and west. Overall, our results indicate that even when preferences are not the major driver of gene flow, ecology is important for interpretation of how widespread mammals respond to complex landscape changes. This research was supported by an ASM Grants-In-Aid of Research awarded to Elizabeth M. Kierepka in 2012.

3 (E, **) ELMER C. BIRNEY AWARD, Plenary I, Salon E, Saturday 15 June 2013

Adam T. Ford¹, Jacob R. Goheen²

¹Department of Zoology, University of British Columbia, Vancouver, BC V6T 1Z4 Canada; ²Departments of Zoology & Physiology and Botany, University of Wyoming, Laramie, WY 82071 USA

Plant Defenses and Prey Behavior Mediate a Trophic Cascade in East Africa

The importance of herbivore behavior in mediating the indirect effects of predators on plants (i.e., trophic cascades) has proven contentious and remains unresolved for large, terrestrial mammals. We evaluated evidence for a trophic cascade driven by resource selection of impala (*Aepyceros melampus*), the numerically dominant ungulate across vast expanses of East Africa. We used a combination of GPS telemetry, habitat manipulations, feeding trials, and a large-scale exclusion experiment to demonstrate a trophic cascade mediated by impala behavior. Habitat selection was driven by visibility, not access to forage. Preferred forage occurred at higher densities in areas with low visibility and inside exclosures; however, unpalatable forage occurred in similar densities across areas with a range of visibilities as well as between exclosures and paired control plots. Feeding trials indicated that palatability decreased

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with increasing spinescence among different forage plants. A combination of predation risk and plant defenses may underlie the distribution of at least some species of shrubs in this system. This represents one of a very small number of studies to identify a behaviorally mediated trophic cascade in a large mammal system and to demonstrate that plant defense may buffer against the cascading effects of risk. This research was supported by an ASM Grants-in-Aid of Research awarded to Adam T. Ford in 2011.

4 (E) A. BRAZIER HOWELL AWARD, Plenary I, Salon E, Saturday 15 June 2013

Jason L. Malaney

Museum of Southwestern Biology, University of New Mexico, Albuquerque, NM 88130 USA

Using Biogeographic History to Inform Conservation: The Case of Preble's Meadow Jumping Mouse

This study explores why the assessment of biogeographic history of organisms is critical to effective implementation of costly strategies in natural resource management. Through comprehensive taxonomic and geographic sampling, use of multiple genetic loci, and integration of niche assessments and fossils, I provide an alternative view of conservation priorities for the highly controversial Preble's meadow jumping mouse (*Zapus hudsonius preblei*) and its relatives in North America. This example highlights how conservation efforts often are predicated on a taxonomy that frequently predates modern evolutionary concepts and does not account for the historical-biogeographic signatures that should be central to informing management actions.

5 (E,**) ALBERT R. AND ALMA SHADLE AWARD, Plenary I, Salon E, Saturday 15 June 2013

C. Miguel Pinto

Department of Mammalogy and Sackler Institute for Comparative Genomics, American Museum of Natural History, New York, NY 10024 USA; The Graduate Center, City University of New York, NY 10016 USA; Centro de Investigación en Enfermedades Infecciosas, Pontificia Universidad Católica del Ecuador, Quito Ecuador

Mammals from Andean Cloud Forests: Studies on Diversity, New Species, and Biogeographic Origins

The Andes are considered one of the world's hottest hotspots of diversity; however, there are still large gaps in our knowledge about their mammalian diversity. This lack of information is particularly pronounced in the Andean cloud forests, located roughly between 1,500 to 3,000 m on the eastern and western flanks of the cordillera, areas highly threatened by deforestation, agriculture, and mining. Here, I present results of several multi-authored projects, divided in 3 main topics, which seek to characterize the mammalian diversity of these forests. First, 3 new species belonging to different clades are being described: a shrew-opossum (Paucituberculata: Caenolestidae: *Caenolestes*), a Mindo rat (Rodentia: Cricetidae: *Mindomys*), and an olingo (Carnivora: Procyonidae: *Bassaricyon*). Second, analyses of nuclear and mitochondrial DNA, including DNA barcoding initiatives, help to clarify phylogenetic relationships of several poorly known groups (e.g., caenolestids), and unveil cases of species that may need further systematic revisions (e.g., several cricetids). Finally, biogeographic analyses of distribution and endemism combined with phylogenetic reconstructions of ancestral areas shed light on the origins of these mammalian fauna. Overall, results indicate that the Andean cloud forests harbor unique mammalian taxa that demonstrate complex biogeographic patterns and high levels of endemism. Also it is shown that further sampling and systematic work still is needed to fully characterize this astounding fauna. This research was supported by an Albert R. and Alma Shadle Fellowship in Mammalogy awarded to C. Miguel Pinto in 2012.

6 (E,**) ASM FELLOWSHIP, Plenary I, Salon E, Saturday 15 June 2013

Ryan A. Long¹, R. Terry Bowyer¹, John G. Kie¹, Warren P. Porter²

¹Department of Biological Sciences, Idaho State University, Pocatello, ID 83209 USA; ²Department of Zoology, University of Wisconsin Madison, Madison, WI 53706 USA

Linking Climate to Behavior and Fitness of Endotherms: A Bioenergetic Approach

The heat-dissipation limit theory posits that tradeoffs in energy allocation by endotherms often may be governed by limits on their capacity to dissipate heat, rather than by availability of energy. Despite its broad ecological relevance, however, behavioral implications of the theory have not been tested. We evaluated relative importance of the thermal environment in influencing behavior and fitness of a large-bodied endotherm (North American elk; *Cervus elaphus*) occupying 2 ecosystems with markedly different climates: 1) a temperate montane forest; and 2) an arid high-elevation desert. We used a mechanistic biophysical model to produce spatiotemporally explicit estimates of metabolic expenditures by elk as they navigated their respective landscapes. Model predictions were combined with location data from GPS collars and data on important fitness correlates to evaluate relationships among the thermal environment, behavior, and fitness of elk. Elk in the desert strongly selected areas that minimized energetic costs during spring-autumn, and showed no selection for forage quality. In the montane forest, relative importance of energetic costs as a determinant of behavior outweighed forage quality only in summer. Nevertheless, variability in energetic efficiency among adult females in the forest prior to parturition was positively correlated with birth mass of

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young. Our results add support to the heat-dissipation limit theory, and provide important clues about how large endotherms are likely to respond behaviorally as global temperatures continue to rise. This research was supported by the American Society of Mammalogists Fellowship in Mammalogy awarded to Ryan A. Long in 2012.

7 Symposium I: White-nose Syndrome: A Deadly Disease of North American Hibernating Bats, Salon E, Saturday 15 June 2013

Jeremy T. H. Coleman¹, Joseph S. Johnson²

¹National White-nose Syndrome Coordinator, US Fish and Wildlife Service, Hadley, MA 01035 USA; ²Department of Biology, Bucknell University, Lewisburg, PA 17837 USA

White-nose Syndrome (WNS) has caused unprecedented mortality in hibernating bats in eastern North America since its discovery in 2007. WNS is caused by the fungus *Geomyces destructans* (Gd), which invades and erodes the skin of affected bats, leading to fatal disruptions in physiology during hibernation. Seven North American bat species have been affected by WNS to date, with infected bats or the causative fungus documented in 24 US states and 5 Canadian provinces. Gd is believed to have been introduced to North America from Europe, where large-scale mortality has not been documented. The rapid spread and devastating impacts of WNS in North America have presented researchers and natural resource managers with considerable biological and social challenges, but relatively few tools have become available to combat the disease. Federal and state listing under the Endangered Species Act provides legal authority for government agencies to manage bats. Several states have begun to list hibernating bat species and the US Fish and Wildlife Service is currently assessing 3 species for potential listing. A national response plan, finalized in May 2011, provides the framework for a comprehensive North American response, and presents a model for responding to future wildlife disease outbreaks. Collaboration between the multifarious groups and individuals engaged in the WNS response remains critical, and is responsible for the considerable advances made towards understanding of this disease.

8 Symposium I: White-nose Syndrome: A Deadly Disease of North American Hibernating Bats, Salon E, Saturday 15 June 2013

Jeffrey Lorch¹, Daniel Lindner², Carol Meteyer³, Laura Muller³, Michelle Verant⁴, David Blehert³

¹Department of Forest and Wildlife Ecology, University of Wisconsin-Madison, Madison, WI 53706 USA; ²US Forest Service, Northern Research Station, Center for Forest Mycology Research, One Gifford Pinchot, Madison, WI 53726 USA; ³US Geological Survey - National Wildlife Health Center, Madison, WI 53711 USA; ⁴Department of Pathobiological Sciences, University of Wisconsin-Madison, Madison, WI 53706 USA

Chilled Chiropterans as Fungal Fodder: Why *Geomyces destructans* is Killing North American Bats

White-nose Syndrome (WNS) is a lethal disease of North American hibernating bats. First photo documented in New York in February 2006, WNS has rapidly spread across the eastern United States and Canada, killing an estimated 5.5 million bats. Prior to the emergence of WNS, such massive population declines in mammal species due to an infectious disease were unprecedented. Also unusual is that WNS is caused by a fungus, a class of pathogens that rarely result in large disease outbreaks among healthy mammals. Laboratory studies have demonstrated that infection by the fungus *Geomyces destructans* causes WNS in healthy bats as characterized by skin lesions that may disrupt physiological processes of the host during hibernation. *Geomyces destructans* is psychrophilic (cold-loving): it grows well at the low temperatures experienced by hibernating bats (approximately 2-10°C), but it does not grow on euthermic animals. However, cave sediments have been shown to harbor the fungus throughout the year (including during warm summer months), indicating that underground bat hibernacula serve as long-term reservoirs for *G. destructans*. Several lines of evidence suggest that *G. destructans* was introduced to North America, possibly from Europe where bats seem to coexist with the fungus. Thus, the substantial population declines caused by WNS on this continent are likely the result of a novel pathogen introduced into a naïve population of hosts.

9 Symposium I: White-nose Syndrome: A Deadly Disease of North American Hibernating Bats, Salon E, Saturday 15 June 2013

Marianne S. Moore¹, Kenneth A. Field¹, Gregory G. Turner², Morgan E. Furze¹, Daniel W. F. Stern¹, Paul R. Allegra¹, Sarah A. Brownlee¹, Chelsey D. Musante¹, Megan E. Vodzak¹, Matthew E. Biron¹, Melissa B. Meierhofer¹, DeeAnn M. Reeder¹

¹Department of Biology, Bucknell University, Lewisburg, PA 17837 USA; ²Pennsylvania Game Commission, Harrisburg, PA 17110 USA

Immune Responses to Infection By *Geomyces destructans* Vary Between Species Exhibiting Differential White-nose Syndrome Population Declines

The emerging fungal disease known as White-nose Syndrome (WNS) does not affect all species or all populations equally. For example, big brown bats (*Eptesicus fuscus*) have significantly lower mortality than little brown myotis (*Myotis lucifugus*) and are probably better able to survive infection because of their larger body size and their

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preference for hibernating for shorter periods, at colder temperatures, and solitarily or in smaller clusters. However, the ability of big brown bats to withstand infection by the causative *Geomyces destructans* (Gd) is not truly known. We experimentally infected both species with Gd and measured immune responses at 3, 7, and 13 weeks postinfection. Methods included total and differential white blood cell counts, microbicidal assays, phagocytic assays, total and anti-Gd immunoglobulin ELISAs, and cytokine profiles. Housed in identical conditions, big brown bats developed much lower levels of infection than little brown myotis and showed larger immune responses to Gd infection. Additionally, uninfected big brown bats exhibited greater immune responses in general and maintained higher immunocapabilities throughout hibernation compared with uninfected little brown myotis. Differences may reflect less hibernation-induced immunosuppression in big brown bats or general differences between the immune systems of these 2 species. Notably, big brown bats may be equipped to respond immunologically to Gd infections more quickly and effectively than little brown myotis, especially as hibernation progresses and the fungus proliferates.

10 Symposium I: White-nose Syndrome: A Deadly Disease of North American Hibernating Bats, Salon E, Saturday 15 June 2013

Winifred F. Frick¹, Tina Cheng¹, Kate Langwig¹, Kevin Drees², Amanda Janicki³, Gary F. McCracken³, Jeff Foster², A. Marm Kilpatrick¹

¹Department of Ecology and Evolutionary Biology, UC Santa Cruz, Santa Cruz, CA 95064 USA; ²Center for Microbial Genetics and Genomics, Northern Arizona University, Flagstaff, AZ 86011 USA; ³Department of Ecology and Evolutionary Biology, University of Tennessee, Knoxville, TN 37996 USA

Patterns of *Geomyces destructans* Infection Across North America

White-nose Syndrome (WNS) has caused devastating impacts on hibernating bat populations across North America since its emergence in 2006. Determining prevalence and intensity of infection in wild bat populations is critical for understanding the impacts and spread of WNS. In collaboration with state agency biologists, we assessed prevalence and intensity of *Geomyces destructans* infection using molecular diagnostics (qPCR) from swab samples collected from hibernating bats during the 2011–2012 and 2012–2013 winter field seasons across enzootic, epizootic, and leading edge regions and along a latitudinal gradient in North America. Prevalence varies by species in highly impacted regions even within the same hibernacula and by region depending on time since WNS was first detected. Prevalence of infection does not appear to be strongly influenced by colony size, which could have negative implications for impacts of the disease. The use of noninvasive swab sampling provides a method of early detection of *G. destructans* presence before disease symptoms of mortality and visible infection are apparent. Our results are useful to track spread of *G. destructans* at a continental scale and for determining factors associated with risk of arrival of *G. destructans*, disease progression, and impacts to populations.

11 Thematic Session I: Recent Advances in Mammalogy, Salon E, Saturday 15 June 2013

Jason Munshi-South

Department of Natural Sciences, Baruch College, City University of New York (CUNY), New York, NY 10010 USA

Evolution in the Anthropocene: Landscape Genomics of White-footed Mice Along an Urban-to-Rural Gradient

Over 50% of humans now live in cities, and urbanization is 1 of the most important drivers of land transformation around the world. Increasingly, humans are also a selective force driving rapid evolutionary change in other species. This presentation describes ongoing efforts to develop *Peromyscus* (white-footed mice) in New York City as a model for examining the evolutionary implications of urbanization. Our lab integrates complementary approaches from landscape ecology, urban ecology, and population genomics. Most recently, we have been using a landscape genomics approach to examine how urbanization structures both neutral and adaptive genetic variation. We have generated high-density, genome-wide SNP (single nucleotide polymorphism) genotypes using RAD-Seq from over 200 mice sampled from 25 populations along an urban-to-rural gradient spanning New York City to rural Connecticut. We are using outlier analyses to identify candidate genomic regions experiencing selection, and spatial approaches to identify SNPs exhibiting a strong frequency threshold along an urban-to-rural gradient. We are also examining environmental correlations between SNP frequencies and variables related to urbanization. Preliminary results indicate that spatial models based on relatively few high-contrast landscape variables (e.g., vegetation versus impervious urban surfaces) explain connectivity between urban-suburban-rural populations. Genomic regions containing coding sequences involved in metabolism, immunity, and reproduction exhibit statistical signatures of selection in isolated urban populations of white-footed mice. Ongoing work examines variation in gene expression and environment-genotype correlations in urban versus rural populations.

12 (ECT) Thematic Session I: Recent Advances in Mammalogy, Salon E, Saturday 15 June 2013

Taal Levi¹, Felicia Keesing², A. Marm Kilpatrick³, Marc Mangel⁴, Christopher C. Wilmers⁵, Richard S. Ostfeld¹

¹Cary Institute of Ecosystem Studies, Millbrook NY; ²Department of Biology, Bard College, Red Hook, NY USA;

³Department of Ecology and Evolutionary Biology, UC Santa Cruz, Santa Cruz, CA USA; ⁴Department of Statistics

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and Applied Mathematics, UC Santa Cruz, Santa Cruz, CA USA; ⁵Department of Environmental Studies, UC Santa Cruz, Santa Cruz, CA USA

Trophic Cascades and Infectious Disease

Recent increases in Lyme disease, long after the recolonization of deer, suggests that other factors may be responsible for the continuing emergence of Lyme disease. A growing body of evidence suggests that Lyme disease risk is dynamically linked to fluctuations in the abundance of small mammal hosts, which infect the majority of ticks. We show that increases in Lyme disease in the northeastern and midwestern United States over the past 3 decades coincide with a range-wide decline of a key small mammal predator, the red fox, due to expansion of coyote populations. Further, we find that coyote abundance and fox rarity predict the spatial distribution of Lyme disease in New York, while deer density is uncorrelated with Lyme disease incidence across 4 states. We then use a landscape-scale field study to test whether tick abundance and infection prevalence is linked to coyote and fox site occupancy. Finally, we use a 30-year time series of wolf, coyote, and fox relative abundance from the state of Minnesota to show that wolves suppress coyote populations, which in turn releases foxes from top down control by coyotes. This cascade is likely to alter the size spectrum of heavily consumed prey with important implications for biodiversity and human health.

13 Thematic Session I: Recent Advances in Mammalogy, Salon E, Saturday 15 June 2013

Felicia Keesing

Program in Biology, Bard College, Annandale-on-Hudson, NY 12504 USA

Ecological Effects of the Loss of Large Mammals in African Savanna Ecosystems

African savannas support an unparalleled diversity and abundance of large mammals. Since 1995, we have been documenting the consequences of this diversity for less obvious species that share these habitats. The exclusion of large mammals results in a cascade of ecological consequences, including increases in the abundance of small mammals and venomous snakes, and decreases in the survival of Acacia tree seedlings. Our recent research has focused on interactions between wild large mammals and livestock through their shared tick ectoparasites. Cattle in East Africa are often treated with an acaricide that kills ticks attempting to feed. While this acaricide is known to be effective at reducing tick burdens on cattle, its effects on ticks in savanna ecosystems are less well understood. Over 7 years, we sampled ticks monthly on replicated plots that controlled for the presence of cattle and for the presence of 2 guilds of large wild mammals. The presence of acaricide-treated cattle dramatically reduced the abundance of host-seeking nymphal and adult ticks but did not affect the abundance of host-seeking larval ticks. The reduction in ticks that results from the presence of acaricide-treated cattle has potential health benefits for humans and wildlife. Our most recent work explores the possibility of integrating cattle and wildlife to reduce disease risk while maximizing economic benefits for humans.

14 JOSEPH GRINNELL AWARD, Plenary II, Salon E, Sunday 16 June 2013

James H. Brown

Department of Biology, University of New Mexico, Albuquerque, NM 87131 USA

How to Train a Scientist?

I have trained more than 50 Ph.D. students and about 20 Master's students and postdocs. Many have gone on to influential careers. Most are not professional mammalogists, but quite a few are. Most are academics, but quite a few work in conservation NGOs, government agencies, and free-lance activities, and 1 is a guitar-maker. Given their successes, maybe I have done some things right. My philosophy of graduate education is simple: 1) choose the most interesting applicants, not necessarily the ones with the highest qualifications; 2) try to provide a stimulating environment where creativity, motivation, and hard work will be rewarded; 3) treat students like scientific colleagues, not like undergraduates or employees; 4) treat them individualistically, because there is no recipe for how to become a successful scientist; and 5) encourage them to follow their interests, question authority, and above all have fun. The most rewarding thing is that I think I have learned just about as much from them as they have learned from me.

15 ALDO LEOPOLD AWARD, Plenary II, Salon E, Sunday 16 June 2013

Dean E. Biggins

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Black-footed Ferret Conservation: A Mix of Scientific Investigation and Operational Tasks

In 1981, black-footed ferrets (*Mustela nigripes*) were discovered near Meeteetse, Wyoming. We gathered information on ferrets during 1981–1984 using newly developed radio-telemetry methods and other techniques. Diseases (plague and canine distemper) caused a rapid decline in the Meeteetse population of ferrets in 1985. We captured remaining ferrets in 1985–1987 for captive propagation, which became increasingly successful after a disappointing start in 1986.

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Reintroductions began in 1991. Supporting research included developing a technique for comparing habitat quality on reintroduction sites and documenting effects of captivity on behaviors using surrogate Siberian polecats (*M. eversmannii*). Rearing experiments suggested a 10-fold increase in survival of pen-conditioned kits compared to their cage-reared counterparts, strongly influencing the design of new facilities and the strategy for raising kits. Plague (caused by *Yersinia pestis*) is now considered to be the most serious biological impediment to recovery of black-footed ferrets. Its epizootic devastation was apparent in 1985, but its virulence in ferrets was underscored after losing multiple captive ferrets in 1995. Serological monitoring of carnivores documented presence of plague at many reintroduction sites, motivating us to investigate effects of enzootic plague using vector control and vaccines to manipulate the disease. Results suggested that enzootic levels of plague can prevent establishment of viable populations of ferrets. The ferret example led to field research implicating plague as a serious conservation concern in other ecosystems.

16 C HART MERRIAM AWARD, Plenary II, Salon E, Sunday 16 June 2013

James A. Estes

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Sea Otters and Kelp Forests: An Ecological History of the North Pacific Ocean

My intent in this lecture is to recount the high points of what my colleagues and I have learned during 43 years of research on sea otters and kelp forests in the North Pacific Ocean. Most of our discoveries, which center on the ecological influences of sea otter predation, were made possible by the maritime fur trade, the decimation of sea otters and the fragmented recovery of surviving remnant populations. The key ecological process is a trophic cascade in which sea otters enhance kelp forests by preying on herbivorous sea urchins. This effect occurs as an abrupt phase shift, which varies with sea otter density both geographically and depending on the directionality of otter population change. The positive influence of sea otters on kelp forests affects numerous other species and ecological processes. Sea otters also appear to have shaped the coevolution of marine plant/herbivore interactions by reducing the interaction strength of herbivores on plants, thus reducing in turn both the need for plants to defend themselves against herbivory and the need for herbivores to resist those defenses. These dynamics explain the inability of plants and herbivores to coexist at high densities in the North Pacific, the ability of similar plants and herbivores to coexist in the southern oceans, and why kelp forests collapsed so spectacularly following the recent decline of sea otter populations in southwest Alaska.

17 Symposium II: Ecological Niche Modeling: Concepts, Applications, Challenges, and Solutions, Salon E, Sunday 16 June 2013

Robert P. Anderson

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Ecological Niche Modeling: Theory, Reality, and Room for Improvement

Recent advances in ecological niche modeling allow harnessing enormous stores of biological and environmental data to study species niches and distributions. Correlative niche models yield geographic predictions of abiotic environmental suitability, which can be processed to estimate the areas a species occupies. I provide a theoretical overview, clarify key issues regarding data and model building, and highlight areas requiring progress. Throughout, I emphasize additional concepts necessary for transferring a model across space/time, and for studies of niche evolution. Based on an emerging consensus, researchers should: 1) select “scenopoetic” predictor variables not affected by the presence of the focal species, especially those that will maintain predictivity across space/time; 2) obtain occurrence records that constitute representative samples of the areas suitable for the species; 3) use comparison data (absences/background information) from regions in which the species is likely at equilibrium with the variables employed; 4) approximate optimal levels of model complexity, for example via “tuning” or “smoothing”; 5) assess stationarity of the species’ response across space/time (including the possibility of niche differentiation); and 6) assess possible truncations of species response curves, exercising prudence when projecting to non-analog conditions (for transfer across space/time). Opportunities for progress exist for including non-climatic abiotic variables, integrating biotic variables, considering local adaptation, quantifying uncertainty, and running simulations of dispersal and establishment in novel landscapes (e.g., for invasive species or after climate change).

18 Symposium II: Ecological Niche Modeling: Concepts, Applications, Challenges, and Solutions, Salon E, Sunday 16 June 2013

Mariano Soley-Guardia

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American Society of Mammalogists 93rd Annual Meeting—Philadelphia, Pennsylvania

Determining Whether Peninsular Populations of Rodents Inhabit Novel Climatic Conditions in Northern South America, by Using Optimally Complex and Habitat-informed Ecological Niche Models

I examined potential population connectivity and niche evolution in small mammals, taking into account model complexity and the effect of occurrence records that are spatially marginal. Specifically, I fit ecological niche models to continental populations of rodents typically inhabiting mesic conditions in northern South America, and project them onto an area occupied by peninsular populations. Because comparisons of niches require optimally complex models that are also transferable, I first build preliminary models with different settings, and evaluate them using subsets of geographically segregated continental records only. Additionally, records that are spatially marginal (representing protrusions of mesic habitat onto otherwise dry regions) might produce overestimations of species niches (due to the nature and resolution of employed variables). To deal with this issue, I calibrate 2 final models: 1 including and another excluding such records. Jointly interpreting both models, it appears that peninsular and continental populations inhabit the same environmental conditions and are kept allopatric by intervening unsuitable habitat. These conclusions are substantially different when models are built with default settings or do not take into account the effect of spatially marginal records. Hence, when use of finer resolutions (or more proximate variables) is not possible, building complementary models can provide a more realistic estimate of connectivity and environmental conditions typically inhabited by the species.

19 Symposium II: Ecological Niche Modeling: Concepts, Applications, Challenges, and Solutions, Salon E, Sunday 16 June 2013

Eliécer E. Gutiérrez

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Testing the Predicted Geographic Pattern of Competitive Exclusion in Two Species of the Marsupial Genus *Marmosa*

In this study, I use ecological niche models to test the geographic pattern predicted by competitive exclusion in *Marmosa robinsoni* and *M. xerophila*, a task challenged by sampling bias and complications for selection of study regions. If 2 species experience competitive exclusion, then 1 species should predominate in areas of potential sympatry along contact zones. To test this prediction, I first georeferenced occurrence records of focal species. The resulting datasets contained signals of geographic biases in sampling; therefore, I spatially filtered them to reduce possible bias in environmental space. Using these filtered datasets, MaxEnt, and bioclimatic variables, I modeled the species' existing fundamental niches. Because Andean highlands and the Río Orinoco represent barriers that prevent *M. robinsoni* from dispersing to large regions with likely suitable climatic conditions for it, I selected a study region that only contained areas to which this species has access. By superimposing the geographic projections of the models for the 2 species, I identified areas of potential sympatry. Within these areas, the vast majority of records along the single known contact zone corresponded to *M. xerophila*. This result matches the prediction of competitive exclusion and suggests that *M. xerophila* might be responsible for the geographic isolation of a population of *M. robinsoni* in northwestern Venezuela.

20 () Symposium II: Ecological Niche Modeling: Concepts, Applications, Challenges, and Solutions, Salon E, Sunday 16 June 2013**

Tereza Jezkova

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Using Phylogeographic Data to Test Biological Hypotheses Generated by ENMs

Ecological niche models (ENMs) transferred to past climatic conditions have been used to infer historical species distributions. The accuracy of these ENMs, however, is often hard to assess due to lack of independent data. Phylogeographic signals imprinted in species genomes can be used to reconstruct historical distributions and therefore test biological hypotheses generated by ENMs. For example, we can distinguish between populations that have persisted in place for a long period of time versus those that have expanded into an area only recently. Similarly, we can distinguish between populations that have been connected versus those that were isolated. I will explain how phylogeographic data can be used to evaluate ENMs and emphasize some common problems and misconceptions accompanying the interpretations of phylogeographic data. As an example, I will demonstrate how I used the phylogeographic structure of 2 rodents from the American Southwest, the desert kangaroo rat (*Dipodomys deserti*) and the chisel-toothed kangaroo rat (*D. microps*), to evaluate the ENMs transferred to the climatic conditions of the Last Glacial Maximum. I will discuss problems with model extrapolation, as these 2 species have experienced nonanalogous climates between the Last Glacial Maximum and present time. I will also show how contrasting ENMs and phylogeographic structure suggested that 1 of the species has undergone a niche shift, a modeler's worst nightmare, yet an exciting evolutionary discovery. This research was supported by an ASM Grants-In-Aid of Research to Tereza Jezkova in 2005.

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21 Symposium II: Ecological Niche Modeling: Concepts, Applications, Challenges, and Solutions, Salon E, Sunday 16 June 2013

Eric Waltari

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Incorporating Model Uncertainty in Ecological Niche Models to Predict Future Species Distribution and Contact Dynamics: A Case Study Using *Sorex cinereus* and *S. ugyunak* In Alaska

Correlative ecological niche models have been increasingly used, albeit rarely with uncertainty quantified, to create both present-day distribution estimates and paleodistribution estimates, with these paleomodels commonly compared with paleontological data and phylogeographic reconstructions. These approaches can equally be applied to future climate reconstructions to predict future species distributional changes. Considering that these future estimates cannot be corroborated with independent data, such models should be made and interpolated with caution. I will show how taking into consideration the 6 modeling suggestions (selection of environmental variables, of occurrence data, and of background extent as well as testing for niche differentiation, model complexity optimization, and clamping) outlined earlier can lead to better quantification of model uncertainty. I will use as exemplar species *Sorex cinereus* and *S. ugyunak*, which come into contact at the taiga/tundra ecotone in Alaska. Considering current and predicted increased warming trends in the Arctic and elsewhere, I will incorporate the 6 sources of uncertainty as well as variation in emissions scenarios and global circulation models to create estimates of their future distributions. These similar species distribution models can be aggregated both in taxonomic and temporal dimensions and used to make conservation recommendations.

22 Technical Session 1: Natural History, Outreach, and Education, Salon A, Sunday 16 June 2013

David J. Schmidly

Department of Biology, University of New Mexico, Albuquerque, NM 87106 USA

The Life and Career of Vernon Bailey: America's Greatest Field Naturalist-Mammalogist

Vernon Bailey (1864-1942) was among the last of the naturalists to achieve professional status through self-education and apprenticeship instead of a formal education. In 1887, he was appointed as a Field Naturalist for the Biological Survey (USBS), and he worked for the agency until his retirement at the rank of Chief Field Naturalist in 1933. Practically every season of employment was marked by fieldwork in some part of the US. His legacy includes publishing > 200 scientific papers, contributing ca. 13,000 specimens to the USBS mammal collection, describing 78 taxa of mammals, and serving as the 8th President of the ASM (1933-1934). Bailey designed and perfected the Survey's live "beaver trap" and the "foothold trap" for which he was awarded prizes by the American Humane Association. On a personal level, he was scrupulously honest and fair and a model of integrity. He was quietly generous and admired by all who knew him. This talk will focus on 5 aspects of Bailey's life and career: 1) his early childhood and adolescent years; 2) his apprenticeship with C. Hart Merriam at the USBS; 3) his marriage in 1899 to Florence Merriam (C. Hart Merriam's sister); 4) his career at the USBS; and 5) his retirement years.

23 Technical Session 1: Natural History, Outreach, and Education, Salon A, Sunday 16 June 2013

Neal Woodman

USGS Patuxent Wildlife Research Center, National Museum of Natural History, Smithsonian Institution, Washington, DC 20013-7012 USA

Rafinesque's Apocryphal Western Mammals: Why the Type Localities of the Mule Deer (*Odocoileus hemionus*) and the Long tailed Deer (*Odocoileus virginianus macrotus*) Are Not Where We Thought They Were

Among the iconic mammals of western North America is the mule deer, *Odocoileus hemionus*, which was formally described and named in 1817 by the eccentric North American natural historian Constantine S. Rafinesque. At the same time, Rafinesque also described the "long tailed deer," which is currently recognized as a Central Plains subspecies of the white-tailed deer, *Odocoileus virginianus macrourus*. Rafinesque based his descriptions of these 2 deer, along with those of 5 other species of mammals, on information he obtained from the recently published journal of the French Canadian fur trader, Charles Le Raye. Le Raye had been captured by a Sioux raiding party along the Osage River in Missouri in 1801, and he remained a captive for 3 years and 5 months. During this time he traveled with his captors north and west along the Missouri River drainage as far as the Yellowstone River of Montana and the Big Horn Basin of Wyoming—several years before the Lewis and Clark Expedition visited some of the same regions. Le Raye described the native peoples he encountered, and, more important to zoologists, he described a number of the animals he encountered. Unfortunately, the veracity of Le Raye's journal has been questioned by historians and ethnographers, as has the very existence of this voyageur. The scientific names of the mule deer and long tailed deer are not endangered—the Code of Zoological Nomenclature makes no provision for mistakenly naming a fictional creature, particularly one whose existence has been established by the credibility of generations of post-1758 biologists and wildlife management professionals. The particular identity of the organisms that bear the names does

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come under scrutiny, however, because the type localities are part of the myth. Fortunately, the author of Le Raye depended upon other, verifiable sources for his descriptions, and, by tracing those sources, we can determine both the original, early 19th-century concept of those taxa and from whence the animals came.

24 Technical Session 1: Natural History, Outreach, and Education, Salon A, Sunday 16 June 2013

John J. Ososky

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True Stories from the Archives: The Emergence of Modern Marine Mammal Science During the Era of Smithsonian Curator Frederick W. True

Frederick W. True, Smithsonian curator of mammals and later head curator from 1883 to 1911, is little known as one of the founding fathers of modern marine mammal science. He continued and expanded the practice of opportunistic natural history collecting instituted by his predecessor, Spencer Baird, through partnerships with whaling companies, fishermen, life-saving station keepers, lighthouse keepers, the military, academic colleagues, and many others to help create the world's largest collection of recent and fossil whales. He helped bring order to the taxonomic disarray of the cetaceans with a review and revision of the family Delphinidae, a review of the nomenclature of mysticetes, and an account of the family Ziphiidae. He described a number of new species including Dall's porpoise (*Phocoenoides dalli*) and Stejneger's beaked whale (*Mesoplodon stejnegeri*). He oversaw development of exhibits, including a blue whale model. A review of the archives reveals that he worked closely with many of the leading natural history scientists of his time, including Roy Chapman Andrews, curator at the American Museum and famed dinosaur collector, anatomist and paleontologist Edward D. Cope, Alaskan explorer and naturalist William H. Dall, whaler turned conservationist Captain Charles Scammon, and collector W. L. Abbott. True was an avid student of the history of whaling, and while curator joined a whaling crew for several months and helped collect a fin whale for the museum.

25 Technical Session 1: Natural History, Outreach, and Education, Salon A, Sunday 16 June 2013

Reginald A. Hoyt¹, James A. Hart²

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Mammal Technical Committee of the Pennsylvania Biological Survey: Triumphs and Challenges

Organized in 1979, the Mammal and Ornithological Technical Committees of the Pennsylvania Biological Survey were designated as official scientific advisory committees to the Pennsylvania Game Commission (Pennsylvania's wildlife management agency). Bringing together wildlife managers, researchers, and academicians, the Mammal Technical Committee (MTC) promotes dialog concerning the conservation of Pennsylvania's mammals. Past efforts of committee members have included *Species of Special Concern in Pennsylvania* (1985), a comprehensive assessment of the status of Pennsylvania's mammals, a survey of cave-dwelling bats, the status of solitary tree bats and the least shrew, and monitoring of Allegheny woodrat (*Neotoma magister*) populations. In 2001, the Pennsylvania Important Mammal Areas Project (IMAP) was initiated. It promotes the conservation of mammals by identifying critical sites and habitats and by educating the public, via ecotourism opportunities, about mammals and their needs. In 2010, Steele et al. edited *Terrestrial Vertebrates of Pennsylvania: A complete guide to species of conservation concern*, updating the work published in 1985. Currently a state-wide Mammal Atlas project is in the planning stages. Significant progress has been made, however, invasive species, wildlife disease, climate change, energy development, and habitat fragmentation present Pennsylvania mammals and the MTC with serious challenges. In addition to the direct threats to mammal populations, political and industry opposition to conservation efforts presents new and substantial obstacles to the mission of the MTC and the Pennsylvania Game Commission.

26 Technical Session 1: Natural History, Outreach, and Education, Salon A, Sunday 16 June 2013

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The Latin American Network for Bat Conservation

Latin America contains more bat species than any other continent. The region contains fully one-third of all bat species in the world, in about 13% of its land surface; more than 380 bat species including 6 endemic families inhabit the region. Latin America also suffers from severe ecosystem degradation and limited conservation professionals. However, over the past decade, many professionals have returned, and this worldwide effort is finally bearing fruit. In 2007, 11 Latin American countries decided to work together towards designing, planning, and implementing a bat conservation agenda. In 2009, 16 countries met to draft the charter documents that would guide bat conservation and research efforts for the next couple of decades. Today, the documents are ready and are being implemented. The Latin American Network for Bat Conservation (RELCOM for its Spanish acronym) is working in almost 20 countries, and has identified 5 top threats to bats: habitat loss, roost destruction and disturbance, human-bat conflicts and

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emerging infectious diseases, indiscriminate use of toxic substances, and other emerging threats such as white nose syndrome and unmitigated wind farm developments. Each threat is addressed with specific goals, objectives, and indicators of success. The work is underway to reduce or eliminate local threats. This model of local empowerment, global partnership, and regional input is promising for many other conservation threats around the world.

27 Technical Session 1: Natural History, Outreach, and Education, Salon A, Sunday 16 June 2013

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eMammal - Citizen Science Camera Trapping as a Solution For Broad-scale, Long-term Monitoring of Wildlife Populations

eMammal is a new initiative integrating camera trap data from researchers and citizen scientists to increase the spatial and temporal scale of wildlife survey data. We use a cloud computing workflow including remote photo upload, expert review of photo ID, and store photos and data in a Smithsonian digital repository. In our 1st field season, 85 volunteers deployed cameras to 687 sites in 12 parks across 3 states and recorded over 25,000 animal detections with camera traps. Our initial research questions evaluate the effects of consumptive and nonconsumptive recreation on wildlife, and preliminary results indicate significant patterns. White-tailed deer, black bear, bobcats, red fox, and eastern gray squirrel were detected more in unhunted areas while coyotes and wild turkeys were detected more in hunted areas. White-tailed deer and black bear were detected more frequently off trails, while coyotes, red fox, and bobcats were detected more often on trails. Volunteers were attracted to the project by the desire to contribute to science but found capturing photos of wildlife the most rewarding experience. The amount of wildlife data collected in a single season shows the potential for camera traps and citizen science to sustainably monitor mammals at a large scale. eMammal combines volunteer and researcher data into a publically accessible dataset to enable conservation and personal connections with mammals in today's rapidly changing world.

28 Technical Session 1: Natural History, Outreach, and Education, Salon A, Sunday 16 June 2013

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Integrating Carnivore Research, Technology, Field Experience and Collaboration in the Undergraduate Biology Curriculum

Ongoing studies of carnivore abundance, density, and behavior in Westchester County, New York, use a variety of techniques to investigate areas of conservation value. An outgrowth of this research was the development of an upper-level core research biology course that incorporated field, technological, and social tools needed in the professional world. The new course strengthens the biology and environmental science research curricula by incorporating: 1) direct field experience; 2) peer-to-peer learning and teamwork; and 3) technological skill building. The course showcases camera-traps, a simple but powerful field tool, the processing of resulting wildlife photos, statistical analysis, and GIS to introduce students to field-based science. An overview of the wildlife data collected, how the data were analyzed by students in the lab, and how we integrated this material into a semester-long, upper-level biology course that combined science and technology will be discussed.

28/257 Technical Session 1: Natural History, Outreach, and Education, Salon A, Sunday 16 June 2013

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Monitoring Wildlife Using Smartphones: The Role of Mobile Devices in Research and the Classroom

Numerous ongoing citizen science projects are mobilizing the public to collect data at a large scale, well beyond the scope of that of a typical researcher. In June 2012 using the open-source Epicollect platform and smartphone app, RoadkillGarneau and WildlifeBlitzGarneau projects were developed to monitor wildlife sightings, both alive and dead. TrackingWildlifeSignGarneau was recently launched to aid wildlife trackers and conservation biologists who are systematically monitoring wildlife corridors. We have incorporated these citizen science projects, emphasizing the use of technology, in our ecology classrooms and research. As of February 2013, RoadkillGarneau has citizen scientists collecting across 12 states (CO, FL, MA, MI, NC, NY, NH, NM, PA, OK, TX, and VT), having logged 248 individuals of 39 species. Similarly, WildlifeBlitzGarneau has participants collecting in 8 states (AK, FL, MA, MT, NC, NY, SC, and

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TX) and Quebec, Canada, having logged 152 individuals of 81 species with. Smartphone technology streamlines data collection and organization, facilitates photo documentation with georeferencing, and encourages public participation in research projects. In the Epicollect platform, data are sent to an open-source Google AppEngine, making real-time data available on a webpage for participants to instantaneously experience their scientific impact. This project has the potential to engage audiences ranging from naturalists to mail carriers and bus drivers and can provide wildlife managers with important information on the timing of wildlife movement.

29 (E) Technical Session 2: Morphology, Salon B, Sunday 16 June 2013

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Quantification of Olfactory Bulb Shape and Patterns of Brain Shape Variation in Procyonidae

Olfactory bulb size and position is not uniform within Carnivora, with the variation in size and position linked to ecological differences between species. Quantitative studies of olfactory bulbs have traditionally focused on measuring their size. This is the 1st attempt to directly quantify differences between the shapes of the brain and olfactory bulbs in the carnivoran family Procyonidae. I used 3-dimensional geometric morphometrics to quantify variation in brain morphology within Procyonidae using endocasts as a proxy for brain shape. Endocasts of 7 procyonid species were digitally rendered from computed tomographic data and 21 surface landmarks were collected. A principal components analysis was then performed to analyze shape variation within the family. Olfactory landmarks represent 3 of the 10 highest loading landmarks on the first 2 principal components (PC), contributing to 22.99% of the variation on PC1 and 24.45% of the variation on PC2, with PC1 and PC2 representing 46.30% and 21.13% of the total variation, respectively. The shape differences in the olfactory bulbs represent some of the greatest variation in overall brain morphology among procyonids. The large contribution of olfactory landmarks to overall differences in brain shape indicates significant variability of olfactory bulb shape and may be related to the diverse ecologies within Procyonidae.

30 Technical Session 2: Morphology, Salon B, Sunday 16 June 2013

Frank E. Fish¹, Paul W. Weber², Laurens E. Howle², Mark M. Murray³, Joy S. Reidenberg⁴

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Association of Flipper Morphology and Hydrodynamics with the Maneuvering Ecology of Large Whales

Cetaceans evolved flippers that are unique in size and shape due to selection pressures associated with hunting, foraging, and body size. Flippers function as control surfaces for maneuverability and stability. Flippers of cetaceans and engineered hydrofoils are similar with streamlined cross-sections and wing-like planforms, which affect lift, drag, and hydrodynamic efficiency. Scale models of the flippers from large-bodied (body length > 6 m) cetaceans (*Balaenoptera physalus*, *Orcinus orca*, *Physeter macrocephalus*) were constructed from computed tomography (CT) scans of flippers. Flipper planforms were highly tapered for *B. physalus*, a rounded, paddle-like design for *O. orca*, and a square geometry for *P. macrocephalus*. Hydrodynamic properties of the models at varying angles of attack (-40 to 40 degrees) were determined in a water tunnel with a multi-axis load cell. The flippers were found to have hydrodynamic characteristics similar to engineered wings. Differences in flipper morphology of the large-bodied cetaceans and their hydrodynamic performance are associated with the requirements of aquatic locomotion involved with ecology of the whales. The flippers of *O. orca* provided the greatest maneuverability, whereas the flippers of *B. physalus* had low drag for lunging, and the flippers of *P. macrocephalus* provided lift for diving.

31 (E, ST) Technical Session 2: Morphology, Salon B, Sunday 16 June 2013

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Seals, Skulls, and Sexual Dimorphism

The Pinnipedia (seals, sea lions, and walrus) includes some of the most dimorphic living mammals. For example, male southern elephant seals (*Mirounga leonina*) weigh 5 times the females and guard harems of around 50 individuals. Pinniped reproductive strategies range from monogamy to extreme polygyny, with males of different species placing emphasis on display or combat to secure a mate. We investigate the influence of these reproductive strategies on the construction of the cranium and mandible. Pinniped skull and jaw shape on 83 specimens, representing 25 species, was quantified using 58 and 9 three-D landmarks, respectively. To further investigate function of the mandible, biplanar X-rays were used to estimate mandibular corpus cortical thickness and estimate

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bite forces on an additional 33 specimens, representing 3 monogamous and 2 polygynous species. Body mass dimorphism is a poor indicator of skull shape dimorphism in pinnipeds. Shape dimorphism is larger in species utilizing display whereas mass dimorphism is larger in combative species. The southern elephant seal exhibits both characteristics. There is less dimorphism in jaw shape than cranial shape. However, males of both phocid and otariid combative species have significantly higher calculated bite force, relative to females, than non-combative species. Males from different pinniped families have convergently evolved similar sexual characteristics.

32 Technical Session 2: Morphology, Salon B, Sunday 16 June 2013

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Ecological Correlates of Morphological Variation in the Tympanic Bulla of Gerbils (Rodentia, Gerbillinae): Testing the Influence of Phylogeny, Adaptation, and Drift

Desert rodents share many distinctive features, perhaps the most characteristic being the hypertrophy of the tympanic bulla. A common functional explanation for this trait is that it is an adaptation for increased sensitivity to sound that is necessary in open habitats where sound dissipates quickly. Most gerbils exhibit bulla enlargement. Bulla morphology of 80 species (1-9 specimens each) of gerbils was quantified from specimens photographed at natural history museums. We tested whether size and shape of the bulla are correlated with the environment (e.g., temperature and precipitation) by mapping these variables onto a newly estimated 40 species molecular phylogeny of gerbils. Species with no sequences were grafted onto their closest relatives. There was significant phylogenetic signal in the size and shape of the tympanic bulla. The relationship between bulla size and shape with aridity was analyzed after correcting for phylogenetic relatedness using the aforementioned tree. The relationship with size appears to be stronger than that with shape. Implications for the adaptive scenario will be discussed.

33 (E) Technical Session 2: Morphology, Salon B, Sunday 16 June 2013

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Functional Anatomy of Mammalian Carnivores: Ecological Role of the Sagittal Crest in Mastication and Bite Force

The functional role of the sagittal crest in the ecology of mammals is difficult to underestimate; as the point of attachment of the temporalis, it is one of the largest muscles involved in mastication and potentially in securing potential prey. We examined this feature using 19 measurements on specimens representing 16 carnivoran species. A principal component analysis (PCA) of untransformed variables distinguished most species. We hypothesized that the sagittal crest may increase in size as skulls size increases with muscular force being proportional to cross sectional area. Since the temporalis is increasing in cross sectional area, it requires a greater surface on the skull for attachment, hence an increase in the size of the sagittal crest. Because of this relationship, we ran a 2nd PCA on sagittal crest measurements only, normalized to greatest length of skull. There were large differences in the magnitude and directionality of the eigenvectors of the size adjusted characters, suggesting shape rather than size based components. Paradoxically, there was less differentiation among species clouds. Similar results were obtained from analysis of the cross sectional areas of the temporalis and bite forces calculated from digital images. Our data suggest that the size of the sagittal crest in carnivores is an invariant ecological property proportional to size, that scales with the cross sectional area of the temporalis muscle.

34 (E) Technical Session 2: Morphology, Salon B, Sunday 16 June 2013

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New Geometric Morphometric Methods for Taxonomic Identification of Fossil Ground Squirrels (Rodentia: Marmotini)

Ground squirrels (*Ammospermophilus*, *Spermophilus* sensu lato) are a diverse group of sciurids well represented in the late Quaternary fossil record of North America. Much like the present day, they appear to have been prominent members of past mammalian communities and are known to have responded acutely to ancient climate and environmental changes. However, a detailed paleobiogeography of North American ground squirrels is currently lacking due to both problematic identification of morphologically-similar taxa and a history of systematic and taxonomic revisions within the group. This limits understanding of: 1) the past geographic ranges of ground squirrels; 2) variability among taxa in the tempo and extent of range shifts; and 3) those factors that contribute most strongly to assembly of sciurid communities across geologic time. In this paper, we present a geometric morphometric methodology for identification of fossil ground squirrel cranial material (crania and mandibles) based on an extensive sample of modern specimens representing 8 distinct genera. The methodology was adapted to maximize

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identification rates of both complete and partial fossil material to either the genus or species level. Further, we tested the effectiveness of the methods by analyzing ground squirrel remains from several late Quaternary fossil localities in New Mexico, USA, and present the results of this work as well as discuss both the biogeographical and paleoecological implications of our findings.

35C Technical Session 2: Morphology, Salon B, Sunday 16 June 2013

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Effects of Harvest, Culture, and Climate on Trends in Size of Horn-like Structures in Trophy Ungulates

In polygynous ungulates, mating success of males is correlated with body size and size of horn-like structures, which are biologically important and of cultural interest. We evaluated trends in horn and antler size of trophy males recorded from 1900 to 2008 in Records of North American Big Game, which comprised > 22,000 records among 25 trophy categories of species occupying North America. We used a weight-of-evidence approach based on differences among trophy categories in life-history characteristics, geographic distribution, morphological attributes, and harvest regimes to discriminate among competing hypotheses for explaining trends in size of trophy horn-like structures. These hypotheses were young male age structure caused by intensive harvest of males, genetic change as a result of selective male harvest, a sociological effect, effects of climate, and habitat alteration. Trends in size of horn-like structures were negative and significant for 11 of 17 antlered categories and 3 of 8 horned categories. Mean predicted declines during 1950–2008 were 1.87 and 0.68% for trophy antlers and horns, respectively. Our results were consistent with a harvest-based explanation, whereby harvest of males has gradually shifted age structure towards younger and smaller males. Long-term trends in the size of trophy horn-like structures may provide the incentive to evaluate the appropriateness of the current harvest paradigm and pursue further investigations to disentangle the relative effects of nutrition and harvest.

35/255 (E) Technical Session 2: Morphology, Salon B, Sunday 16 June 2013

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Structure and Function of the Tympanoperiotic Complex in Odontocete Cetaceans

Vibration is intrinsic to all structures. Any object can be characterized by its own distinct family of resonant frequencies. Vibrational analysis allows us to calculate these resonant frequencies based on an object's geometry and its material properties. The odontocete tympanoperiotic complex (TPC) contains the ossicles and the cochlea. Measuring TPC variation is a key to understanding the functional morphology of sound reception. Recent work suggests that this apparatus selectively filters and/or amplifies various vibrational components of the incoming sounds. The TPCs from 8 toothed whales were scanned with microCT, subjected to vibrational analysis, and examined with geometric morphometrics. In the TPC vibrational analysis, the first 60 resonant frequencies, or modes, were calculated for 2 porpoises, 4 dolphins, 1 sperm whale, and 1 river dolphin. All 60 modes for each specimen occurred below 190 kHz. There is no distinct trend across species between modes 1-10. Frequency diverged gradually between modes 10-60. The dolphins had both the lowest and highest modes over the entire range. The plots for the spotted dolphin, the porpoises, and the sperm whale were remarkably similar between modes 10-60. The modes for the left and right TPCs from the same specimen were nearly identical, indicating symmetry. Geometric morphometric analysis parses major sources of shape variation in TPC geometry, allowing odontocete TPCs to be sorted into complex morphotypes that are linked to functional differences.

36 (E) Poster Session I, Franklin B, Sunday 16 June 2013

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Fungal Diseases of Mammals and Other Wildlife Species: Factors Influencing Disease Dynamics and Host Mortality

Since 1970, there has been a steady rise in infectious disease cases in wildlife, even when controlling for reporting bias. Fungal diseases in particular have caused unprecedented die-offs of wildlife populations, threatening biodiversity and ecosystem services. Although these diseases have affected a wide range of wildlife species, host mortality among and within species has been highly variable. White-nose Syndrome, a disease caused by the

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pathogenic fungus *Geomyces destructans*, has been a particularly severe emerging threat to bat species of North America. We reviewed the literature on White-nose Syndrome in bats and a suite of other fungal diseases in wildlife, including chytridiomycosis in amphibians. We sought to evaluate the epidemiology of these diseases and gain a broader understanding of factors that may commonly influence disease dynamics and host mortality. Our research identified characteristics of fungal pathogens that make them particularly severe threats to mammals and other wildlife, characteristics of mammals and other wildlife that correlate with mortality from fungal pathogens, and criteria by which to prioritize species for conservation attention.

37C Poster Session I, Franklin B, Sunday 16 June 2013

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Role of Mammalian Species as Hosts for *Trypanosoma cruzi*

The protozoan *Trypanosoma cruzi* parasite causes Chagas disease and relies on triatomine insects as vectors. Most species of triatomines are associated with free-ranging vertebrates. Several mammalian species serve as reservoir hosts; however, the role of free-ranging mammals in maintenance of Chagas disease is not well understood. This information is critical for control and risk management efforts. As previous studies report that *T. cruzi* infection of working dogs in Southern Texas may be chronic, I am conducting my research at the Military Working Dog (MWD) facility on Lackland Air Force Base (AFB) in San Antonio, Texas. The overall goal of the project is to understand the parasite-vector-host interaction in the environment surrounding the MWD facilities. I am determining the relative densities of free-ranging mammalian species by season and vegetation type. Additionally, I am estimating the prevalence rate of *T. cruzi* in blood samples from major mammalian species. Preliminary serological results show that raccoons (*Procyon lotor*) and Virginia opossums (*Didelphis virginiana*) have high prevalence rates of *T. cruzi* antibodies. I anticipate that my research will identify the levels of infection in different mammalian hosts and will help focus control efforts on those species most likely to contribute to Chagas disease transmission.

38 Poster Session I, Franklin B, Sunday 16 June 2013

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Evaluating Host Specificity Assessments of Bat Flies (Diptera: Streblidae) from Ecuador

Bat flies (Diptera: Streblidae and Nycteribiidae) are blood-feeding parasites of bat populations worldwide but reach their zenith of diversity and abundance in the Neotropics. As a group, bat flies encompass myriad morphological and behavioral adaptations for life on the host. Host specificity is an intriguing emergent property of parasite-host systems and is the degree to which single parasite species are restricted to single host species. Despite host and parasite characteristics that should decrease specificity, there is an emerging consensus of high host specificity for the group. Using specificity indices and a dataset of over 2,000 bats and 6,000 bat flies, we evaluated the degree of host specificity among Ecuadorian bat flies. Although historically viewed as unspecific, we add to other recent findings that bat flies are highly host specific. No single fly species was found to have more than 4 primary host species, or resulted in a high specificity index value. Most fly species were absolutely host specific or parasitized congeneric hosts, and specificity assessments increased when strict sampling protocols were followed. Research on parasite-host associations promises to increase our knowledge of both parasite and host groups but also the myriad ecological, evolutionary, and epidemiological properties that emerge from the intimate parasite-host relationships. Various potential mechanisms may drive evolution and maintenance of high specificity.

39 Poster Session I, Franklin B, Sunday 16 June 2013

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Habitat Use of Mule Deer on Agricultural Lands: Implications for Survival and Reproduction

Extensive use of agricultural lands by deer is common throughout the west, especially in desert environments where native forage and water is limited. Artificially high densities of deer on fields can lead to increased disease risk due to close association with livestock and conspecifics. Also trace mineral or nutritional imbalances may result from inability to digest a diet comprised primarily of alfalfa, a high energy, high protein forage, resulting in sickness or decreased body condition. For these reasons agricultural fields have the potential to act as a population sink. We have monitored habitat use, survival, and occurrence of disease symptoms (diarrhea and emaciation) for deer associated with agricultural fields. We have identified 3 strategies for use where animals either remain in the uplands throughout the spring and summer, remain in the uplands through the spring and early summer then transition to the fields during late summer, or remain on the fields throughout the spring and summer. We have identified variation in seasonal use of agricultural lands with greater numbers of individuals using the fields as the summer progresses and increasing

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numbers of symptomatic individuals during late summer and fall. We have also identified higher iron and molybdenum levels in the livers of sick individuals, which can cause secondary copper deficiencies. Using this information we can identify how habitat relationships influence health and subsequent survival.

40 (E) Poster Session I, Franklin B, Sunday 16 June 2013

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Biogeographic Patterns, Life-history Trends and Conservation Status of Wild Canids

The family Canidae is comprised of 36 extant species that exhibit a wide range of morphological, ecological, behavioral and social traits. Currently, 33% of the world's canids are recognized as species of conservation concern (threatened, vulnerable, endangered, or critically endangered) by the IUCN, and even more are experiencing population declines. We examined the relationship between IUCN conservation status and macroecological patterns in all of the world's living canid species. We mapped body size, geographic distribution, range size, and a suite of life-history variables for canids onto a phylogenetic supertree, and evaluated whether these factors predicted IUCN conservation status. Body size, gestation period and geographic range size were all significant predictors of conservation concern, and insular geographic distribution and high degree of sociality (especially obligatory pack-hunting) were strongly associated with endangered or critically endangered status. We also evaluated the relative representation of each species in the scientific literature (an index of scientific knowledge and research effort). Three species (*Canis lupus*, *C. latrans*, and *Vulpes vulpes*) are significantly over-represented in the literature, accounting for approximately 75% of all publications. In contrast, all 3 critically endangered canid species combined are represented in only 2% of the literature. Our combination of meta-analytic synthesis of conservation risk factors and quantification of knowledge gaps for species at risk of extinction yields new insights into important further directions for canid conservation efforts.

41 Poster Session I, Franklin B, Sunday 16 June 2013

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Bat Response to Oak Regeneration Silviculture

Concern over declining bat populations has generated increased interest regarding the role of forest management in bat habitat conservation. Management for timber production alters forest habitat, potentially affecting bat roosting and foraging resources. Bat activity is generally higher in harvested than in unharvested forest stands. However, species activity patterns often differ from overall bat community trends. Our study examined the influences of harvest practices on bat activity in 2 state forests in south-central Indiana as part of the Hardwood Ecosystem Experiment, a long-term investigation of the effects of oak regeneration management on forest communities. We sampled bat activity with stationary acoustic detectors in clearcut, patch cut, and first-stage shelterwood harvests and in unharvested (reference) stands. We measured vegetation characteristics at acoustic sites to examine relationships between microhabitat characteristics and bat activity. The most frequently detected species were eastern red bats (*Lasiurus borealis*), tricolored bats (*Perimyotis subflavus*), and northern long-eared bats (*Myotis septentrionalis*). Hoary bats (*L. cinereus*) were least commonly detected. Total bat activity was higher in clearcuts and shelterwoods compared to unharvested sites. *Myotis* species were more active in shelterwoods, where overstory stem density was reduced by 30%, than in unharvested sites. *Myotis* activity was similar among clearcut and shelterwood treatments. Our results indicate that management that creates a mix of structurally diverse forest stands can maintain habitat for a diverse bat community.

42 Poster Session I, Franklin B, Sunday 16 June 2013

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Heavy Metal Contamination and Accumulation at Abandoned and Untreated Copper Mines in Keweenaw, Michigan

Mine tailings can result in elevated levels of heavy metals that may persist at multiple trophic levels. There is little information on heavy metal accumulation in proximity to abandoned copper mines in Keweenaw, Michigan, where mining began in 1845 and continued until 1968. During that time approximately 11 billion pounds of copper were extracted through underground mining practices. In the present study, small mammals were trapped adjacent to tailing piles at nine abandoned mine sites. Three reference sites in the copper rich basaltic deposits that were distant from the mines served as internal controls; 3 reference sites in the same county on sandstone deposits served as

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external controls. Mine sites yielded 45 *Peromyscus maniculatus* captures; basaltic sites yielded 14 *P. maniculatus*; sandstone deposits yielded 10 *P. maniculatus*. Triplicate samples of Balsam Fir, Sugar Maple, and soil were collected within 10 m of each capture. All samples were digested with nitric acid, peroxide, and hydrochloric acid following EPA method 200.3. Metal analysis was done in triplicate for each sample collected using atomic absorption spectrophotometry. Preliminary soil analysis from this region revealed elevated soil copper and arsenic concentrations. The present study is expected to reveal elevated metal concentrations in soil, water, plant, and mammal species from mine sites in comparison to basalt and sandstone reference sites implying persistence at multiple trophic levels.

43 (E) Poster Session I, Franklin B, Sunday 16 June 2013

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Impacts of Mining on Mule Deer Migrations in Nevada

Over the past century, mule deer (*Odocoileus hemionus*) have suffered dramatic declines throughout the western US due, in part, to loss of migratory corridors. An increase in mineral exploration across Nevada has raised the level of concern over the protection of ungulate migration routes throughout the state. In January 2012, the Nevada Department of Wildlife and University of Nevada, Reno captured and applied radio collars to 12 female mule deer in the proximity of an active mine in the Ruby Mountains of eastern Nevada. Collars were scheduled to collect locations at 1-hour intervals during migrations to give an accurate depiction of migratory behavior in and away from mining facilities. We used Brownian Bridge Movement Models to delineate stopover sites for each individual during both the fall and spring migration periods. We calculated route efficiency and movement rate between stopover locations and throughout the mining area to determine the effects of the mine on movement patterns. We hypothesized that mule deer would show higher route efficiency and movement rates between stopovers than through the mining complex. Mule deer showed an increase in route efficiency and movement rate between stopover locations when compared with movement through the mine. These results suggest an increase in energy expenditures of mule deer forced to navigate these mining complexes, which may negatively impact migratory behavior.

44 (E) Poster Session I, Franklin B, Sunday 16 June 2013

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Factors Influencing Mortality of Translocated Northern River Otters (*Lontra canadensis*) in Utah

Translocations of northern river otters have been common throughout the United States from the 1970s to the 2000s. In Utah, managers are actively working with otters to reestablish presence throughout the state. From 2009 through 2012, we translocated 27 radio-marked otters to the Provo River in Utah. Many otters did not survive translocation and died from various causes within 2 weeks of release. Our objective was to determine what factors had the most influence on translocation-related mortality of otters. We developed a series of *a priori* models and used logistic regression to determine what factors were the most important. Using Akaike's Information Criterion, we found that the univariate models including body mass bore the most model weight, and that body mass was the most important factor influencing the initial survival of translocated otters. Model-averaged β estimates indicated that otters at the large end of body mass were 4 times more likely to survive than otters at the low end of body mass. Sex was the next most important factor influencing survival, as odds ratios indicated that males were more likely to survive than females. We urge ecologists and managers to delay the trapping and translocating of otters until juveniles are likely large enough to have a high probability of survival. We further recommend female-biased translocations, as females were less likely to survive translocations.

45 (E) Poster Session I, Franklin B, Sunday 16 June 2013

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Hind Foot and Tail Length in Mustelid Climbers and Diggers

The family Mustelidae contains animals with a wide range of habitats and bodies adapted to their niches. Within this family are partially arboreal martens and terrestrial badgers. To climb trees for protection and to hunt, martens most likely have longer hind feet and tails relative to their body size, as this enables them to grip branches and keep their balance. Because badgers are diggers that rely on their forefeet to burrow through soil, their hind feet and tails are most likely shorter so as not to be a hindrance to digging. To see if there is a relationship between these different behaviors and the morphologies of the mustelids, we collected literature values and measurements from museum specimen for head-body length, hind foot length, and tail length in martens and badgers. We compared the ratios for

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hind foot length to head-body length and for tail length to head-body length. Overall, the ratios for hind foot length and the ratios for tail length were greater for martens than for badgers. The ratios for all species of martens were similar. The ratios for badgers were much more varied, and the species that spend more time in trees had ratios similar to those of the martens. In summary, arboreal mustelids tend to have longer hind feet and tails than terrestrial mustelids.

46 Poster Session I, Franklin B, Sunday 16 June 2013

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Taking Measure of Mustelids: Morphological Diversity

The small carnivores of the Mustelidae include such diverse members as the weasels, martens, badgers, and otters, as well as species not so easily recognized, such as the taira and lynx. The Mephitidae and Procyonidae are more closely related to each other than either is to the Mustelidae. The genus *Potos* is basal to these 3 families. This study compares the morphology of the mustelids, mephitids, procyonids, and *Potos* to see if patterns of sexual dimorphism emerge across different taxonomic levels. Morphological data (head-body, tail, hind-foot, and ear lengths, and mass) were obtained from 7,500 specimens from 3 natural history museums, online databases, and the literature. Dimorphism was expected to be similar to the basal lineage, *Potos*. *Potos* shows a pattern of a larger male head-body length (2.2%), tail length (5.7%), hind foot length (8.7%), and ear length (9.0%) but a larger female mass (8.4%); however, the number of specimens with weight measurements was low (female=4, male=3). Excluding weight, 34 of 44 mustelid species show similar patterns of dimorphism, 8 of 11 mephitid species, and 6 of 8 procyonid species. Reverse sexual dimorphism is rare and not usually significant. Therefore, sexual dimorphism emerges as a pattern for a majority of mustelid, mephitid, and procyonid species, but each family contains species that have departed from the basal lineage for at least 1 morphological measure.

47 (E) Poster Session I, Franklin B, Sunday 16 June 2013

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Body Mass as an Estimate of Body Condition in a Hibernating Small Mammal, the Golden-mantled Ground Squirrel (*Callospermophilus lateralis*)

Seasonal variation in food availability is a central problem for animals living at high elevations, where the vegetative growing period is short. Hibernation is 1 life history adaptation to this problem, and fat storage is essential to its success. Hibernating mammals must store large amounts of fat in summer when energy is abundant, enough to fuel basic metabolic processes through winter when energy is scarce. In hibernating squirrels (family Sciuridae), the amount of energy stored as fat further influences important demographic traits such as natal dispersal, overwinter survival, timing of reproductive maturity, and female reproductive success. In the absence of accurate measures of body condition (defined as percent body fat) of live animals, researchers have used total body mass as a proxy. However, the validity of this measure has not been established. Using total body electrical conductivity (TOBEC) on live golden-mantled ground squirrels (*Callospermophilus lateralis*), we determined that body mass is a valid indicator of percent fat. However, reliability varies seasonally; the relationship between body mass and body condition changed through the active season as energetic needs apparently shift from expenditure on reproduction to acquisition before hibernation. Correcting for skeletal size did not improve reliability, though its effect on fat storage also varies seasonally. Our results have implications for research in basic behavioral ecology and predictions of body size evolution under climate change.

48 Poster Session I, Franklin B, Sunday 16 June 2013

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Immunohistochemical Study of Merkel Cells in Verrucae of *Artibeus jamaicensis*

Phyllostomid bats have unique morphological facial features, including patterns of glabrous facial verrucae that lack typical, integumentary, sensory end-organs but are well-endowed with Merkel cells and free nerve endings (neurites or *Haarscheibe*). Routine paraffin histology, immunohistochemical staining, and immunofluorescence were utilized to elucidate the nature of Merkel cells found in the epidermal rete pegs of facial verrucae, terminal hair follicles, and vibrissae hair follicles of *Artibeus jamaicensis*. We found an abundance of dermal afferent nerves branching widely as they approach the epidermal-dermal junction. Many axons terminated at the rete pegs forming a delicate meshwork of nerves suggesting the presence of Merkel cell-neurite complexes, whereas other nerves penetrate the epidermis terminating within various epidermal strata as free-nerve endings, some with terminal enlargements. Terminal and vibrissal, follicular Merkel cells were found in the outer root sheath, with some populations being innervated. Merkel

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cells in root sheaths and verrucae responded variably to antibodies. Most notable was positive immunoreactivity (IR) for Serotonin (5-HT), Vasoactive Intestinal Peptide (VIP), Neuron Specific Enolase (NSE), and Protein Gene Product 9.5 (PGP 9.5) in Merkel cells of vibrissae hairs, while only IR for NSE and PGP9.5 was found in epidermal rete pegs. These findings suggest multiple Merkel cell populations with diverse functional attributes.

49 Poster Session I, Franklin B, Sunday 16 June 2013

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Locomotor Performance in the Pacific Marten: Are Semi-arboreal Mustelids More Efficient Runners than Semi-aquatic Ones?

The relatively long body and short limbs of mustelids allow them to exploit resources from a diversity of habitat types. This body plan also has important implications for energetics because of increased heat loss from a high surface to volume ratio and muscular support of an elongated spine. Past research suggests that dorsal flexion of the spine enables semi-aquatic mustelids to be relatively efficient runners at faster speeds. We evaluated locomotor performance in a semi-arboreal mustelid, the Pacific marten (*Martes caurina*), and compared our results to those previously observed in semi-aquatic mustelids. We measured the energetic costs of locomotion using flow-through respirometry methods and described stride characteristics. At slower speeds, when martens were using a trotting gait, they were less efficient than predicted by allometric equations; at higher speeds, when bounding, martens were significantly more efficient than predicted. Nonetheless, they did not revert to a bounding gait earlier than expected. These observations suggest that unlike the semi-aquatic river otters (*Lontra canadensis*) and mink (*Neovison vison*), martens do not use spinal flexion but instead employ other adaptations that result in energy savings.

50 (E) Poster Session I, Franklin B, Sunday 16 June 2013

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Differential Dispersal of Two Codistributed Species of *Pteropus* in the South Pacific

Pteropus samoensis and *P. tonganus* (Chiroptera: Pteropodidae) are 2 species of flying foxes found on southern Pacific islands, with regions of sympatry in the Samoan and Fijian archipelagos. Although their roosting habits differ significantly, with *P. samoensis* roosting singly or in small family groups and *P. tonganus* roosting colonially, both are dietary generalists with 61% overlap in their food plants. Also, both species have experienced repeated population bottlenecks as a result of periodic cyclones. Based on these similarities in their geographical distributions, ecological niches, and recorded demography, we explored the null hypothesis that the 2 species have experienced similar evolutionary histories. Using mitochondrial sequence data and microsatellite genotypes, we reconstructed the genetic demography of the 2 species, focusing on patterns within and between Samoa and Fiji. Descriptive analyses of the 2 datasets show very different patterns, including patterns consistent with male-biased dispersal in *P. samoensis* but not in *P. tonganus*. Using coalescent-based ABC analyses, we will illustrate the extent to which the 2 species have experienced different evolutionary trajectories. Additionally, we will use these data to estimate the effective size and spatial limits of populations for these 2 threatened species. This study will address the extent to which similarities in extant populations are generalizable into the past, and help to illustrate how 2 species might arrive at similar traits through distinct evolutionary pathways.

51 Poster Session I, Franklin B, Sunday 16 June 2013

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Experimental Tests of Interactions Between Woodrats Across A Zone of Secondary Contact: Asymmetry in Body Size and Aggression Limit Interspecific Mating

When 2 closely related species come into secondary contact, individuals that mate with heterospecifics may have lower fitness if hybrids are inferior to purebred offspring. Under these conditions, we expect the evolution of behaviors that minimize hybridization and promote assortative (conspecific) mating. We conducted mate choice trials between *Neotoma fuscipes* and *N. macrotis* in coastal California to examine the evolution of mate preference in an area of sympatry. We examined patterns of mate choice exhibited by females in a zone of secondary contact in comparison to females from allopatric populations. We quantified each female's behavior when given a choice to interact and

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mate with both a conspecific and heterospecific male over a 2-hour period. We did not find strong evidence of increased assortative mating in sympatric females. However, we observed strong asymmetry in the preferences of the species in both sympatry and allopatry. Females of the smaller *N. macrotis* interacted and mated more assortatively than the larger *N. fuscipes*. Moreover, aggressive male-female interactions increased in both species in sympatry compared to allopatry. Our results suggest that body size and aggression are determinants of mate choice between these species. Specifically, when these species come into contact, there may be augmented competition for shared resources, selecting for increased aggression, which may ultimately interfere with reproductive interactions.

52 Poster Session I, Franklin B, Sunday 16 June 2013

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Reproductive Success of Male Prairie Voles (*Microtus ochrogaster*) Displaying Alternative Reproductive Tactics

In many species, males display alternative reproductive tactics (ART); some males are territorial while others adopt a non-territorial wandering tactic. Typically residents are considered to display a superior reproductive tactic than wanderers although there are few studies where parentage was estimated using genetic techniques to verify this hypothesis. We tested this hypothesis with data from multiple years of live trapping, radio tracking, and genetic parentage analyses within natural and semi-natural populations of prairie voles (*Microtus ochrogaster*). In the natural populations, wandering males sired more offspring than residents, apparently because they mated with more females. In the semi-natural populations, the reproductive success of wandering and resident males was not significantly different. Thus, wandering males did not have lower reproductive success in any population. The difference or lack of difference in body mass may explain the patterns we found with regard to reproductive success of males. In the natural population in Kansas, wanderers were significantly heavier than residents and they sired more offspring. In populations where there was no difference in body mass between males displaying different tactics, there was also no difference in reproductive success. Thus, the hypothesis that residents are displaying the preferable reproductive tactic may be too simplistic since relative reproductive success of males displaying particular ARTs may vary depending on their body condition.

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A New Model of Ricochetral Locomotion in Mammals

Small mammal saltatorial adaptations maximize escape from predators in patchy environments where sudden positional changes are more effective than dashing away in 1 direction. Saltation is an independent series of longer jumps than body size predicts; saltators also alter trajectory midleap using elongated tails as rudders. Although from species differing in biogeographic range, phylogenetic origin, and time of appearance in the fossil record, their ecological niches constrain saltators to showing common morphologies. These include bipedal hopping, long, tufted tails, large eyes and auditory bullae, elongated feet and hind limbs with proximal muscle bellies. This study examines saltatory adaptations among forms of common appearance by comparing saltation to the atlatl, a device for increased human hunting efficiency that propels projectiles farther and more accurately than can be accomplished by arm movements alone. Such animals are atlatl saltators. The body parts determining these locomotor capabilities compare to those of an atlatl, but are analogous only when it is inverted. The atlatl saltator's foot corresponds to the atlatl projectile and launcher, the calcaneus to the atlatl spur and the lower leg to the atlatl handle. The knee corresponds to the human wrist holding the device. Knee straightening equals a forward wrist snap. In parallel, the animal uses large thigh muscles to move forward, while the human movement allows large trunk muscles to effect a corresponding atlatl movement.

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Influence of Resource Abundance on Two Echimyid Rodents in Central Panama

A main goal in ecology is to understand the origins and the maintenance of biodiversity. Questions, such as how can morphologically and ecologically similar species coexist when resources are limiting, arise. The biologically rich Neotropics are a focal point for exploring these questions due to their high levels of biodiversity and seasonal limitations in resources that may lead to direct competition. *Proechimys semispinosus* and *Hoplomys gymnurus* are closely related species that are morphologically similar and overlap greatly in habitat and resource use. Seasonal

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fluctuations in resources should increase the potential for direct competition as individuals try to secure access to resources. Studies have demonstrated that *P. semispinosus* is behaviorally dominant over *H. gymnurus*, however questions remain as to how *H. gymnurus* is able to persist in the presence of *P. semispinosus*. My goal is to understand how the presence of resources affects intra-/interspecific interactions during periods of resource abundance and scarcity. Paired behavioral trials will be performed to examine interactions when 1 individual has initial access to a resource. In understanding their interactions, we can enhance our understandings of species coexistence.

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The Importance of Sensory Information in the Foraging of Wild Nine-banded Armadillos

Nine-banded armadillos (*Dasyopus novemcinctus*) have been expanding their distribution in the United States since the 1850s. This expansion may have been possible due in part to their generalized insectivore diet. Information on foraging has been limited to identifying stomach or fecal contents; little has been done to investigate how individuals identify and locate prey items. The relative importance of sensory information was examined while collecting information on foraging preferences in an attempt to find attractants for baiting purposes. Twenty-eight wild armadillos were caught at various locations in northern Florida and individually tested for preferences to 18 items in choice experiments. Trials were videotaped and analyzed for: 1) time to first contact; 2) whether an item evoked interest (i.e., the number of times the animal was within 1 m and oriented toward the item); and 3) whether that item sustained interest (i.e., amount of time spent oriented toward the item while within 1 m). Live prey items, such as pond worms (*Lumbricus terrestris*), wigglers (*Pheretima hawayanus*), red worms (*Wisenia fetida*) and crickets (*Acheta domestica*), elicited faster responses than others. We determined that olfactory and auditory/vibrational cues were important in evoking a response. The perceptual range of armadillos appears limited. Our results suggest that attracting animals with effective baits may prove difficult. Further investigations of the specific roles of sensory cues used by foraging armadillos are warranted.

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Influence of Crayfish on Diet and Summer Habitat Selection by American Mink

The American mink (*Neovison vison*) is an economically important furbearer native to the human-dominated landscapes of the Midwestern US. Mink are a well-documented generalist carnivore, but no studies have examined habitat selection by mink as it relates to prey availability within its native range. We collected 107 scats across east-central Illinois between September 2011 and July 2012 to examine changes in diet between seasons and across an urbanization gradient. Common food items included multiple species of crayfish, mammals, fish, birds, and insects; with crayfish being especially prevalent in summer. From May-July 2012, we conducted occupancy surveys at 60 sites (200 m stream segments) and concurrently sampled these sites to estimate density of crayfish. We examined the relationship between mink occupancy and crayfish density to explore crayfish density as a potential driver of mink habitat selection during summer. Naïve occupancy by mink was 0.316 (19 of 60 sites). Mean crayfish density was 10.5/m² at sites occupied by mink and 4.9/m² at unoccupied sites. Crayfish densities were spatially variable within sites, and further analyses will examine finer-scale habitat associations between mink and crayfish. Because mink also consume terrestrial prey, we evaluated whether landscape context (e.g., urbanization, riparian buffer width) also affects site occupancy in Midwestern streams.

57 (E) Poster Session I, Franklin B, Sunday 16 June 2013

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Preliminary Analysis of Niche Partitioning Among Mammals of Riparian Corridor

Interspecific interactions play a vital role in the dynamic processes and functions of ecological communities. The linear nature of the habitat of animals inhabiting riparian corridors leads to inevitable interactions between such species and, therefore, competition for space and food resources. Niche theory states coexisting species within a community must partition their environmental resources. We examined temporal niche partitioning between river

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otters (*Lontra canadensis*) and mink (*Neovison vison*) as well as between river otters and raccoons (*Procyon lotor*) based on patterns of use at 10 river otter latrine sites along the Provo River in northern Utah. We sampled sites using infrared remote trail cameras that recorded the date and time of each image, and we identified all species within each image. Results from contingency analysis indicated otter activity patterns are different from both raccoon and mink. However, both river otters and raccoons were primarily active at night, while mink, previously shown to be nocturnal, were primarily active during diurnal hours. Therefore, there may be temporal partitioning occurring between mink and otters, as mink have likely altered their behavior to avoid nocturnal competitors. As river otter populations expand their range across North America, otter interactions with competing carnivores will likely increase. River otters may outcompete other carnivores, so understanding temporal niche partitioning can help wildlife managers predict impacts of increasing river otter populations on potential competitors.

58 (E) Poster Session I, Franklin B, Sunday 16 June 2013

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Foraging Behaviors of Field Mice Under Direct Cues of Predation Risk

Increased predation risk on nocturnal mice has been shown to decrease activity levels, predominately in foraging efforts. Few studies have tested the differences among olfactory cues in relation to predation risk. Enclosure experiments using predator and competitor scents were conducted to determine the effects of direct cues of predation risk on foraging behavior among deer mice (*Peromyscus maniculatus*) collected from the Upper Peninsula of Michigan. Six mice were observed for 6 nights, influenced by 6 different olfactory cues, and studied over a 6-month period from June to November of 2012. Feeding trays, consisting of sunflower seeds in a sand matrix served as artificial resource patches and giving-up densities (GUD) were measured to test for foraging tendencies among patches exposed to different olfactory cues. Each rodent was observed to assess its initial decision entering a treatment or control enclosure. The objective was to examine whether these mice recognize specific terrestrial predator odors. Mice had lower GUD in the non-treatment enclosure than in the treatment enclosure containing the predator scent: coyote, red fox, or bobcat. There was little difference in GUD between control and competitor scent enclosures and mice initially favored movement into the control enclosures. These results suggest that mice have the inherent ability to recognize potential threats presented through olfactory cues.

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The Influence of Habitat Structure and Predation Risks on Seed Dispersal by Scatter Hoarding Rodents

Many rodents serve as agents of seed dispersal by scatter hoarding seeds during food shortages and subsequently failing to recover some of these caches. Traditional models of scatter hoarding hold that seeds are distributed in a manner to reduce pilferage and at that same time balance the costs of cache recovery. Recent studies, however, suggest that habitat structure and predation risks also influence cache placement and ultimately seed establishment. To test this, we followed the dispersal of 12,000 seeds over 2 years to identify natural caches by small mammals (predominantly *Sciurus carolinensis*). We then measured GUDs (giving up densities) at cache sites, random sites, and sites along logs and rocks where rodents were likely active. At each of 496 sites, we presented feeding chambers containing 200 sunflower seeds, mixed in a 3-L matrix of sand, and determined the number of remaining seeds (GUDs) after 2-3 days in the field. We also measured vegetation parameters at the 3 site types. We found that GUDs (a proxy for predation risks) were higher at cache sites than near logs and rocks and that cache sites were placed in more open areas with less canopy cover. We suggest that small mammals select cache sites in the open where higher predation risks reduce the probability of cache pilferage. Such patterns of cache selection may also enhance seed establishment.

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Whistling Land Mammals: Groundhogs, Tapirs, and Dholes

A whistle is a vocalization comprised of a frequency sweep. It is most commonly associated with bats and dolphins that use them for sophisticated echolocation. It is quite rare, and more simply used, among land mammals. This paper presents 3 distinctly different examples: groundhogs, tapirs, and dholes. For the groundhog, typically out in the open during daylight in a quiet environment, it is a quick warning signal to alert others to visually scan for a threat and head for safety. It sweeps up in frequency, which is the quickest means of generation. In contrast, tapirs, with poor eyesight, operate alone in the jungle at night so a strong whistle is their primary means of communication. The whistle's frequency sweep avoids interference in the noisy jungle environment and sweeps downward to provide low

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frequencies, which travel further. Dholes, which have excellent eyesight, operate in packs during daylight in similar jungle conditions. They use very short low level whistles just to keep in touch, since jungle vegetation often obstructs their line of sight while they are trying to surround their prey.

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Vigilance Strategies of Bush (*Heterohyrax brucei*) and Rock (*Procavia capensis*) Hyraxes While Basking

Bush (*Heterohyrax brucei*) and rock (*Procavia capensis*) hyraxes are spatially associated in Matobo National Park (MNP) in Zimbabwe. While basking on rock kopjes (hillsides) before foraging bouts, hyraxes are exposed and vulnerable to predation, especially by Verreaux's eagle (*Aquila verreauxii*). Thirty-five individuals, categorized as either adult solitary, adult in adult-only homospecific group, subadult in homospecific group (*H. brucei* only), or juvenile in homospecific group (*P. capensis* only), were observed for vigilance behavior. Collectively, hyraxes spent 87.2% of total time vigilant, most of this in a low state of vigilance (e.g., prone but alert, with eyes open). Within species, no relationship existed between percent time adults spent vigilant and adult group size. Adult *H. brucei* spent more time vigilant (99.3% of total time observed) than did the larger adult *P. capensis* (86.0%). Subadult *H. brucei* spent less time vigilant (61.5%), and groomed (nonvigilant activity) more frequently, than did adult *H. brucei*. Juvenile *P. capensis* (vigilant 98.6% of total time observed) exhibited a greater frequency of abrupt head turns – a behavior signaling heightened vigilance – than did adult *P. capensis*. While basking, adult hyraxes spend much time vigilant, especially so for the smaller, more vulnerable *H. brucei*. Subadult *H. brucei*, in the presence of conspecifics, devote comparatively less time to vigilance and more to grooming. Juvenile *P. capensis* are vigilant and readily aroused.

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Using Cameras to Estimate *Peromyscus* Activity Levels Relative to Predator Risk

Knowledge of activity patterns is a critical component of many ecological studies. Small mammal activity changes in response to moonlight to reduce the risk of encountering predators. Activity patterns of free-ranging nocturnal rodents have been examined using numerous techniques including live trapping and short-interval observations. Direct observation, while desirable, can be challenging. As an alternative, we monitored activity of wild *Peromyscus* in a restored prairie using automated cameras. We hypothesized that the frequency of photographs of *Peromyscus* will decline during periods of increased predation risk. Trap nights were classified into 3 predation risk categories (high, moderate, and low) based on moonlight intensity and cloud cover. An ANOVA was used to compare the frequency of *Peromyscus* detection between the risk categories. Additionally, a covariate quantifying detection of predators on cameras within the trapping grid was added to this ANOVA. Our results indicate that automated cameras provide a viable approach for estimating activity patterns of small mammals consistent with previous studies of risk sensitive declines in small mammal activity levels.

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Influence of Male avpr1a Genotype on Social and Reproductive Behavior in Prairie Voles (*Microtus ochrogaster*)

Many animal species exhibit considerable intraspecific variation in behaviors associated with reproduction such as pair bonding and parental care. This variation has generally been examined with respect to varying environmental conditions, but neurogenetic factors also appear to influence sociosexual behavior. For example, it has been demonstrated that some social behaviors in male mammals including pair formation and paternal care are mediated by the neuropeptide vasopressin through its action on the vasopressin 1a receptor (V1aR). Data from laboratory and semi-natural populations of prairie voles suggest that microsatellite length polymorphism in the gene (avpr1a) that codes for the V1aR contributes to variation in male sociosexual behavior. We tested the hypothesis that a male's avpr1a genotype is contributing to variation in social and reproductive behavior observed under field conditions by releasing adult voles, in which all the males possessed 2 avpr1a alleles that were either substantially longer or shorter than the mean length in their population of origin, into semi-natural enclosures. Illinois males with long avpr1a alleles were more likely to be residents at a nest with a female than males with shorter alleles but the converse was true for males from Kansas. Males with long avpr1a alleles from Illinois, but not Kansas, also sired offspring with

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more females than males with short alleles. However, avpr1a genotype was not correlated with the number of offspring sired by males.

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Variations of a Small Mammal Community in a Changing Landscape in Southeastern Virginia

In 2005, an ongoing monitoring program of the small mammal community began on a secondary successional wetland site owned by The Nature Conservancy. We hypothesized the spatial distribution of the herbivorous small mammal community and populations would be related to that of vegetation. Our study site consisted of an 8 x 8 grid, at 12.5-m intervals, and had 2 modified Fitch traps per station. We trapped for 3 days each month, averaging 4,600 trap nights per year. After determining the spatial densities for the small mammal community and populations, we used ArcGIS to map and conduct cluster analyses using a combination of LiDAR data and ground surveys, with respect to the small mammal community and population densities. With the progression of succession, this site experienced a general and parallel decline of all old field species, both for vegetation and the small mammal community.

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The Impact of Precipitation on Insectivore and Arthropod Abundance in Prairie Dog (*Cynomys ludovicianus*) Towns in Southwest North Dakota

Studies have indicated a positive correlation exists between precipitation and arthropod abundance. Arthropod numbers increase with increasing precipitation. Consequently, an increase in arthropods may lead to an increase in insectivores. Little research involving trophic and climatic interactions among shrews, arthropods, and precipitation has been conducted in temperate climates. Arthropods were sampled at 20 prairie dog (*Cynomys ludovicianus*) towns in 2011 and 2012. Samples were obtained using Y-shaped pitfall arrays with drift fences. Pitfall arrays were operated for five consecutive nights over 4 sampling periods. Arthropods representing 6 terrestrial orders were collected. All orders showed a significant increase in abundance from 2011 to 2012. This growth is potentially correlated with a change in yearly precipitation from 2011 to 2012. Shrews may also exhibit a secondary response to precipitation by responding to an increase in arthropod abundance.

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Small Mammal Diversity in Edge Versus Forest Interior Habitats

As forests become fragmented, creating edge habitat, small mammals may change their home range and activity patterns in response. They may also be subject to increased predation or competition. The goals of this study were to measure small mammal diversity and describe distributions and home ranges of white-footed mice (*Peromyscus leucopus*) populations. We hypothesized that more white-footed mice would be found in interior habitat rather than edge habitat because of increased high canopy cover and decreased overlap with other small mammal species. Mammals were trapped and released in meadow-wood edge habitats and deciduous forest interior. Sex ratio, population density, microhabitat, home range, reproductive status, and weight data were collected. Weather, moon phase, and trapping effort were also measured. More mouse activity and captures were recorded in areas of less dense woody stem growth. Females stayed further apart from each other when compared to male/male and male/female distance averages. Trees near traps that caught mice had a higher average diameter than traps that did not catch mice. Species diversity and possible competition were greater in edge habitat than forest interior. More shrews were captured than mice in edge habitat, whereas more mice were caught in deep woods habitats than shrews, showing an inverse correlation between mice captures and shrew captures, alluding to possible competition.

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An Experimental Test of Small Mammal Dispersal of Arbuscular Mycorrhizal Fungi Spores

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We tested whether small mammals disperse arbuscular mycorrhizal fungi (AMF) in a mesophytic forest. We examined fecal pellets from small mammals trapped in alternating months from April to October 2011 and 2012 at the Towson University Field Station in Monkton, Maryland, and monitored AMF spore dispersal via wind. We compared plots of sterilized soil that were exposed to small mammals, and either baited or not baited, to associated plots that excluded small mammals from May to September 2012. At the end of the field experiment, we transferred sterile soil to a greenhouse and assayed inoculum potential with *Sorghum bicolor*. Our data indicated small mammals consumed AMF spores in June and August 2011 and June and October 2012. Mice in the genus *Peromyscus* composed the majority of captures (86.8%). The frequency of mice containing AMF spores ranged from 3.6 – 14.3%. We identified AMF spores in 9.1% of eastern gray squirrels (*Sciurus carolinensis*) and 50% of woodland voles (*Microtus pinetorum*). AMF spores dispersed via wind at a rate of 0.77 spores/m²·day in 2011 and 0.74 spores/m²·day in 2012. In the field experiment, more open plots contained AMF (4/10 baited and 5/10 not baited) than closed control plots (2/10 exclusions). This study provides experimental evidence that small mammals disperse AMF spores in a patchy manner, and wind dispersal also plays a role.

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Biogeographical Patterns of Energetic Compensation in Desert Small Mammal Assemblages

Investigating the mechanisms by which coexisting or competing species utilize limited resources is useful in elucidating patterns of niche space and species diversity. Research in the Chihuahuan Desert showed that Bailey's pocket mouse consumed up to 90% of the energetic resources left unused when kangaroo rats were experimentally excluded. We excluded the ecologically dominant degu (*Octodon degus*) from replicate sites in north-central Chile and documented no energetic compensation by other small mammals over 19 years. In this poster, we will present the results of analyses on small mammal assemblages in arid regions elsewhere to evaluate the probability of ecological replacement at a wide range of sites. We predict that energetic compensation will be likely within desert small mammal assemblages in North America, reflecting the diversification of largely granivorous heteromyid rodents. Because most other desert regions lack such extensive trophic specialization, we expect such compensatory dynamics to be unlikely elsewhere. We posit that energetic compensation documented in North America reflects: 1) the serendipitous presence of the heteromyid radiation; and 2) dietary specialization by rodents on seeds produced during 1-2 seasons of predictable annual rainfall. Furthermore we predict that such compensation will be uncommon elsewhere, as the pool of species available to colonize sites generally is smaller and lacks the trophic redundancy of North American deserts.

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Resource Partitioning Among Sympatric Congeners of *Reithrodontomys*

A primary goal of ecology is to understand the maintenance of biodiversity and the underlying interdependent mechanisms allowing species to coexist. To avoid competition, coexistence of species is afforded by niche differentiation through differential patterns in life histories, morphologies, times of activities, and resource partitioning. Competition among congeners is predicted to be especially strong due to their shared evolutionary histories and similar ecological and morphological characteristics. To elucidate co-occurrence mechanisms of congeners, stable carbon and nitrogen ratios ($\delta^{13}\text{C}$ and $\delta^{15}\text{N}$) were assessed from nails of multiple individuals of *Reithrodontomys* (harvest mice) collected on the Volcán de Colima in Colima, Mexico. *Reithrodontomys* were trapped in 2008-2009 at ground and elevated levels on the Volcán de Colima where multiple species of harvest mice overlap at fine spatial scales. Results revealed variation in $\delta^{13}\text{C}$ levels at the intraspecific level. Interspecific comparisons showed varying degrees of dietary overlap and trophic structuring among harvest mice on the Volcán de Colima. *Reithrodontomys* demonstrated plasticity in their diet that was associated with microhabitat use. This study demonstrates how stable isotopes are useful to help understand dietary overlap and trophic differentiation within and among co-occurring harvest mice. Furthermore, this study contributes to our overall understanding of the ecological roles of sympatric congeners in their native habitats.

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Expansion of the Semi-arboreal White-footed Mouse In Tallgrass Prairie: Three Decades of Fire, Woody Invasion and Land-cover Change

Since its inception in 1981, temporal variation in the experimental “application” of fire to the Konza Prairie Long-Term Ecological Research Project has maintained native tallgrass prairie with varying success. Konza is comprised of a patchwork of treatment units that vary in prescribed fire frequency (annually or quadrennially burned, or long-term unburned), occurrence of native grazers (bison), topography, and weather conditions. Over much of the last century (since 1939) and especially during the last 3 decades (since 1981), a documented increase in woody vegetation has occurred across the ~3,500-ha site (Briggs et al. 2005); furthermore, during the last 30+ years, woody expansion has occurred in treatment units that undergo fire less frequently. Concurrently, we have assessed the community and population dynamics of small mammals at Konza, among 14 sampling sites in 7 treatment units. Concomitant with the increase of woody vegetation, the semi-arboreal white-footed mouse (WFM; *Peromyscus leucopus*) has generally expanded its presence at Konza during the last 3 decades. Furthermore, WFM has increased sharply at sites with less frequent burns (> 4 years between fires) and, in some cases, has become the dominant species. At the same time, its prairie cousin, the deer mouse (*Peromyscus maniculatus*), has tended to decrease at these sites, suggesting that some degree of ecological replacement in small mammal communities has accompanied the land-cover change.

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Fire and Land Use Interact to Affect Patterns of Rodent Granivory

Understanding how pervasive anthropogenic disturbances, like prescribed fire and past agricultural land use, influence rodent granivory may be important to understanding patterns of plant abundance and composition. To assess the effects of fire and land-use history on patterns of rodent and arthropod granivory for 2 plant species, *Tephrosia virginiana* and *Vernonia angustifolia*, we deployed 2 seed depot types (rodent and arthropod access; arthropod access only) at 27 sites in the longleaf pine ecosystem that differed in fire frequency (high or low) and land use (forested sites used for agriculture ~60 years ago vs. historically forested sites). Average seed removal was 25% for *T. virginiana* and 36% for *V. angustifolia*. Allowing rodent access significantly increased seed removal of both species. Removal of *T. virginiana* by rodents was greater than removal by arthropods for high and low fire frequency sites. Rodent removal of *V. angustifolia* depended upon an interaction between fire frequency and land use: rodents removed more seeds at post-agricultural sites regardless of fire frequency, and at historically forested sites with low fire frequencies, but not at historically forested sites with high fire frequencies. Our results add support to the role of rodents as significant agents of seed removal in the longleaf ecosystem. Moreover, we show that the effects of fire frequency and land use on seed removal by rodents differ depending upon the plant species.

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A Standardized Design for Small Mammal Sampling Across Habitats, Decades, and Spatial Scales for the National Ecological Observatory Network

A major component of the National Ecological Observatory Network (NEON) is continental-scale terrestrial sampling, including the temporal dynamics in: 1) the demography and disease prevalence of small mammals; and 2) small mammal community diversity and structure, as they relate to climate, productivity, and land use. The standardization of protocols across sites, varying in area from 1 km² to 500 km², and across multi-decadal time scales is critical. Sampling at these spatial and temporal scales is unprecedented; I relied on members of a technical working group and existing long-term data to inform how to best concentrate sampling to achieve objectives and maximize efficiency. All of the data produced by the Observatory will be freely available to communities of mammalogists, ecologists, scientists, and the public, as well as associated voucher specimens and additional archived samples. The Observatory’s success is dependent upon the community’s support of the design and implementation and ultimately the use of the data to advance scientific knowledge. I present the current design for the small mammal sampling for NEON as a means of communicating and engaging with the diversity of experts in mammalogy.

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The Expansion of Pinyon-juniper Woodland and the Appearance of *Peromyscus truei* in the Toiyabe Range of Central Nevada

In the early 20th century field biologists from the Museum of Vertebrate Zoology at Berkeley conducted vertebrate surveys in the Great Basin region. Over the past several years, we have been conducting resurveys of many of the localities visited by MVZ scientists. Our resurvey of the Toiyabe Range of central Nevada revealed the presence of the pinyon mouse, *Peromyscus truei*. This species was not recorded in the Toiyabes during the original survey of 1930-31, but in the recent survey, the species was widespread and abundant. The appearance of *P. truei* is correlated with the expansion of its primary habitat, pinyon-juniper woodlands. The regional expansion of single-leaf pinyon, *Pinus monophylla*, is evident through comparisons of landscape photographs taken by the original surveyors in 1930 and photographs taken more recently. Our aim is to understand the nature of the pinyon expansion over the past 80 years through dendrochronology techniques using tree cores obtained from pinyon in the area. The correlation of tree ring patterns with climate data reveal the conditions favorable to recruitment and growth of trees and allow us to assess the relative importance of climate warming as a factor behind pinyon expansion. Understanding the causes behind such dramatic habitat shifts and the associated changes in small mammal assemblages has important implications for conservation and management of biotic communities in the Great Basin.

74 Poster Session I, Franklin B, Sunday 16 June 2013

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Detection and Characterization of Bat Hotspots: A Fusion Test of Local Spatial Autocorrelation

Mammalogists commonly seek to identify spatial autocorrelation in their capture datasets, in some instances to negate its effect on design or analysis, in others to elucidate the processes behind the phenomenon itself. Although there are several tests of local spatial association, each has different strengths and weakness and hence tends to capture different aspects of the data. Here we present a fusion approach to characterize clusters in spatially-explicit capture data of rainforest bats from Malaysia, using 3 disparate, but commonly-used tests of local autocorrelation: a traditional spatial analytical approach (*G* statistics); a permutation method designed for ecological count data using distance indices (SADIE); and a cluster detection test that uses a moving window of variable size to identify sets of points or regions (SatScan). We demonstrate that the fusion approach significantly improves hotspot detection and characterization, provides explicit representation of confidence for individual clusters, and generates an integrated map that incorporates spatial autocorrelation of the data.

75 Technical Session 3: Evolutionary Biology, Salon A, Monday 17 June 2013

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Sex-biased Dispersal Drives High Error Rates in Mitochondrial Tree-based and Distance-based Species Delimitation

Species delimitation using mitochondrial sequences promises to identify species in the face of declining morphological expertise and a catastrophic biodiversity crisis. It has become common for species delimitation to rely in part, or completely, on 2 criteria: 1) reciprocal monophyly; and 2) a threshold of sequence divergence between putative species. Using coalescent simulations of continuous and interrupted gene flow, we show that these commonly applied criteria incur high false positive and high false negative error rates in species delimitation, particularly if gene flow is male-mediated. We posit that mitochondrial species delimitation requires additional supporting data to ensure that sex-biased dispersal is not the basis for the species limits proposed. To reduce error rates, species delimitation requires hypothesis testing that accounts for multiple inheritance systems (including morphology), divergence times, and criteria other than monophyly and sequence divergence.

76 Technical Session 3: Evolutionary Biology, Salon A, Monday 17 June 2013

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The Influence of Reproductive Ecology on Genome Evolution in Rodents

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Behavioral traits, such as the male reproductive strategy, potentially influence genome evolution through their impact on effective population size. Murid rodents are thought to generally have high variance in male reproductive success as a result of sperm competition, and many species have large testes, suggesting a high degree of competition for reproductive opportunities. Some species, however, have proportionately smaller testes—a phenotypic signature of relatively low sperm competition and low among-male variance in reproductive success. To explore the effect of male reproductive strategy on genome evolution, we used next-generation sequencing to quantify genome-wide polymorphism and divergence in 4 species of murids spanning a 30-fold difference in relative testes mass. Our results illuminate, for the 1st time, the degree to which cryptic reproductive behavior varies among these animals over evolutionary timescales.

77 (ECT) Technical Session 3: Evolutionary Biology, Salon A, Monday 17 June 2013

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Genetic Analysis of a Hybrid Zone Between Two Species of Woodrats (*Neotoma*)

Hybrid zones, areas of interbreeding between divergent taxa, have been documented in a number of plant and animal species. Hybridization is no longer considered a rare phenomenon and is often an important generator of genetic diversity. The degree to which closely related species can interbreed is determined by ecological, behavioral, and genetic factors, and hybridization is most often limited by the genetic diversity between species. Using 15 microsatellite loci, mitochondrial sequence data, and genome-wide sequence data, we assessed the genetic diversity across and adjacent to a hybrid zone between 2 species of woodrats (*Neotoma fuscipes* and *N. macrotis*). The zone exists across a 2 km continuum from pure *macrotis* to pure *fuscipes* with no strict segregation between the parental species. Using marker appropriate analyses, we found clear signals of admixture and introgression in all 3 genetic datasets. Approximately 20-30% of the individuals occupying the contact zone are of hybrid origin, and we find evidence of multigenerational hybrids and backcrosses to both pure species. Divergence between the 2 species is 11% based upon cytochrome *b* sequences, and F_{ST} values are equally divergent. Principle component analysis of the genome-wide dataset shows 3 distinct groups of animals (pure *fuscipes*, pure *macrotis*, and hybrids) with hybrids being more divergent from the 2 pure species than the 2 pure species are from each other.

78 Technical Session 3: Evolutionary Biology, Salon A, Monday 17 June 2013

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Reproductive Success Across a Hybrid Zone in *Neotoma*: Differential Fitness Effects Among Pure and Hybrid Genotypic Classes

When closely related species come into secondary contact, a wide range of ecological and genetic interactions may occur. Specifically, when the boundary between species is still permeable to genetic exchange, patterns of mate choice and reproductive success play central roles in the degree of genetic introgression that will occur between the interacting species. We examine patterns of reproductive success in populations of *Neotoma macrotis* and *N. fuscipes* in an area of secondary contact. Despite substantive genetic and morphological differences between these sister lineages, they readily hybridize in the field. We use a multilocus microsatellite dataset and detailed mark-recapture information to quantify patterns of reproductive success for individuals of both pure and hybrid classes. The fitness effects that emerge from differential patterns of reproductive success among pure and hybrid genotypic classes, in combination with our growing understanding of other pre- and post-zygotic isolating mechanisms in this system, are leading to a particularly detailed view of the nature of this species boundary.

79 Technical Session 3: Evolutionary Biology, Salon A, Monday 17 June 2013

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Some Animals are More Equal Than Others: Functional Diversity vs. Functional Group Richness in Large Quaternary North American Mammals

Functional groups and guilds are commonly used in modern and paleontological studies to represent the range of ecological diversity within a community. Functional groups simplify analysis by lumping together multiple species assumed to be functionally equivalent and therefore ecologically redundant. Many species can go extinct without the functional group disappearing. However, there is no objective method for creating these groupings, and the assumption that species are either completely similar or completely distinct from one another is restrictive and unrealistic. Continuous, quantitative functional diversity measures are an alternative to functional groups that can be calculated from similar types of data. Previous modeling work suggests that the redundancy of species within functional groups is unrealistic as most species are relatively ecologically distinct from each other. Most modeling

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only considers random, theoretical extinctions though. Few studies have examined the functional diversity and functional group richness of actual communities going through a large extinction event. Using both qualitative and quantitative trait data for large (> 10 kg) Quaternary North American mammals, we can see how functional group richness, functional diversity, and taxonomic richness changed through the Pleistocene extinction and the last 40,000 years. Continuous measures of functional diversity should be used over functional groups as they allow for more realistic, varying degrees of ecological similarity between species.

80 (E, ST) Technical Session 3: Evolutionary Biology, Salon A, Monday 17 June 2013

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Multiple Trait Combinations Predict Brain Size in Mammals

Brain size relative to body size (i.e., encephalization) is thought to reflect a species' cognitive ability to integrate and process information from the environment using various sensory modalities. On the one hand, comparative studies of brain size have focused on the social and ecological benefits of cognition that may enhance survival. On the other, brains are energetically expensive; increased energy allocation to support large brains must detract from an organism's energy budget with consequences for life history. The meaning and validity of these correlations continue to be debated. To begin to understand the tradeoffs associated with brain size, we must first understand how multiple intrinsic and extrinsic traits interact with each other in producing brain size in a context dependent fashion. We use machine learning techniques and a new dataset of brain sizes for 1,455 species, phylogenetic relationships, and 12 ecological, behavioral, and life history traits to determine the multiple trait combinations that lead to brain size in mammals. Deviations from the brain and body size allometry provide a metric of encephalization. Machine learning techniques reveal multiple combinations of intrinsic and extrinsic factors, and their interactions, in association with relative brain size. Our analysis suggests that natural selection has provided multiple trait combinations, mediated via life history, in order to balance the cognitive requirements of lifestyles with the energetic costs of brain size.

81 (E) Technical Session 3: Evolutionary Biology, Salon A, Monday 17 June 2013

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Defining Extreme: A New Perspective on Insular Mammalian Body Size Change

Organisms colonizing islands often undergo dramatic shifts in size. This is especially evident among insular mammals, where shifts towards larger body sizes in small species and smaller body sizes in large species are often referred to as the "island rule." Despite early assertions that mammals followed a rule with law-like regularity, it is now clear that any island "rule" is an oversimplification of a complex process where exceptions abound. Multiple factors have been hypothesized to influence the size shifts, and no single variable has sufficed to explain the size differences observed on islands. In addition, previous analyses of the island rule have ordinarily focused on the differences between single mainland and island pairs without considering the intraspecific variation found within a lineage on the mainland. To address this issue, we assembled a data set of mainland rodent populations to obtain an estimate of body size variation typically observed on the mainland. We then applied this estimate to another, previously assembled dataset of insular rodent populations and examined how island populations that fell within the boundaries of normal mainland variation differed from those that fell outside those boundaries. We find significant differences between these 2 groups for several island-specific factors (climate, island area, etc.) and explore to what extent this approach could be applied to other orders.

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Climate Change and Body Size: A Review and Plea for Standards

Inquiry into the effects of recent climate change on organismal biological attributes has precipitated a renaissance of studies on ecogeographic or "ecochronologic" variation as well as a renewed appreciation of the value of museum collections in ecological research. Recent studies investigating shifts in body size and/or dimensions over centennial and even decadal time scales have led some authors to propose such changes as a universal response to climate change. However, methodological and reporting inconsistencies not only render many individual studies unrepeatably but also severely limit both their long-term utility and comparability with other studies. Here I review recent studies of ecochronologic variation in mammals and suggest standards that, if adopted, would greatly facilitate comparison among published studies (and therefore maximize opportunities for synthetic reviews and/or meta-analyses) while also ensuring that data are better, and permanently, associated with voucher specimens.

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83 Technical Session 4: Population Ecology, Salon B, Monday 17 June 2013

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Effects of Elk Population Density on Immune Function Mediated by Body Condition

A primary tenet of life history theory is that trade-offs occur because resources are limited and individuals must allocate resources among important functions for survival and reproduction. Long-lived species occupy the slow-paced end of the pace-of-life continuum, and have evolved strategies to maximize reproductive success over their lifetime by placing greater emphasis on adult survival and less emphasis on any single reproductive event. Most ecoimmunology studies predict a trade-off between reproduction and immune function because both are energetically costly. Most studies, however, have used fast-paced species. We used North American elk (*Cervus elaphus*), a slow-paced species, to investigate trade-offs between immune function and reproduction mediated by body condition. Because elk invest in survival over current reproduction, we expected no trade-off between reproduction and immune function. Instead, we predicted that immune function would be high in reproductive females, but that immune function would decrease with body condition in non-reproductive females. We experimentally altered body condition by manipulating population density of elk at Starkey Experimental Forest and Range; we experimentally increased population density and observed that body condition was negatively correlated with population density. We quantified 3 aspects of constitutive immune function (bactericidal competence, hemolytic complement activity, and haptoglobin concentration) and correlated those results with body condition and reproductive status of adult female elk.

84 (E) Technical Session 4: Population Ecology, Salon B, Monday 17 June 2013

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Population Dynamics of a Forest Ungulate Respond to Winter Severity and Habitat Alteration

Changes to habitat and climate have become ubiquitous and can strongly influence wildlife population dynamics, including species of high ecological and economic importance such as ungulates. These effects often impact vital rates differentially, as certain life history processes are more vulnerable than others. We examine the effect of timber harvest and variable winter weather on a long-lived vertebrate, deer in the coastal temperate rainforest of Southeast Alaska. Sitka black-tailed deer (*Odocoileus hemionus sitkensis*) are the dominant herbivore and a key resource for subsistence hunters. Timber harvest plans for the Tongass National Forest incorporate deer density into management goals but exclude environmental variability from calculations. We derived vital rates from life history data for 63 adult and 154 juveniles and population growth rates from matrix-based life table response experiments. Timber-harvested areas produced a lower population growth rate than unharvested areas ($\lambda = 1.06$ and 1.12), explained primarily by variability in adult female fecundity and juvenile survival. Winter severity had a larger effect, with population growth rates ranging from 0.84 to 1.19, driven primarily by variability in juvenile survival. Climate models predict increasing winter precipitation and stochasticity, which along with continuing timber harvest may reduce future deer populations. Timber managers calculate deer carrying capacity using average winter severity. Instead, such plans should incorporate and monitor changing climate in an adaptive-management framework to ensure sustainable deer populations.

85 Technical Session 4: Population Ecology, Salon B, Monday 17 June 2013

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Pinyon-juniper Expansion in the White Mountains: Implications for Mule Deer Demographics and Habitat Use

Grazing, fire suppression, and altered land use regimes have led to shifts in vegetation composition, in particular increases in distribution and density of pinyon-juniper woodlands. This shift can lead to loss of important habitat for wildlife. As woodlands extend into shrub steppe and riparian communities, soil moisture is reduced causing declines in understory biomass and reduction in forage availability. This study examines habitat relationships of mule deer in an arid ecosystem, with a focus on the influence of pinyon-juniper woodland. GPS locations of female mule deer were gathered between mid-June through August, when nutritional demands are highest; fawn rearing and accumulation of energy stores for winter. The data were analyzed using mixed-effects logistic regression to identify selection or avoidance of various habitat types and landscape features. We found that deer strongly selected riparian areas and stayed relatively close to those habitat types. We also identified very little selection or avoidance for pinyon-juniper habitat at a fine scale (within 5 m of the location), however, strong avoidance as densities increase, at a larger scale (250 m). These results emphasize the importance of riparian habitat during summer months and supports our

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hypothesis that pinyon-juniper woodland may provide critical thermal or anti-predatory environment at low to mid densities, but as densities increase and understory biomass declines this habitat would become less desirable.

86 (E, ST) Technical Session 4: Population Ecology, Salon B, Monday 17 June 2013

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Migration Behavior, Body Condition, and Sex Differences in Survival of Mule Deer

Migration is an important adaptation for species inhabiting variable ecosystems. Many ungulate populations make seasonal migrations between summer and winter ranges; however, peer-reviewed literature indicates migration routes and distances travelled can be highly variable. Few studies have quantified these migration strategies in the context of true measures of fitness such as body condition or population-level effects on survival. We used data from 424 radio-collared mule deer (*Odocoileus hemionus*) to test hypotheses relating survival to body condition, sex, environmental conditions, and migratory strategy. We used a known-fate survival framework in Program Mark to obtain seasonal estimates of survival for each sex and age class in relation to body condition and migration distance. Adult survival was most parsimoniously explained by models containing covariates for sex, season, body condition, and migration distance. Over-winter survival of juvenile mule deer was best explained by models containing covariates for sex, body mass, and a winter severity index. Adult and juvenile survival was lower for males than for females, even after accounting for mortality caused by human harvest. These results suggest population models may overestimate male survival outside of harvest reporting. We also provide preliminary results that suggest adult survival varies with respect to migratory behavior and body condition, which may have direct management implications for decisions affecting harvest quotas, habitat improvements, and energy development policies.

87 (E) Technical Session 4: Population Ecology, Salon B, Monday 17 June 2013

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Distance Sampling as a Technique to Monitor Pronghorn in Kansas

Accurate and reliable survey results are crucial for proper pronghorn (*Antilocapra americana*) management. Aerial strip transect counts have been conducted biannually in Kansas since 1963. Summer counts (15 July–15 August) were conducted to obtain buck:doe:fawn ratio estimates. Winter counts (15 December–28 February) were conducted to obtain population abundance estimates. We conducted strip transect counts 18–19 July 2012 and distance sampling surveys 13–14 August 2012. The date surveys and counts were conducted had an impact on survey results. Pronghorn cluster size (group size) increased by 57% (3.98 to 6.23) between July and August. Consequently, encounter rate decreased by 70%, from 0.127 pronghorn/km to 0.038 pronghorn/km. The population abundance estimate obtained from the distance sampling survey was 1,638 pronghorn (CV = 23.1%). The strip transect count from the previous winter (2011-2012) was 1,437 pronghorn. The distance sampling survey produced statistically precise estimates (CV = 23.1%) albeit with a small sample size ($n = 65$) and required less flight time than the strip transect counts. To obtain statistically reliable population estimates and buck:doe:fawn ratios in Kansas, we preliminarily suggest the optimal time for distance sampling surveys to be mid-July.

88 (E,**) Technical Session 4: Population Ecology, Salon B, Monday 17 June 2013

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Insights into the Reproductive Ecology of Fishers (*Martes pennanti*) at the Southernmost Extent of the Range in California

The fisher (*Martes pennanti*) is a rare forest-dwelling carnivore of conservation concern in the western United States. The population in the southern Sierra Nevada is of particular interest because it is isolated, genetically distinct, and at the southernmost extent of the species' range. In recent years, much effort has focused on improving our understanding of fisher ecology and implications for forest management in the Sierra Nevada. However, insight on denning needs and even basic reproductive parameters have been hindered by the fact that few reproductive dens have been found in this region. Between 2008 and 2012, we identified reproductive dens of 27 female fishers using radio telemetry on the Sierra National Forest and documented parameters and behaviors associated with reproduction. Earliest den initiation date was 23 March, and mean number of kits per female across years was 1.59 ($n = 78$ litters, range = 1 to 3). On average, individual females used 3.35 (range = 1 to 6) den structures in a given

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year; earliest move from a natal to maternal den was 6 April. In addition, we documented male visitation at dens after parturition and summer rest sites used by females with kits. Data from this project will help inform local biologists and forest managers and provide guidance for conservation plans. This research was supported by an ASM Grants-in-Aid of Research awarded to Rebecca E. Green in 2011.

89 Technical Session 4: Population Ecology, Salon B, Monday 17 June 2013

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The Effects of Translocation on Reproductive Success in Newly Released Fishers

The objective of most translocations is to establish increasing populations of animals immediately. Yet, for most translocations, few data are collected on the reproductive success of animals immediately following release to a new area. Further, information is lacking on how reproductive success following translocation affects the establishment of a new population. Prior to releasing fishers (*Pekania pennanti*) into the Northern Sierra Nevada of California, we hypothesized that the timing of their release would affect their reproductive success. Specifically, we hypothesized that females released relatively early would be able to develop home ranges and acquire sufficient resources to allow implantation of blastocysts and that females released 24 months (October–December) prior to the implantation of blastocysts would have a higher probability of giving birth than would females released 0–1 months (January–February) prior to implantation. We tested these predictions on 40 female fishers released on 2 independent translocations in California and Washington. We determined successfully giving birth by tracking females to dens and by observing kits using remotely active cameras. We observed differences in denning rate between sites, but females released early denned and produced kits more often (75% in California and 33% Washington) compared to females released later (33% California and 17% Washington). Preliminary modeling of this effect suggests that releasing fishers early may result in populations > 30% larger after 10 years than those released late.

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Hormonal Patterns Reflect Social Instability in a Heavily Hunted Wolf Population

Often the effects of hunting are measured in terms of population numbers and distributions, but exploitation can also affect social dynamics, reproductive rates, morphological traits, population structure, and genetic structure. Stress and reproductive hormones in hair, which reflect long-term endocrine activity integrating concentrations as the hair grows, provide a novel approach for investigating the social and physiological consequences of hunting. Accordingly, we compared steroid hormone levels in hair of wolves (*Canis lupus*) living in Canada's arctic tundra ($n = 103$) that experience heavy hunting rates with those in the boreal forest ($n = 45$) where hunting pressure is lower. We predicted that tundra wolves would show hormonal evidence of an unstable social structure, including elevated stress and reproductive hormones. The hair samples showed that the stress hormone cortisol was higher in tundra wolves compared with those in the boreal forest. Tundra wolves also had higher levels of testosterone, which might be indicative of unstable social structure in tundra wolves compared with those in the boreal forest. Moreover, progesterone was higher in tundra wolves, possibly reflecting the reproductive activity typical of a situation where social organization is disrupted. Although ecological differences in prey specialization and habitat could also contribute to the hormonal differences we observed between regions, our findings are consistent with social and physiological consequences of human exploitation.

91 Technical Session 5: Behavior, Salon C, Monday 17 June 2013

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Steering Sound Beams: The Influence of Social Context on Acoustic Radiation Patterns in Neotropical Singing Mice

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The efficacy of animal communication depends upon signal detection by receivers following propagation through an often-cluttered environment. Most studies of acoustic displays used in sexual contexts focus on the role of spectral and temporal characteristics in signal evolution. However, sound waves generally radiate from a vocalizing animal with unequal amplitude in different directions, favoring adaptations that exploit or compensate for this directionality. We used a hemispheric microphone array to record from male Alston's singing mice (*Scotinomys teguina*) before and after playback of a conspecific vocalization. In this species, males commonly emit highly stereotyped and elaborate vocalizations that serve to repel rival males. Upon hearing conspecific song, males oriented towards the speaker and produced vocalizations with greater intensity (3 dB). Our data suggest that males dynamically adjust vocal output and acoustic directionality to expand the signals' active space and advertise aggressive intent.

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Mammalian Plural Breeding: Why Bother?

An emerging trend in mammalian sociality is that plural breeding with communal care, a reproductive strategy in which multiple females in a group breed and rear offspring in a communal nest, does not enhance the direct fitness of females. Much of our knowledge about mammalian plural breeding comes from relatively short-term (< 3 years) studies. Moreover, we lack a strong understanding of the mechanisms underlying sociality-fitness relationships in mammalian plural breeders. Since 2005, we have been studying the ecological, physiological, and social underpinnings of direct fitness variation in the plurally breeding rodent, *Octodon degus*. Our study suggests that plural breeding is costly to females in large groups. The per capita number of offspring produced and surviving to breeding age decrease with increasing group size. Inequality in direct fitness increases with increasing group size and heterogeneity of social network structure. *Degu* social groups are not kin-biased, suggesting that females do not compensate for reduced direct fitness with increased indirect fitness. Mechanistically, females in large groups do not maintain elevated baseline cortisol levels but experience reduced immunocompetence. This cost does not reduce the fitness of females or the immunocompetence of offspring. The results of our long-term study beg the question: "Why do *degu* breed plurally?" To answer this question, we are quantifying neuroendocrine and environmental correlates of social group size and direct fitness.

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The Effects of Perinatal Behavior and Maternal Decisions on Neonate Survival in a Hiding Ungulate

The periods immediately preceding and following parturition are times of heightened vulnerability for mothers and neonates. In ungulates, maternal behavioral strategies such as isolation and birth-site selection can mitigate predation risk during the perinatal period. We investigate the effects of maternal behavior and decision-making on the survival of newborn Thomson's gazelles (*Gazella thomsoni*). We observed parturition events and perinatal behavior of free-ranging gazelle. We documented high frequencies of disturbance of the mother-calf pair in the hour following parturition, which often resulted in neonate predation. We discuss the role of maternal behavioral variation in generating or avoiding disturbances and predation. Our results suggest that much infant mortality occurs within an hour of parturition, a time period overlooked by many studies of ungulate infant mortality. Knowledge of infant mortality rates and the factors contributing to them is important in understanding and managing ungulate populations.

94 (**, ST) Technical Session 5: Behavior, Salon C, Monday 17 June 2013

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A Positive Interaction Between Reciprocal Help and Relatedness Predicts Cooperative Food Sharing in Common Vampire Bats

Hamilton's rule states that selection favors helping behaviors when relatedness exceeds the fitness ratio of actor cost to recipient benefit ($r > c/b$). By altering this cost-benefit ratio, reciprocity can create interactions between direct and indirect fitness benefits. I examined how reciprocal help, relatedness, and barriers to physical contact influenced food-sharing decisions in 28 common vampire bats (*Desmodus rotundus*) under captive conditions of variable relatedness and equal association. I induced food-sharing multiple times over 3 years, measured social grooming, and estimated relatedness using 15 microsatellite loci and matrilineal pedigrees. I also tested whether bats would provide food to caged conspecifics through a cage wall. The food-sharing network was consistent, reciprocal, kin-biased, and correlated with social grooming. Donors typically initiated sharing, and in a few reciprocated cases, close

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kin regurgitated food through a cage wall. Reciprocal help was the strongest predictor of food sharing (8 times more predictive than relatedness), yet the degree of reciprocity increased with relatedness. These findings suggest that: 1) food sharing is explained by cooperative social bonds involving a positive interaction between relatedness and reciprocal help; 2) the evolution of vampire bat food sharing is not explained solely by harassment or kin selection; and 3) cooperation experiments that prevent physical social contact can alter naturally occurring cooperative behavior. This research was supported by 2 ASM Grants-in-Aid of Research awarded to Gerald Carter in 2010 and 2012.

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Scansorial and Arboreal Behavior in Northern Red-backed Voles in Alaska

The northern red-backed vole (*Myodes rutilus*; NRBV) is the predominant small rodent in Alaska's boreal forests. While NRBVs are thought to be strictly terrestrial, their largely allopatric North American congener, the southern red-backed vole (*Myodes gapperi*) has been observed climbing in trees and in a laboratory setting, but is thought to be outcompeted for the arboreal niche by other sympatric small mammals with superior climbing skills. We conducted field trapping at multiple localities in interior Alaska to determine if NRBVs might also be exploiting the arboreal niche. Results indicate that NRBVs readily climb trees, a phenomenon heretofore undocumented in the literature, and frequented traps up to 2 m off the ground. When comparing adjacent arboreal and terrestrial trap lines, we found that 31% of trap success was arboreal. Video captured from camera traps shows NRBVs exhibiting climbing techniques and dexterity, such as climbing on fine terminal branches and descending head-first using rotation in the hind legs for stabilization, that are generally associated with more scansorial or arboreal species. Throughout most of its range in Alaska, *Myodes rutilus* is not sympatric with *Peromyscus* or any other similarly-sized arboreal or scansorial mammal. This suggests that the vacant arboreal niche might lead to an increase in the opportunistic use of the unexploited 3rd-dimension of NRBVs' habitat, which may in turn lead to morphological and/or behavioral adaptations.

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Stem diameter and Toughness Affect Vole (*Microtus* spp.) Foraging Patterns in Tallgrass Vegetation

Voles (*Microtus*) in tallgrass prairie habitats clip and fell stems to access much of the vegetation they consume. Stem characteristics, such as diameter and toughness, should influence vole stem-clipping patterns, though these aspects have not previously been explored. I used field censuses of clipped and unclipped stems and captive feeding trials to determine how stem characteristics affect vole foraging. The field censuses showed that voles were selective about the stems they clipped, and that the species they selected varied over the course of the growing season. In contrast, feeding trials showed that plant species voles preferred remained constant throughout the growing season, demonstrating that palatability alone does not drive vole foraging patterns in the field. Stem census data indicates that stem diameter is an important factor in vole foraging. Voles preferentially cut smaller diameter forb stems (3.5 ± 0.1 versus 4.9 ± 0.2 mm for clipped and unclipped stems, respectively), and larger diameter grass stems (2.0 ± 0.1 versus 1.9 ± 0.1 mm for clipped and unclipped stems, respectively) while forb stems above 7 mm in diameter were never cut, indicating a size refugium from vole herbivory. Additionally, a plant species' average stem toughness correlated with the frequency of vole clipping; in general, species with less tough stems were more likely to be clipped. Stem characteristics play a significant and underappreciated role in vole foraging patterns in tallgrass habitats.

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Multiphasic Movement Patterns of Florida Panthers

How animals move within heterogeneous landscapes is a process influencing many aspects of ecology and population dynamics, because survival depends on food acquisition and predator avoidance and reproduction depends on finding mates. The interactions of animals with their environment can result in complex movement patterns. We investigated the movement patterns of the endangered Florida panther (*Puma concolor coryi*) using location data collected via GPS collars. We quantified several descriptors of movement and tested for the effect of intrinsic and extrinsic factors on these descriptors. We tested the multiphasic movement hypothesis that animals alter movement patterns as a function of internal state, social, ecological, and demographic variables. Finally, we

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assessed whether correlated random walks and Lévy flights adequately described Florida panther movement patterns within and across movement phases. Our results indicate that movement patterns vary greatly depending on several factors, including sex and age of panthers, photoperiod, and season. We identified several movement phases on different scales: movement differed between day and night, movement of dispersing animals was different from that of adults with established home ranges, and females with kittens moved differently than those without. We found no evidence for Lévy distributed movement lengths. Movement of dispersing panthers resembled correlated random walk more closely than movement of adult panthers. Correlated random walk constrained in a home range area was more similar to movement of adult panthers.

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Ecological Drivers of Antipredator Defenses in Carnivores

Although we know a good deal about the evolution of aposematism (bold contrasting coloration advertising unpleasant antipredator defenses), we know less about the evolution of defensive morphologies themselves. Some mammalian carnivores have the ability to spray noxious anal secretions in defense and use bold black-and-white color patterns to advertise these traits, whereas other species lack such weaponry. We demonstrate that enhanced spraying ability evolves in those nocturnal Carnivorans that are at greater risk of predation from large carnivores due to their nocturnality and small size but that sociality evolves in species that are at greater risk of predation from birds-of-prey owing to their diurnality and small size. These results provide the 1st evidence that noxious defenses and sociality are alternative antipredator strategies targeting different predator guilds that predominate predation risk at different times of the day.

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Are There Taxonomic Patterns of Population Variability, Density Dependence, and Conservation Status?

The preservation and persistence of many mammalian species are affected by anthropogenic related activities. In this study, we used mammalian population data from the Global Population Dynamics Database to test for relationships among population size variability, the strength of density dependence, and risk of extinction. Based on theoretical expectations, populations with greater fluctuations in abundance can be predicted to have increased risks of extinction. Because strong density-dependence (DD) might be expected to dampen fluctuations in abundance, increases in DD can be predicted to be associated with decreases in extinction risk. We tested these predictions and the relationship of these population parameters with current conservation status, average mass at maturity, and average age at reproductive maturity. Statistical modeling demonstrated that as the strength of DD increases, extinction risk also increases and population size variability decreases. This suggests that populations with strong DD are at or close to their carrying capacity that allows for population stability over time. We also found that age to sexual maturity was positively associated with decreased rates of population size variability and increased extinction risk.

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Analyzing the Geography of Extinctions and Climate Change in the Sierra Nevada

During the early part of the last century, Joseph Grinnell had the foresight to document the distributions of terrestrial vertebrate fauna in California. Subsequent research has shown a variety of responses in terms of range dynamics, morphology, and genetics in birds and mammals to a century of climate and land use changes. We sought to better understand extinction dynamics of several species of small mammals by analyzing connectivity of habitat and patterns of climate change within the Sierra Nevada. We used landscape features such as local topography and hydrology and a dataset of downscaled climate variables to identify characteristics that signal potential local climate refugia, where climate has not shifted significantly from historical patterns. Additionally we estimated potential

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isolation of populations by elevational constraints and environmental predictability and compared these to extinction trends and genetic isolation to assess landscape connectivity. Our results show that heterogeneity in the geography of climate change plays a strong role in the patterns of species' responses and that future climate change likely will further isolate populations of sensitive mammals.

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Impacts of Climate Change on the Distributions and Diversity Patterns of Ungulates on the Tibetan Plateau

We used the maximum entropy approach to predict current and potential distributions of 22 ungulates on the Tibetan Plateau in 2020, 2050, and 2080. The results showed that these ungulates would lose on average over 50% and 30% of their ranges, much more severe range reductions than has been documented in previous studies. About 68% and 55% of these species would be locally endangered, and 32% and 23% of them would be listed as locally critically endangered, four endemic species (Tibetan elk *Cervus elaphus wallichii*, Thorold's deer *Cervus albirostris*, kiang *Equus kiang*, and Przewalski's gazelle *Procapra przewalskii*) would be globally endangered. The ungulates on the plateau showed latitudinal shifts of approximately 300 km and upward elevation migrations of approximately 650 m. We found patterns of reductions from west to east in ungulate species richness on the Tibetan Plateau. Southeastern mountainous areas had the highest current species abundance and yet may face the greatest diversity decreases, whereas the northwestern and northeastern areas would increase species numbers in the latter half of the 21st century. Ungulates on the Tibetan Plateau will be faced with severe distributional reductions, and the species richness pattern will be dramatically changed under climate change. For conserving the unique ungulates on the plateau, we suggest that securing existing protected areas and establishing new nature reserves to counterbalance the impacts of climate change.

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Small Mammal Distribution and Diversity Throughout Ghana, West Africa

West Africa is experiencing rapid environmental change with the growth of economies through natural resource exploitation, increasing habitat degradation and human expansion. These growing pressures raise much concern for the persistence of wildlife species. Here, I conducted a survey of small mammals within and outside 3 National Parks in Ghana. These parks represent an environmental gradient with rainforest in the south, grassland in the central region, and savanna in the north. I captured 214 individuals across 14 species within 6,597 trap-nights. I found the highest species richness at the northernmost park, which receives the least amount of rain and is the largest in size. Species composition and parasite prevalence varied both between inside and outside protected areas and across the 3 study areas. For example, *Lophuromys sikapusi* was detected only inside 2 national parks. Though all species captured were expected to occur in Ghana, several species thought to be habitat-specialists were found elsewhere. Ultimately, results from my study inform natural history for small mammals of Ghana and contribute to our understanding about species distributions and fine-scale patterns of diversity.

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Morphological and Phylogenetic Community Structure of North American Desert Bats

Understanding mechanisms governing mammalian community assembly has long interested ecologists. Traditionally, ecomorphological data have been used to infer resource partitioning among taxa within a community. Recent approaches have used a regional species pool phylogeny and community membership data to make inferences about processes shaping local communities, thereby tying ecological to evolutionary processes. Here we integrate morphological community structure data with our previous work on phylogenetic community structure to evaluate effects of spatial and taxonomic scale on bats in the 4 great deserts of North America. We calculated community structure metrics from a distance matrix of log-transformed morphological measurements of 55 taxa. Community membership data for each desert were compiled from fieldwork, MaNIS specimen records, and published reports. We found that communities were both morphologically and phylogenetically clustered at the largest spatial (all deserts) and taxonomic (all

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bats) scales. At smaller spatial and taxonomic scales, communities were phylogenetically overdispersed, suggesting an important role for interspecific interactions (such as competition) in structuring communities. However there was an ambiguous pattern for individual deserts based on morphological results, with most communities not significantly different from those randomly assembled at all three taxonomic scales. This research was supported by an ASM Grants-in-Aid of Research awarded to Lorelei E. Patrick in 2011.

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Identifying Landscape Characteristics that Promote Taxonomic, Functional and Phylogenetic Dimensions of Bat Biodiversity

Over 77% of ice-free land has been modified by humans. These alterations have contributed to the accelerated loss of biodiversity and ecosystem services. Nonetheless, such environmental variation does not affect all species equally due to differences in life history traits. Thus, species characteristics, as well as species richness and abundances, are important for understanding dynamics of biodiversity and can be measured by 3 dimensions of biodiversity (taxonomic, functional, phylogenetic). We assessed taxonomic biodiversity (Simpson's diversity), and functional and phylogenetic biodiversity (Rao's quadratic entropy) for phyllostomid bats along a forest loss and fragmentation gradient in northeastern Costa Rica. Via hierarchical partitioning, we identified the best explanatory landscape characteristics for each dimension at each of 6 combinations of season (wet and dry) and spatial scale (1, 3, 5 km radius). The effects of landscape characteristics were season-specific and dimension-specific. The identity of important landscape characteristics, as well as the scale and strength of their effects, differed between seasons. The magnitude and scale of landscape effects were larger in the dry season. Moreover, the dimensions did not respond to landscape variation in a similar manner. Consequently, 1 dimension is not a good surrogate for another. Overall, landscape characteristics associated with intermediate amounts of forest, intermixed with other land-cover types, promote all 3 dimensions of biodiversity. Thus, non-forest land-cover should also be considered in conservation strategies. This research was supported by ASM Grants-in-Aid of Research awarded to Laura M. Cisneros in 2009 and 2010.

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Comparative Biodiversity of Bats And Rodents Along an Extensive Tropical Elevational Gradient: Taxonomic, Functional, and Phylogenetic Dimensions

Environmental gradients in multiple dimensions of biodiversity provide considerable insight into processes that mold the structure of local assemblages. We quantified biodiversity from taxonomic (TB, species richness), functional (FB, Rao's Q using functional traits), and phylogenetic (PB, Rao's Q using a mammalian supertree) perspectives for bats and rodents along an extensive elevational gradient in a hot spot of tropical biodiversity (Manu Biosphere Reserve). We used orthogonal polynomial regression to compare elevational rates of change (linear and non-linear) among dimensions and between taxa, and used simulation analyses to evaluate the extent to which gradients in FB or PB arises as a consequence of variation in species richness. For bats, elevational variation in TB was strong ($R_{TB}^2 = 0.98$), with significant linear and non-linear components, whereas elevational variation in FB ($R^2 = 0.30$) and PB ($R^2 = 0.02$) was stochastic. For rodents, elevational gradients of all dimensions were strong ($R_{TB}^2 = 0.91$; $R_{FB}^2 = 0.82$; $R_{PB}^2 = 0.91$), with significant linear and non-linear components. For both taxa, linear and nonlinear components of elevational rates of change in FB were no different than expected, given empirical patterns of species richness. In contrast, elevational rates of change in PB differed in taxon-specific ways from those expected given patterns in species richness. Strong phylogenetic signals are reflected in elevational gradients of bat and rodent biodiversity.

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Comparing Species-specific Tuning Versus AICc to Select Optimally Complex Ecological Niche Models

We compare 2 strategies for identifying optimal model complexity for ecological niche models (ENMs): species-specific tuning versus information criteria (AICc). ENMs are widely used, yet selecting optimal model complexity remains an outstanding issue. One strategy uses omission rates and AUC/ROC, calculated on withheld test data. Another uses AICc, which selects models that predict training data most accurately without being overly complex. Here, we compare the strategies using occurrence records that were spatially filtered to reduce the effects of sampling bias. We do so for a species with few records, the Malagasy tenrec (*Oryzorictes hova*), using 19 bioclimatic layers and MaxEnt. We vary model complexity, employing different combinations of feature classes and regularization-multiplier values. First, for species-specific tuning, we implement a jackknife approach on occurrence data, calculating the average AUCs and omission rates of the withheld (test) records for each feature-class/regularization-multiplier combination. Second, for the same combinations, we calculate AICs using ENMtools using all occurrence records for model training. Species-specific tuning indicated the optimal settings to be Linear + Quadratic with a regularization multiplier of 2.5. Similarly, AICc led to Linear + Quadratic and a regularization multiplier of 2.0 as optimal. Additional research is needed to determine the generality of the current conclusions for similar datasets, as well as for those with larger sample sizes and/or affected by stronger sampling bias.

107 Technical Session 7: Systematics and Biogeography: New World Mammals, Salon A, Monday 17 June 2013

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Quaternary Bat Diversity in the Dominican Republic

The fossil record of bats is extensive in the Caribbean but few fossils have previously been reported from the Dominican Republic. In this paper, we describe new collections of fossil bats from two flooded caves in the Dominican Republic and summarize previous finds from the Island of Hispaniola. The new collections were evaluated in the context of extant and fossil faunas of the Greater Antilles to provide information on the evolution of the bat community of Hispaniola. Eleven species were identified within the new collections, including 5 mormoopids (*Mormoops blainvillii*, †*Mormoops magna*, *Pteronotus macleayii*, *P. parnellii*, and *P. quadridens*), 5 phyllostomids (*Brachyphylla nana*, *Monophyllus redmani*, *Phyllonycteris poeyi*, *Erophylla bombifrons*, and *Phyllops falcatus*), and 1 natalid (*Chilonatus micropus*). All of these species today inhabit Hispaniola with the exception of †*Mormoops magna*, an extinct species previously known from only from the Quaternary of Cuba, and *Pteronotus macleayii*, which is currently known only from extant populations in Cuba and Jamaica although Quaternary fossils have also been recovered in the Bahamas. Differences between the fossil faunas and those known from the island today suggest that dispersal and extirpation events, perhaps linked to climate change or stochastic events such as hurricanes, may have played roles in structuring the modern fauna of Hispaniola.

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Diversification of the Yellow-shouldered Bats, Genus *Sturnira* (Chiroptera, Phyllostomidae), in the New World Tropics

Yellow-shouldered bats, genus *Sturnira*, are widespread, diverse, and abundant in the Neotropics, but little is known of their phylogeny and biogeography. We collected 4,409 bp of DNA from 3 mitochondrial (cytochrome *b*, ND2, D-loop) and 2 nuclear (RAG1, RAG2) sequences from 138 individuals representing all but 2 recognized species of *Sturnira* and 5 other phyllostomid bats used as outgroups. Sequence data were subjected to maximum parsimony, maximum likelihood, and Bayesian inference analyses. Results overwhelmingly support the monophyly of the genus *Sturnira* but not continued recognition of *Corvira* as a subgenus. A total of 21 monophyletic putatively species-level groups were recovered; pairs were separated by an average 7.09% ($SD = 1.61$) pairwise genetic distance in cytochrome *b*, and 3 of these groups are apparently unnamed. Several well-supported clades are evident, including a complex of 7 species formerly confused with *S. liliium*, which is restricted to Brazilian Shield biomes. *Sturnira*

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apparently appeared in the mid-Miocene, and 3 basal lineages were present by the end of that epoch (5.3 Ma); most living species date to the Pliocene. Both parsimony (DIVA) and likelihood (Lagrange) methods for reconstructing ancestral ranges indicate that *Sturnira* began radiating in the Andes and only later did it colonize Central America and the Antilles. *Sturnira* species that are endemic to Central America arose after the final emergence of the Panamanian land bridge ~3 Ma.

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BAT-Scan: Phylogenomics of *Myotis* Using Retrotransposon Capture

Phylogenomics can be technically challenging and costly which has negatively impacted the utilization of novel, high-throughput sequencing methods for inferring phylogenies in nonmodel taxa. To address this problem, we have extended a retrotransposon based capture and sequence method to generate a large scale phylogenomic data set of New World *Myotis*. Short INterspersed Elements (SINEs) are 100-500 bp retrotransposons often reaching copy numbers of thousands to millions in a single genome. As SINEs mobilize, older SINEs accumulate in the genome while new insertions are also acquired. As lineages diverge, SINEs present prior to the divergence will be shared among taxa, while new, lineage-specific SINE insertions will be found at unique loci. Using our method, we have identified SINE insertion patterns in New World *Myotis* and generated a retrotransposon-based matrix in addition to megabases of DNA sequence data for phylogenomic analyses. Preliminary results from > 207 million reads corresponding to 20.7 gigabases of data have been obtained. Over 92% of reads map to the *M. lucifugus* genome draft and form the foundation of a phylogenomic dataset that will eventually encompass 28–40 taxa. In applying this method, we hope to demonstrate a phylogenomic technique that can be applied using resources available to researchers studying a broad array of nonmodel taxa.

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Phylogeography of the Hoary Bats (*Lasiurus*): Molecular Evidence for Species Diversity and Multiple Invasions of the Hawaiian Islands

Molecular phylogenetic analyses of DNA sequences were performed to examine the relationships of 3 taxa of hoary bats. Estimated divergence times are indicative of species-level divergence of the group, and we recognize the following taxa: North America hoary bat *Lasiurus cinereus*, South American hoary bat *L. villosissimus*, and the Hawaiian hoary bat *L. semotus*. Phylogenetic analysis shows the relationships among these 3 taxa to be ((*cinereus*, *semotus*) *villosissimus*). Phylogeographic evidence indicates there are 2 deeply divergent clades in the Hawaiian Islands. This indicates at least 2 invasions of hoary bats to the Hawaiian Islands, both originating from North America. The current taxonomic status of Hawaiian hoary bats is in question. Both lineages occur on the Island of Maui, but the other lineage is as yet known only from the Island of Hawaii. Whether or not the 2 forms are reproductively isolated is as yet untested.

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Multilocus Phylogeography and Phylogenetics of *Thylamys* Mouse Opossums: The Impact of Pleistocene Glacial Cycles on Andean Taxa

Global climate fluctuations during the Pleistocene may have promoted the diversification of montane species. During cool, dry periods, species that currently inhabit montane areas likely had a broader distribution at lower elevations.

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When climates warmed, previously contiguous populations may have been split among isolated highland regions. We tested predictions about how climate fluctuations are expected to affect the geographic distributions and phylogeographic structure of Andean *Thylamys* species. We predict that present-day sister lineages diverged during warm periods of the Pleistocene. As climates warmed after the Last Glacial Maximum, we expect effective population sizes of montane species to decline and gene flow between sister lineages to decrease. To assess the timing of lineage splitting, we inferred a fossil-calibrated ultrametric tree based on 15 nuclear loci and 3 mitochondrial loci. We densely sampled the same loci within montane lineages to assess effective population size fluctuations and gene flow. Results indicate that several intraspecific haplogroups arose during the Pleistocene, but assessments of gene flow and population size shifts do not support our predictions. Population expansions of one particular *Thylamys* lineage (the widespread *Thylamys pallidior* B haplogroup) are likely due to the expansion of “montane-like” cool and dry habitats in Patagonia after the Last Glacial Maximum. This research was supported by an ASM Grants-In-Aid of Research awarded to Thomas Giarla in 2008.

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Phylogeny and Evolution of Body Size in Caviidae (Rodentia, Hystricognathi, Cavoidea): Approach of a Combined Analysis with Morphology and Molecular Data

Caviidae forms part of the highly diverse South American hystricognath rodents and includes 3 major living lineages: Caviinae (cavies), Dolichotinae (maras), and Hydrochoerinae (capybaras and rock cavies). Caviids have the broadest range of body sizes among extant rodents, but so far the evolution of body size has never been properly analyzed in this group. In this contribution, we include new sequences of 4 genes (Coll, 16S, Rag-1, Vwf) for extant caviids and integrate them with published sequences of 4 other genes (cyt b, 12S, Tth, Ghr) as well as a recently published morphological dataset scored for extant and extinct taxa (including the extinct “eocardiids,” which form the successive sister groups of Caviidae). The resultant topologies are used to infer the evolution of body size in this group through the optimization of body mass estimates. The analysis reveals static body size across “eocardiids” and a much more dynamic history of body size changes within the crown group Caviidae. Hydrochoerines and dolichotines both increased in size but through 2 independent and temporally separated transitions. In turn, caviines reduced their body size during the middle-late Miocene, as major environmental changes were altering the South American biomes. This research was supported by an Oliver P. Pearson Award awarded to Maria Encarnacion Perez in 2012.

113 Technical Session 7: Systematics and Biogeography: New World Mammals, Salon A, Monday 17 June 2013

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A Preliminary Test of the Traditional Taxonomy of New World Deer (Cervidae: Rangiferini) and its Implications for Conservation

Deer in North, Central, and South America form the monophyletic tribe Rangiferini, whose taxonomy, evolution, and biogeography to date are poorly understood. Herein, we report 1st steps to improve this situation, testing the monophyly of most genera and species traditionally recognized for the tribe Rangiferini. We conducted phylogenetic analyses of cytochrome-*b* gene sequences using more extensive geographic and taxonomic sampling than previous studies. Our ingroup comprised the genera *Blastocerus*, *Hippocamelus*, *Odocoileus*, *Ozotoceros*, *Pudu*, *Rangifer*, and members of clades traditionally referred to *Mazama*; members of the remaining telemetacarpalian genera were designated as outgroups. Consistent with previous studies, our results support the monophyly of *Blastocerus*, *Ozotoceros*, and various lineages traditionally referred to as “*Mazama*,” and provide further evidence for the polyphyly of *Mazama* and the parphyly of *M. americana*. Novelty in our results include support for the monophyly of *Pudu pudu* and the genera *Hippocamelus* and *Rangifer*. Our results are equivocal with regard to the monophyly of *Odocoileus*, and neither *O. hemionus* nor *O. virginianus* were recovered as monophyletic. We discuss implications of these findings for conservation, providing examples of how uncritical taxonomic lumping of species has probably hidden several valid taxa from protection.

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114 Technical Session 8: Disturbance Ecology, Salon B, Monday 17 June 2013

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Large Mammal Diversity, Abundance, and Activity Patterns at Jean Lafitte National Park, Louisiana: Pre- and Post-Katrina

Established in 1978, the Barataria Preserve of Jean Lafitte National Park has been used and modified by people of the region for nearly 2,000 years and is currently undergoing major urban and environmental impacts. We conducted the 1st mammal inventory of the park in 2003-2005, with field studies terminating just prior to Hurricane Katrina. Bat monitoring, live trapping small and medium-sized mammals, and motion-triggered cameras documented occurrence and habitat distribution of 24 species. Field work for a re-assessment of mammal diversity and habitat use was just completed (2012), and results for large mammals are reported here. Sampling localities for the re-assessment included the sites studied in the pre-Katrina survey but added many other sites, especially in swamp habitats. Large mammals are very abundant in all habitats, with significant increase in the abundance of deer and carnivores (coyote, bobcats), post-Katrina. Feral hogs were not present pre-Katrina but have now established a large breeding population that is expanding into all major habitats within the park. These results speak to the resilience of mammals in an area impacted by major hurricanes but also to the opportunities presented for introduction of invasive species (feral hogs) that are now reshaping the functional ecology of the park.

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Bat Response to Differing Fire Severity in Mixed-conifer Forest California, USA

Wildlife response to natural disturbances such as fire is of conservation concern to managers, policy makers, and scientists, yet information is scant beyond a few well-studied groups (e.g., birds, small mammals). We examined the effects of wildfire severity on bats, a taxon of high conservation concern, at both the stand (< 1 ha) and landscape scale in response to the 2002 McNally fire in the Sierra Nevada region of California, United States. One year after fire, we conducted surveys of echolocation activity at 14 survey locations, stratified in riparian and upland habitat, in mixed-conifer forest habitats spanning 3 levels of burn severity: unburned, moderate, and high. Bat activity in burned areas was either equivalent or higher than in unburned stands for all 6 phonic groups measured, with 4 groups having significantly greater activity in at least 1 burn severity level. Extent of high-severity fire damage in the landscape had no effect on activity of bats in unburned sites suggesting no landscape effect of fire on foraging site selection and emphasizing stand-scale conditions driving bat activity. Results from this fire in mixed-conifer forests of California suggest that bats are resilient to landscape-scale fire and that some species are preferentially selecting burned areas for foraging, perhaps facilitated by reduced clutter and increased post-fire availability of prey and roosts.

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The Role of Life History Traits in Post-fire Recovery of Small Mammals in the Chaparral Shrublands of Southern California, USA

Chaparral shrublands in southern California exhibit significant biodiversity but are prone to large wildfires. Under 3 climate-change scenarios, total area of California burned annually is expected to increase 9–15% above the historical norm by the end of the century. As fire frequency increases, understanding species' responses to fire is essential for making informed management decisions. Fires in 2002 and 2003 burned ~25% of vegetated area in San Diego County and for 6 years following, the San Diego Natural History Museum coordinated multiple studies examining effects of the fires on small mammals. We synthesized the data and used a mark-recapture framework to test how life history traits affected post-fire recovery, while accounting for spatial variation by site and temporal variation in rainfall and vegetation recovery. Whereas fire severity and distance from unburned perimeter had little effect on small mammal recovery, rainfall and vegetation characteristics interacted with life history traits, such as nest location (above or below ground) and diet breadth, to create species-specific patterns in recovery. Results suggest management of the mammalian community should focus on maintaining a diverse assemblage of chaparral plants to

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provide for varied life history traits and needs. Doing so may require novel management strategies given increasing development, ignition sources, and invasive species in southern California.

117 (E) Technical Session 8: Disturbance Ecology, Salon B, Monday 17 June 2013

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Environmental Change and Habitat Occupancy of Semiaquatic Mammals: Insights from the Midwest Drought of 2012

Climate change effects, such as increased droughts and increased frequency and intensity of seasonal precipitation, are predicted to negatively influence wildlife populations. Habitat specialists occurring in landscapes dominated by human land use may be more susceptible to climate change because dispersal to suitable habitat or temporary refugia may be unlikely. Using 6 years of presence-absence data (2007–2012) spanning years of record-breaking drought and flood conditions, we evaluated the habitat occupancy dynamics of American mink (*Neovison vison*) and muskrat (*Ondatra zibethicus*) occurring in a highly altered ecosystem. In this region, > 90% of historic wetlands have been drained, thus limiting both species' distributions to flashy streams and agricultural ditches. Habitat occupancy by mink (0.92) and muskrat (0.69) were high during a year of above-average precipitation (2008). However, occupancy declined substantially for both mink (0.55) and especially muskrat (0.08) after the severe drought of 2012. Mink are generalist predators and may switch use to upland habitat during periods of low precipitation. However, muskrats have limited mobility in terrestrial areas and may have suffered high mortality during the drought. Of the 5 sites occupied by muskrats in 2012, 4 were located in urban watersheds. Urban streams may serve as temporary refugia for muskrats during drought because of higher base flows. Semiaquatic mammals could be particularly sensitive to increases in summer droughts and winter-spring flooding expected under predicted climate change scenarios.

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Small Mammal Community Responses to a Severe Drought in Tallgrass Prairie Managed with Fire and Grazing

Three main drivers maintain tallgrass prairie in North America: fire, grazing, and a highly variable continental climate. General circulation climate models predict that extreme climate patterns, such as floods and droughts will become more common in the Great Plains due to climate change. Knowledge of population and community level responses of organisms to extreme weather events is crucial to understanding the effects of global change on ecosystems. Climatic variability has been shown to affect survival, recruitment, and abundance of small mammals in the tallgrass and mixed-grass prairies of the central Great Plains. We studied small mammal responses to an alternative rangeland management strategy that produces conditions thought to mimic those that were present in the prairies of North America prior to European settlement. During our 2-year study at Konza Prairie Biological Station, the site experienced 1 year with average precipitation and 1 severe drought year. We detected community-level shifts in small mammal abundance in the drought year. Moreover, population-level responses of deer mice (*Peromyscus maniculatus*) to drought were inconsistent with results of previous studies of climate effects on this species. Our results have important implications for other trophic levels because small mammals play an important ecological role as seed predators and prey for raptors and carnivores.

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Small Mammal Community Structure at a Dried Wetland Site

Cheyenne Bottoms is an internationally recognized wetland in Kansas, United States. Known for its importance to avian fauna, little is known about its small mammal community. Live trapping of small mammals with Sherman live traps, vegetation analysis, and soil sampling were conducted monthly (May through August 2012) to determine the effects of drought on small mammals at wetland and nearby grassland sites. Species richness differed by only 1 between sites, with 6 species being recorded in the wetlands and 5 in the grasslands. However, species' abundances were significantly higher in the wetlands than the grasslands. The relative abundance of species differed between sites, but the most frequently captured individuals were *Peromyscus maniculatus*, *Sigmodon hispidus*, *Mus musculus*, and *Reithrodontomys megalotis*. Two other species, *Cryptotis parva* and *Microtus ochrogaster*, were captured in low numbers. Soil conductivity was significantly higher at wetland sites than grassland sites; however, soil moisture showed no difference between the sites. Vegetation data will be analyzed and compared to the soil and small

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mammal data to determine the effects of the drought on these environmental variables and their effects on small mammal abundance and species richness.

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Changes in Small Mammal Populations Following Capping of Artesian Wells in Great Sand Dunes National Park and Preserve

We studied short-term influences of capping artesian wells on small mammals in Great Sand Dunes National Park and Preserve, Colorado. From 2011–2012, we live trapped small mammals and measured disturbance at 6 sites: 2 wells capped in 2010 (C), 2 flowing wells (F), and 2 reference areas (R). Most wells were established between 1920–1940 for cattle; since the removal of cattle starting in the 1980s, disturbance by ungulates, primarily elk (*Cervus elaphus*) and/or bison (*Bison bison*), is the major influence. We characterized disturbance using percent bare ground, downed vegetation, and ungulate tracks. For small mammals, we estimated density (program DISTANCE), survival (program MARK), and species richness. Over the study, we captured 1,150 individuals of 7 species, but only *Dipodomys ordii* and *Perognathus* had sufficient captures for density and survival analyses. *D. ordii* was the most abundant species and its density followed a pattern of C > R > F, while for *Perognathus* R > C > F. Survival was consistently greater for *Perognathus* and the survival pattern for both was R > C > F. Species richness was greatest at references and capped wells with some species never captured at flowing wells. Despite the 80-year presence of artesian wells, our results suggest that these sites can quickly recover and approach a more natural state for small mammal communities.

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The Effect of Resource Development on Arctic Fox Survival on the Arctic Coastal Plain of Alaska

Mesocarnivores adapted to life near humans often increase their fitness by supplementing their needs, for example food and shelter, by using anthropogenic resources. In Prudhoe Bay, the largest oil field on the Alaskan Arctic Coastal Plain, arctic foxes (*Vulpes lagopus*) forage on anthropogenic foods at garbage accumulation sites. It is not known whether this confers a benefit to arctic fox survival when compared to foxes living in undeveloped sites. The primary objective of this study was to determine whether arctic fox survival was higher in a developed area, Prudhoe Bay (PB), than an undeveloped area, the National Petroleum Reserve-Alaska (NPR-A). Arctic foxes were captured and fitted with satellite collars in PB and NPR-A in 2004, 2005, and 2009. We used data from satellite collars to analyze the effects of development (PB versus NPR-A), sex, season, distance traveled, and sea ice use on adult and juvenile arctic fox survival. Both development and sea ice use had 2 times more support than any other factor. The relatively small difference in arctic fox survival between PB and NPR-A suggests that either access to anthropogenic foods has only a small survival benefit or there is a trade-off between positive effects, such as supplemental food, and negative effects of development, for example competition with a recently increased red fox (*Vulpes vulpes*) population or increased vehicular traffic.

122 (E,**, ST) Technical Session 9: Physiology and Community Ecology, Salon C, Monday 17 June 2013

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Genetic Differences in Hemoglobin Function Between High and Low Altitude Pika Species

There are good theoretical and empirical reasons to expect that high-altitude animals have an elevated blood-O₂ affinity relative to closely related lowland taxa. Under severe hypoxia, an increase in blood-O₂ affinity can preserve an adequate level of tissue oxygenation by enhancing pulmonary O₂ uptake while simultaneously maintaining the pressure gradient that drives O₂ diffusion from the peripheral capillaries to the cells of respiring tissues. Adjustments in blood-O₂ affinity often stems from structural changes in hemoglobin (Hb) brought about by amino acid mutations that increase the intrinsic O₂-affinity of the tetramer and/or mutations that suppress the sensitivity of Hb to the inhibitory effects of allosteric cofactors in the red blood cell, such as 2,3-diphosphoglycerate (DPG) in mammals. We tested for differences in Hb-O₂ affinity between 2 closely related pika species that have contrasting altitudinal distributions, *Ochotona princeps* from the Rocky Mountains in Colorado (4,300 m) and *O. collaris* from Alaska (~1,040 m). We measured O₂-binding properties of purified Hbs from both species, and found that *O. princeps* has a higher Hb-O₂ affinity than *O. collaris*. We sequenced the genes that encode the alpha- and beta-chain subunits of Hb

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to identify the amino acid substitution(s) responsible for the observed functional differences. A few candidate residues ($\alpha 78$, $\beta 5$, $\beta 58$, $\beta 62$, $\beta 123$, $\beta 126$) may be responsible for the increase in O_2 affinity of high altitude *O. princeps*. This research was supported by an ASM Grants-In-Aid of Research awarded to Danielle M. Tufts in 2012.

123 Technical Session 9: Physiology and Community Ecology, Salon C, Monday 17 June 2013

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Aquatic Sound Reception in Cetaceans

Cetaceans possess highly derived auditory systems because a conventional pinna and air-filled ear canal are ineffective at collecting and guiding sound towards the middle ears in an aquatic environment. Odontocetes, or toothed whales, receive sound through specialized “acoustic fats” associated with the mandibles and ears. Although sound reception mechanisms of mysticetes (baleen whales) are unknown, we found that some mysticete species also have large, discrete fat bodies associated with their auditory bullae. In this study, we investigated the biochemical composition of this fat and used Finite Element Modeling to determine sound propagation through the whale head. Our results indicate that the mysticete fats are composed of different lipids than the odontocete acoustic fats but share some characteristics, including having fewer dietary signatures than blubber and being conserved under starvation. Finite Element models indicate that the lower sound speeds and densities of these fats provide a slight increase in peribullar sound pressures compared to other local soft tissues. Consequently, we propose that both odontocete and mysticete cetaceans have incorporated fatty tissues into their auditory systems for aquatic sound reception.

124 (E,**) Technical Session 9: Physiology and Community Ecology, Salon C, Monday 17 June 2013

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Seasonal Variation in the Degu (*Octodon degus*) Endocrine Stress Response

Many wild mammals show seasonal variation in circulating levels of stress hormones. Seasonal changes in the stress response may help animals better cope with the different challenges faced during each life history stage. We determined the seasonal stress profile of wild, free-living degus in Chile. Female degus were sampled during non-breeding (January), mating (June), late pregnancy (August), and lactation (1st litter-September, 2nd litter-January). Male degus were sampled during the first 3 time-points. We measured baseline cortisol (CORT), stress-induced CORT, and negative feedback efficacy. Our results show that during mating, male baseline CORT was highest and stress-induced CORT was lowest. Female baseline CORT was highest during late pregnancy and stress-induced CORT was highest during late pregnancy and lactation. Both male and female negative feedback efficacy was strongest during late pregnancy. During all seasonal time-points, females had higher stress-induced CORT compared to males. Females also had higher baseline CORT than males at all time-points except mating. Our data suggest that baseline CORT levels are highest during periods of high energy expenditure, but stress-induced levels of CORT are highest during periods with increased chance of stressor exposure. Consequently, CORT concentrations appear to be regulated in response to different life-history needs. This research was supported by ASM Grants-In-Aid of Research awarded to Carolyn M. Bauer in 2011 and 2012.

125 Technical Session 9: Physiology and Community Ecology, Salon C, Monday 17 June 2013

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Female Sperm Storage: How Can We Distinguish Sperm Storage from Simple Sperm Longevity in Mammals?

The terms sperm longevity and sperm storage are not synonymous. Longevity primarily operates via selection on the male, and sperm storage by females implies selection on the female. It is important to take time to distinguish between the 2 phenomena. What does it mean to store sperm? The answer has clear implications for mating system evolution and sexual conflict, but the criteria for defining female sperm storage are unclear. This is particularly true of mammals that generally lack specialized storage structures. We discuss ways to refine thinking about sperm storage, outline gaps in our knowledge, and nuances of accurately determining if a species stores sperm or has long-lived sperm. Focusing on mammals we synthesize information on reproductive physiology, evolutionary ecology, and

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behavior to explore the question; what is sperm storage and how does it differ from sperm longevity? We review the taxa for which data suggest female sperm storage despite an absence of specialized structures.

126 (E) Technical Session 9: Physiology and Community Ecology, Salon C, Monday 17 June 2013

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Using Multi-species Occupancy Modeling to Identify Suitable Habitat for Bats in Indiana with Focus on the Endangered Indiana Bat

The Indiana bat (*Myotis sodalis*) is a federally endangered species under threat from White-nose Syndrome. Thus, the identification of areas critical for Indiana bat summer habitat is needed. To characterize these areas, we collected acoustic recordings of bat echolocation calls from state forests in Indiana. Echolocation calls were identified using automated call classification software and detection histories for each species at each site were constructed. Data were analyzed using a hierarchical multi-species occupancy approach that estimates occurrence and detection probability for all species. Because the differentiation of bat species through automated techniques is controversial (particularly for *Myotis*), we took a 2-step approach. First, we used multi-species occupancy modeling for all bats recorded but *Myotis* species were combined into a single group. Models were constructed using a suite of habitat covariates (e.g., proportion of area forested within 1 km), and the effect of these features on the occupancy of each species (or group) was determined. Second, we used the same occupancy modeling approach with *Myotis* echolocation calls distinguished to the species level. Both models were validated with independent data from concurrent mobile acoustic surveys. Our 2-tiered method allowed us to independently assess factors that affect occupancy for the genus and for individual species, thus allowing for the identification of features that could be used to classify critical habitat at both taxonomic scales.

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Testing Efficacy of Hairtube Sampling at Detecting Presence of Small Mammals

Small mammals play crucial roles in ecosystem function (e.g., pollination, seed dispersal, prey source, and insect control) yet are suffering increased rates of extinction due to their intimate relationship with microhabitats. Small mammal species are also thought to be significantly impacted by climate change, anthropogenic activity, and other environmental perturbations. Therefore accurate and reliable sampling techniques are paramount; however, small mammals can present challenges to sampling due to their small size, inconspicuousness, and cryptic behavior. We investigated hairtube sampling as a viable method for detecting small mammal presence and biodiversity. Hair is collected on sticky tape as an animal passes through a baited plastic tube, and collected hair is viewed under a microscope, where distinctive features (i.e., medulla, scale, and cross section) permit identification of species. We deployed hairtubes over 2 study sites of high montane forests on Mount Graham within the Pinaleno Mountains of southeastern Arizona. We collected over 1,800 samples and identified 10 different species. Hairtubes show not only a high probability of species detection but demonstrate ability to detect multiple species as well. Hairtubes may prove an attractive tool for researchers due to the noninvasive nature, ability to extend sampling periods and areas, potential to sample multiple species, and cost effectiveness

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Using Camera Trap Surveys to Address Terrestrial Mammal Biodiversity and Conservation in Sumaco National Park, Ecuador

It is crucial to have a worldwide, fine, and clear understanding of species richness, density, and distribution in order to create appropriate conservation management plans. Unfortunately, “Wallacean” and “Linnean” shortfalls point to numerous gaps in our knowledge of those variables, thus slowing down our attempt at reversing the current trend of global biodiversity loss. Ecuador’s Sumaco National Park (SNP), ranging from 1,600 m to 3,800 m in elevation, is an unstudied International Biosphere Reserve located in the heart of the Tropical Andes hotspot, one of the most biodiverse regions of the planet. Using camera traps, a noninvasive sampling method, we investigated the species richness and distribution of medium to large nonarboreal mammals, as well as the density of those listed as species of conservation concern (classified as threatened, vulnerable, endangered, or critically endangered) by IUCN for SNP’s lower montane and montane cloud forest (1,600 m–2,300 m). The sampled ecosystem was divided into 4 transects, each sampled by 10 cameras placed at least 350 m apart for 4 months. We captured species significantly

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higher than their known elevational ranges and described different community assemblage across the ecosystem, which had previously never been documented. This study, being the 1st one of its kind, provides information necessary to form a plan for mammalian conservation in SNP's cloud forest and a baseline for Ecuador's Tropical Andean cloud forests.

129 (ECT) Technical Session 10: Conservation Genetics: Carnivores, Salon E, Monday 17 June 2013

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Are Corridors Important for Tigers?

Understanding the patterns and processes of an endangered species metapopulation occupying a fragmented habitat is crucial for devising effective conservation strategies. Corridors facilitate dispersal and gene flow and thus are vital for metapopulation persistence. Multiallelic genotypic information from 273 individually identified tigers (*Panthera tigris*) was used in Bayesian and coalescent-based analyses to answer questions about spatial genetic structure and gene flow in the tiger metapopulation of the Satpura-Maikal landscape. We found that the tiger metapopulation in central India has high rates of historical and contemporary gene flow. Population subdivision began about 1,000 years ago and accelerated about 200 years ago due to habitat fragmentation, leading to 4 spatially separated populations that have been in immigration-drift equilibrium maintained by high gene flow. We also found the highest rates of contemporary gene flow in populations that are connected by forest corridors.

130 (E, ST) Technical Session 10: Conservation Genetics: Carnivores, Salon E, Monday 17 June 2013

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Distribution and Population Connectivity of San Joaquin Kit Foxes in the Panoche Valley, California: The Power of Non-Invasive Surveys

The endangered San Joaquin kit fox (SJKF) is adapted to arid landscapes and strongly linked ecologically to kangaroo rats and environmental conditions. Despite steady habitat loss, the elusive nature of SJKF has limited surveys to being site specific or broadly descriptive of range-wide trends. Thus, its status is unknown in the northern and central parts of California's Central Valley. Because the Ciervo-Panoche area contains the largest, high-quality habitat for SJKF in their northern range, we conducted systematic transect surveys for SJKF scats with detection dog/handler teams throughout the area during 2009-2011. We collected almost 600 scats and documented the age and location of each. Using molecular methods, we identified 93 SJKF individuals (56 males and 37 females) from 332 samples. Half of the individuals carried a previously unknown mitochondrial haplotype with a 16 bp deletion. We recaptured 4 individuals in 2010 and 5 in 2011, including 1 female found every year. Despite short distances between individuals, our analyses revealed 2 subpopulations with low connectivity separated by the low eastern ridgeline of the Panoche Valley (PV). We documented more individuals across a wider area of the PV than expected as well as unique genetic diversity and signatures of structuring. These results illustrate the importance of thorough non-invasive surveys to inform management of current distributions and important pieces of land to connect populations of endangered species.

131 Technical Session 10: Conservation Genetics: Carnivores, Salon E, Monday 17 June 2013

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Recovery of Wolverines in the Western United States: Recent Extirpation and Re-colonization or Range Retraction and Expansion?

Wolverines (*Gulo gulo*) were greatly reduced in number and possibly extirpated from the contiguous US in the early 1900s. Since that time, wolverines have re-occupied much of their historical range in the western contiguous United States but remain absent from California, Utah, and Colorado. Whether this recovery represents recent range expansions by relictual populations in the contiguous United States or the recolonization of this region from Canadian populations is unknown. To investigate these hypotheses, we amplified the mitochondrial control region of 13 museum specimens, dating from the late 1800s to early 1900s, and 202 wolverines from modern populations in the contiguous United States and Canada, and we combined resulting data with previously published haplotypes. Two haplotypes (Cali1 and Cali2) that were present in the contiguous United States historically do not occur anywhere else in North America and likely evolved in isolation in the southern ice-free refugium that encompassed most of the contiguous United States during the last glaciation. Collectively, our data indicate that historical wolverine populations in the contiguous United States were extirpated in the 20th century and that extant populations in Washington, Idaho, Montana, and Wyoming were established by subsequent range expansions southward by Canadian populations. For the reintroduction of wolverines to California, Colorado, and other areas in the western United States, potential source populations in the Canadian Rocky Mountains may provide the best mix of genetic diversity and appropriate learned behavior.

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Estimating the Extent of Interspecific Hybridization Across the Range of the Endangered Red Wolf (*Canis rufus*)

Restricting interspecific hybridization in wild populations has been a challenge for the conservation of numerous rare mammal species. Such issues have been a serious threat to the preservation of the critically endangered red wolf (*Canis rufus*) in eastern North Carolina, USA. A management plan focused on restricting hybridization with nonnative coyotes (*C. latrans*) has been in place since 2000. We conducted a noninvasive genetic survey (NGS) of scat across a 2,880 km² region adjacent to the Red Wolf Experimental Population Area (RWEPA) to evaluate the success of the program in limiting hybridization. Using nuclear microsatellite loci obtained from scat DNA, we estimated individual ancestry using Bayesian clustering methods. We detected 87 individuals from this survey, most of which were coyotes. When combined with samples from scat surveys conducted both within RWEPA, we genotyped a total of 392 individuals. Red wolf ancestry decreased along an east-west gradient across the RWEPA. No red wolves were found outside the RWEPA, yet one-half of individuals found within the RWEPA were coyotes. Hybrids composed only 4% of individuals within this landscape and the distribution of genotypes showed a bimodal distribution dominated by the 2 parental species. These results suggest that there is no well-defined contact zone between these species. The rarity of hybrids suggests that some isolating mechanisms are operating to limit hybridization between these species.

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Genetic Population Structure of Neotropical Cougars (*Puma concolor*)

Cougars (*Puma concolor*) were extirpated from much of their native range and are considered “near threatened” in Argentina, Brazil, Colombia, and Peru by the IUCN. Most cougars reside in the Neotropics; however, little is known about these populations as most studies focus on North American populations. Detailed information regarding cougar populations is difficult to obtain via traditional methods (e.g., camera trapping, blood sampling) due to their elusive behavior and the cost of such techniques. This study used DNA extracted from noninvasively collected scat samples to examine the genetic diversity of Neotropical cougars. Diversity amongst 4 mitochondrial gene regions (16S rRNA, 12S rRNA, ATP-synthase 6, and cytochrome *b*) revealed 16 unique haplotypes and broad population structuring. Additionally, overall mitochondrial nucleotide diversity was low, indicating a potential loss of genetic diversity. Amplification of 21 puma-specific microsatellite loci identified 223 individuals (85 males, 108 females, 30 unknown

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sex) and found evidence of fine-scale population structuring, with isolated clusters present in Argentina and Costa Rica. Landscape genetic analysis of the South American individuals revealed agricultural fields as a potentially important driver of fine-scale population structuring resulting in genetic isolation. This research is the 1st project examining the population genetic structure of cougars across their Neotropic range and will help prioritize cougar management plans.

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Variability and Population Genetic Structure of the White-nosed Coati (*Nasua narica*) in Mexico

Genetic variability is an important evolutionary trait for the survival of individuals allowing individuals to adapt to environmental changes. It is estimated that wild populations have high genetic variability; there are exceptions such as rare, threatened, or endangered species. Throughout its distribution populations of white-nosed coati (*Nasua narica*) have declined or even disappeared. It is estimated that Mexican populations of white-nosed coati have gradually become genetically isolated, which can potentially lead to their local extinction. We analyzed 5 populations of white-nosed coati from México using 12 specific microsatellites (individuals sampled = 62). The results showed medium to high levels of heterozygosity ($H_E = 0.682$, $H_O = 0.784$). Most of the microsatellites are in Hardy-Weinberg equilibrium. All loci were polymorphic in all populations, and average alleles per locus was 5.033 ± 1.794 (SD). Regarding Wright's F statistics, we found conservative values except for the inbreeding coefficient, which was low, probably reflecting that this parameter does not significantly affect the population ($F_{IT} = 0.310$, $F_{ST} = 0.203$, and $F_{IS} = 0.134$). We found marked differences in the presence of alleles in populations of the Pacific coast compared to the population of Central Mexico as well as the population of the Yucatán Peninsula, resulting in significant genetic structure and indicating the presence of 5 subpopulations.

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Genetic Connectivity in Sloth Bear (*Melursus ursinus*) metapopulation in the Central Indian Highlands

Sloth bears (*Melursus ursinus*) are an evolutionary distinct bear species that is endemic to the Indian subcontinent. They are listed as vulnerable in the IUCN red-list and are also protected under Schedule I of the Indian Wildlife Protection Act, 1972. As a result of continued habitat loss and degradation, declining sloth bear populations now exist in isolated or fragmented habitat. We investigated the genetic connectivity of the sloth bear metapopulation in the Satpura-Maikal landscape of central India. We used noninvasively collected samples (fecal and hair) to obtain genotypic information using 8 polymorphic loci from 62 individuals from this metapopulation. We found that the sloth bear metapopulation in the Satpura-Maikal landscape has high genetic variation and high genetic subdivision. We also found that habitat connectivity and corridors has a major role in maintaining gene flow and genetic connectivity in this metapopulation. These corridors are under threat due to various anthropogenic activities, and any change in these corridors will further enhance the genetic subdivision of sloth bear metapopulation of central India.

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Impact of Genetic Drift on Island Populations of Mesocarnivores Established on Cumberland Island, Georgia

Processes such as genetic drift and founder effects are important processes that can govern the success of mammalian reintroduction programs. Understanding the process of drift following a reintroduction effort is important for gauging the population viability of a population. In this study, we examined 2 mesocarnivores on Cumberland Island, Georgia, to quantify the genetic impact of founder effects several decades after population establishment. In the early 1900s, a native mesocarnivore, the bobcat (*Lynx rufus*), was extirpated from the island. Thirty-one bobcats were reintroduced in 1989–1990 to repopulate the island. In the early 1990s, coyotes (*Canis latrans*) populated the

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island by swimming across a water barrier from the mainland. The objective of this study was to compare the genetic composition of both populations to the founder groups to examine how founder effects have impacted their genetic composition. In January 2012, scat samples were collected from the island for genetic analysis. Using microsatellite genotyping techniques to identify individuals, we estimated population sizes and genetic diversity of both species. Both species experienced a decline in genetic diversity compared to founder populations. We were also able to estimate the potential number of true genetic founders for the bobcat population. These results provide insight into how population and genetic processes operate in isolated mesocarnivore populations and assess the long-term success of the bobcat reintroduction program.

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Evaluation of NexGen Sequencing Technology for Mammalian Genomes

Although currently considered the gold standard in some fields (e.g., microbial diversity), the usefulness and cost effectiveness of NexGen sequencing has not been effectively realized in mammalian biology. However, over the last year a number of platforms have become available that allow for cheaper and faster next gen sequencing. One of these, the Ion Proton, was announced as having the potential to sequence a human genome in 1 day for \$1,000 (cost). With this technology, the ability to sequence mammalian genomes comes into the affordability and feasibility realm of many academic labs. Using the Ion Proton, we sequenced the genome of an *Oryzomys couesi*. We will discuss the quality and reliability of the sequence generated, as well as whether sales claims match up to reality. Further, we will provide an overview of the workflow.

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A Tale of Three Squirrels: Comparative Mitochondrial and Nuclear DNA Data Highlight Disparate Phylogeographic and Evolutionary Histories

The genetic structure of contemporary species results from mutation, drift, gene flow, and selection. These processes interact in complex ways against a backdrop of historic change in climate, geology, geographic range, and biotic composition. Differences in effective population size and recombination between the mitochondrial and nuclear genomes should produce different patterns of population structure. We present 3 case studies of sciurid rodents in which a strong geographic break in mitochondrial DNA has been identified. Examination of nuclear microsatellite DNA reveals sharp contrasts among the 3 cases. *Ammospermophilus leucurus* shows a pattern of nuclear homogeneity across the geographic area of the mitochondrial break, indicating ongoing gene flow. *Glaucomys sabrinus* shows a strong phylogeographically congruent break in both nuclear and mitochondrial DNA, suggesting reproductive isolation resulting from a lack of gene flow. A similarly congruent break of both nuclear and mitochondrial DNA between *Tamiasciurus hudsonicus* and *T. douglasii* corresponds with speciation, but in this case, the species are able to hybridize where they have established secondary contact. On Vancouver Island, an isolated population of *T. hudsonicus* bearing typical nuclear DNA for that species shows an essentially complete introgression of mitochondrial DNA from *T. douglasii*, reflecting a signal of ancient hybridization. These comparative studies highlight the significance of environmental history in generating variation in the process of speciation.

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Diversification and Gene Flow in Island and Mainland *Tamiasciurus* spp.: Unraveling the Mystery of Vancouver Island's Squirrels

Insular populations provide an opportunity to study processes and timing of lineage diversification that may lead to speciation. Pleistocene climate fluctuations and associated glacial coverage in temperate latitudes have created incipient divergence in many boreal forest mammals. We use phylogenetic and population genetic analyses with multilocus genetic data on pine squirrels (*Tamiasciurus*) to test several hypotheses for the refugial origin and colonization of squirrels on Vancouver Island, which holds a biogeographically peculiar population. We found that the

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nuclear DNA of island squirrels (*T. hudsonicus*) is most closely related to populations of *T. hudsonicus* from the interior continent and indicates that the island was colonized by interior montane lineages around the Last Glacial Maximum. Surprisingly, the mitochondrial DNA of squirrels on Vancouver Island is most closely related to *T. douglasii*, which is presently distributed along the immediate coastline across from Vancouver Island. Vancouver Island is near the hybrid zone between these 2 squirrel species on the mainland and, therefore, it is possible that the founding *T. hudsonicus* population on Vancouver Island may have carried introgressed mtDNA from *T. douglasii*. Our bioclimatic modeling results suggest that nonclimatic factors must have favored colonization of Vancouver Island by *T. hudsonicus* rather than *T. douglasii*. The patterns of gene flow and isolation that we have observed illustrate a dynamic evolutionary response to climate change and geographic features. This research was supported by an ASM Grants-In-Aid of Research awarded to Andreas S. Chavez in 2011.

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Analysis of Nuclear and Mitochondrial DNA Reveals Cryptic Speciation in North American Flying Squirrels (*Glaucomys*)

Phylogeographic studies of North American boreal forest mammals have frequently demonstrated a marked mitochondrial DNA (mtDNA) discontinuity in the Pacific Northwest. This pattern apparently results from historic vicariant event(s) that divided ancestral populations into coastal and interior lineages, followed by more recent secondary contact. We examined mtDNA sequence variation in 210 northern flying squirrels, *Glaucomys sabrinus*, from across their range, with an emphasis on the Pacific Northwest. This analysis documented a strong phylogeographic break between a highly differentiated coastal clade and an interior clade and also allowed us to identify several locations where the 2 clades come into contact in the Pacific Northwest. To assess levels of nuclear gene flow between these 2 divergent lineages, we examined microsatellite variation at 8 loci in 64 individuals straddling the mtDNA phylogeographic break. This analysis revealed no evidence of recent or ongoing gene flow between the coastal and interior lineages, despite close proximity of samples from the 2 groups. A similar suite of microsatellite loci have previously demonstrated recent gene flow and apparent hybridization in northeastern North America between the same interior lineage of *G. sabrinus* and a sibling species, the southern flying squirrel, *G. volans*. Our new evidence strongly supports the existence of a cryptic species of flying squirrel in the Pacific Northwest, which would add a 3rd species to the genus *Glaucomys*.

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Ancient DNA Supports Southern Survival of Richardson's Collared Lemming (*Dicrostonyx richardsoni*) During the Last Glacial Maximum

Collared lemmings (genus *Dicrostonyx*) are circumpolar Arctic arvicoline rodents associated with tundra. However during the Last Glacial Maximum (LGM), *Dicrostonyx* lived along the southern ice margin of the Laurentide ice sheet in communities comprising both temperate and boreal species. To better understand these communities and fate of these southern individuals, we compare mitochondrial cytochrome *b* sequence data from 3 LGM-age *Dicrostonyx* fossils from south of the Laurentide ice sheet to sequences from modern *Dicrostonyx*, sampled from across their present-day range. We test whether the *Dicrostonyx* populations from LGM-age continental USA became extinct at the Pleistocene-Holocene transition, ~11,000 thousand years ago or, alternatively, if they belong to an extant species whose habitat preferences can be used to infer the paleoclimate along the glacial margin. Our results indicate that LGM-age *Dicrostonyx* from Iowa and South Dakota belong to *D. richardsoni*, which currently lives in a temperate tundra environment west of Hudson Bay, Canada. This suggests a paleoclimate south of the Laurentide ice sheet that contains elements similar to the more temperate shrub tundra characteristic of extant *D. richardsoni* habitat, rather than the very cold, dry tundra of the Northern Arctic. Although more data are required to determine whether or not the LGM southern population is ancestral to extant *D. richardsoni*, it seems most probable that the species survived the LGM in a southern refugium.

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Molecular Analysis of Current Subspecies Classification of the Prairie Vole (*Microtus ochrogaster*)

Historically, taxonomic classifications have been constructed using morphological traits. However, established phylogenies based on morphological data may not resemble those constructed for the same taxa using molecular data. In some cases, the inclusion of molecular data has resulted in a dramatic reclassification of organisms. Thus, as more DNA and protein analyses are being conducted across a broad range of taxa, scientists are beginning to reassess current classifications based only on morphological data. Early work divided the prairie vole (*Microtus ochrogaster*) into 7 subspecies based on morphological characteristics, but subsequent quantitative examination of morphological features measured from 3 subspecies (*M. o. haydenii*, *M. o. ochrogaster*, *M. o. taylori*) showed no consistent differences among them. We tested the hypothesis that the *M. ochrogaster* subspecies delimitation based on molecular data will be congruent with the current subspecies classification based on morphology. Preliminary analyses of microsatellite data from the 6 extant subspecies suggest high gene flow among the populations. A cluster analysis of the data indicates there are fewer genetic groups than the number of putative subspecies. Therefore the subspecific classifications may need to be reevaluated using a more integrative taxonomic approach.

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Genetic Consequences of a Range Expansion in Two Congeneric Rodents (Genus *Dipodomys*)

Phylogeographic signals can inform us about how a species has responded geographically and demographically to environmental history. We explored genetic consequences of a postglacial range expansion in 2 congeneric species with different ecological characteristics: the desert (*Dipodomys deserti*) and Merriam's (*D. merriami*) kangaroo rats. *Dipodomys deserti*, a psammophilic substrate specialist, has a patchier distribution and lower population sizes than *D. merriami*, a substrate generalist. These 2 species currently inhabit the warm Mojave and Sonoran deserts, but their ranges reach northern limits along a low-elevation corridor into the cold Great Basin Desert. Paleontological evidence suggests that both species expanded into the Great Basin only after the Last Glacial Maximum. We first contrasted, for both species, genetic diversity within and among "stable" populations within the Mojave and Sonoran deserts with "expanded" populations within the Great Basin. We recovered a genetic pattern of low diversity within the expanded areas and high diversity within the stable areas for both species, supporting the paleontological hypothesis of recent range expansion. Next, we contrasted the genetic signature associated with range expansion between the ecologically divergent *D. deserti* and *D. merriami*. The psammophilic substrate specialist *D. deserti* experienced more rapid loss of diversity in the direction of the expansion. We therefore suggest that this ecological trait has played a strong role in determining genetic architecture associated with range expansion.

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Distribution and Phylogeography of an Alaskan Endemic: The Alaskan Hare

The Alaskan hare (*Lepus othus*) is one of 2 mammals endemic to the Alaskan Arctic and is one of the least studied mammals in North America, due in part to its limited distribution in the vast roadless tundra of western Alaska. Long-term management of this important subsistence species requires baseline occurrence and demographic data. However, the distribution of *L. othus* is inconsistent among published accounts, particularly with regard to its occurrence north of the Brooks Range, and genetic diversity within the species has not been evaluated. This study aims to exhaustively review and update the distribution of *L. othus*, examine its phylogeographic structure, and test morphological and genetic subspecies limits. We are georeferencing *L. othus* specimens from museums across North America and collecting additional voucher specimens from poorly-sampled regions in western Alaska. We are also examining phylogeographic structure using coalescence-based methods and DNA sequences from the mitochondrial genome as well as hypervariable nuclear markers, which will allow for estimates of genetic variation and population connectivity. To fully represent the known geographic range of the species, we will obtain antique DNA from historic museum specimens. Using principle component and conical variates analyses, we will test morphological

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distinctiveness between purported subspecies. This research will allow for better-informed management decisions in the face of traditional subsistence harvest, environmental change, and industrial development.

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The Effects of Climate Change on Body Size in the Masked Shrew in Alaska Revisited

The effects of climate change on mammal body size have become an active field of inquiry in recent years. Whereas an overall decrease in mean body size (and surface area to volume ratio) within a given population over time is often predicted based on Bergmann's rule, the opposite response may also be expected due to increased resource availability, owing to longer growing seasons and milder winters. Any such effect is expected to be most pronounced in regions undergoing inordinately rapid increases in annual temperature. A recent study found that *cinereus* shrews in Alaska have increased in body size over the second half of the 20th century based on analyses of museum specimens housed in the University of Alaska Museum, supporting the resource availability hypothesis. We repeated this study using the same specimens and statistical methods while accounting for potential sex and age dimorphism and found that there was no significant change in body length but that average body mass actually decreased between 1950 and 2000, as would be expected based on Bergmann's rule. We suggest that the previously reported size increase over time can be attributed to demographic phenomena and that both the resource availability hypothesis and Bergmann's rule can simultaneously influence response to a shifting temperature regime.

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Surrogate Habitats for Urban Mammals: Quantifying Survival and Occupancy in Constructed Wetlands

The main consequences of urbanization include the destruction of terrestrial and wetland habitats, resulting in degraded systems and species loss. To mitigate the effects of urbanization on affected watersheds, land management plans require the construction of stormwater ponds, which temporarily retain polluted runoff from impervious surfaces, allowing contaminants to settle before the water is slowly released into the watershed. With intentions to maintain natural hydrology, temperature, and nutrient inputs, stormwater ponds also attract wildlife. Some stormwater ponds might better support or attract urban wildlife when their hydrology, size, and vegetation are considered. In 30 stormwater ponds, we employed a 2 year capture-mark-recapture and presence-absence study to determine the small mammal and mesopredator community in Baltimore County, Maryland, USA. Overall, we encountered 16 native, 2 domestic, and 1 exotic species. Grass cover inside the stormwater pond negatively affected the capture probability of *Peromyscus*, while vegetation density impacted their survival. Detection probability of mesopredators varied by sampling method (camera trap and track plate) and their occupancy was affected by forest cover in the surrounding landscape. Our results indicated that stormwater ponds are being utilized extensively and that small changes in management could further promote urban mammalian diversity in a fragmented landscape.

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Mammals in a Coffee-dominated Landscape in the Highlands of Central Kenya: Implications for Conservation

Coffee is the world's most valuable tropical cash crop. Arabica coffee in Kenya is grown in the highlands, which contain most of their remaining forest systems. Species composition of the mammal communities of the coffee-dominated portions of the Kenyan highlands is unknown, while these habitats are becoming more isolated and increasingly diminished by threats ranging from encroachment by coffee farming to global climate change. Lack of information on the taxonomy and diversity of these communities has limited our ability to formulate conservation strategies. We surveyed the mammalian fauna from 13–27 June 13 2011 within the coffee-growing region of the Central Highlands of Kenya near Nyeri. From tissue samples, we sequenced mitochondrial DNA from the cytochrome *b* (*cyt b*) and 16S ribosomal RNA genes to determine taxonomic designations. We identified 19, 3, and 3 *cyt b* haplotypes for the sequences that aligned with existing sequences from Rodentia, Soricomorpha, and Carnivora,

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respectively. Most species captured in coffee were those associated with open or lowland habitats. Forest plots showed consistently higher richness compared to coffee and comprised mainly recognized forest species. Forest plots also showed a higher species diversity and included 3 mesopredators, *Nandinia binotata*, *Galerella*, and *Genetta*. Only 4 species were shared between coffee and forest plots. Better understanding the assemblage of taxa living in the Kenya highlands is the 1st step in conservation efforts there.

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A Risk Assessment of Road Proximity and Road Crossings of Radio-collared Mule Deer (*Odocoileus hemionus*) on the US Air Force Academy

From 1990 to present, the Colorado Division of Wildlife (CDOW) and USAFA Natural Resources (NR) implemented a lethal management program to reduce the resident mule deer population on the 7,465-hectare USAFA reservation due to concerns of winter-browse overuse, decreasing deer health and fitness, and high deer-to-vehicle collisions. In 1988, the estimated deer population of 1,600 was reduced to current levels of 200 to 250 animals. Over this period, a reduction in deer-to-vehicle collision fatalities also occurred ranging from a high of 124 in 1988 to a yearly average of 15 to 25 from 2000 to present. To date, no evaluation of “potential risk” of deer relative to vehicular roadways has been accomplished. Thus, we evaluated both deer proximity to roadways (10 m from road centerline) and actual deer road crossings of 14 radio-collared (LOTEK Wildcell) mule deer from Jan 2011 through June 2012 using both static and time-sequenced ARCGIS methods. Our results suggest potential “high risk” for deer-to-vehicle collisions at current population numbers. Using pooled data of all 14 deer over the 18-month period, we recorded 824 total mule deer road proximity values (46 per month) and 22,026 actual road crossings (1,234 per month). These results may necessitate future public safety and wildlife management actions to decrease potential deer-to-vehicle collisions.

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Barrier Effects of Roads on an Endangered Forest Obligate: Role of Forest Structure

Roads and traffic can influence animal movements and may act as barriers, especially for small-bodied forest obligates. The barrier effect is driven by several distinct mechanisms, including edge, gap, and traffic avoidance. An understanding of these factors is important to develop appropriate mitigation of road impacts. We combined radio telemetry and traffic monitoring with 3-dimensional remote sensing imagery (LiDAR) to examine edge, gap, and traffic effects and determine the relative importance of each to road avoidance. Our study species is the Mt. Graham red squirrel (*Tamiasciurus hudsonicus grahamensis*), an endangered subspecies of red squirrel endemic to high elevation forests in southeastern Arizona. To investigate edge, gap, and traffic avoidance, we compared probability of red squirrel home ranges that cross linear features between random lines in forests, road edges, low to high canopy cover lines, and roads with low and high traffic volume. We assessed environmental characteristics of road segments that red squirrel home ranges overlapped to identify features associated with improved road permeability. Red squirrels do not avoid crossing road edges but rarely cross roads. Canopy cover is the most significant factor affecting probability of crossing. As canopy cover decreases, probability of overlap is decreased. Our results show narrow dirt roads with low traffic volume can be partial barriers for forest dependent species and gap avoidance may play an important role in road avoidance.

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Patterns of Activity and Diversity of Bats at the Urban-wildland Interface in Southern California

Habitat loss and fragmentation pose a significant threat to bat populations. Urbanization can decrease roosting sites and foraging habitat for many species in southern California; however, the factors that allow some species to persist in cities and suburban areas, while others decline, are unclear. We used acoustic detectors (Pettersson D240X) to record bat echolocation calls at 4 sites in the eastern San Gabriel Valley that differed in their local site characteristics and the degree of urbanization of the surrounding landscape. Each site was sampled for 10 nights between March and August 2012. Using Sonobat software to identify 6,448 calls, we detected 8 bat species. Activity of the 4 most common species differed among sites: *Tadarida brasiliensis* was recorded at all sites but was the most active species at 2 golf courses, *Myotis yumanensis* was the most common species at a large regional park, and *Eptesicus fuscus* and *Lasiurus cinereus* were the most common species at an ecological reserve. Although the reserve had the least bat activity and lowest mean species richness (based on calls), it had the highest species richness after adjusting for

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the number of calls. Community composition differed significantly between the sites except for the golf courses, which were not different from one another. Our results suggest that bats are abundant in areas of southern California where suitable roosting and foraging habitats are available.

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Life at the Urban Interface: Potential Effects of Parks, Golf Courses, and Bicycles on Desert Bighorn Sheep

The response of wildlife to human disturbance can be placed into 3 broad classes: avoidance, attraction, or habituation. Predicting how these behaviors interact at the urban interface is a significant challenge to research and management. Desert bighorn sheep (*Ovis canadensis nelsoni*) in the River Mountains (RM) of southern Nevada have experienced increasing human encroachment over the last 4 decades. We compared habitat use, availability, and anthropocentric land use between historic (1970–1978) and present-day (2003–2004) periods in the RM to determine the cumulative effects of human disturbance. Human activity affected ewes and rams differently, resulting in a 17.8% and 13.7% habitat loss, respectively. The addition of a municipal park and golf course altered bighorn sheep habitat, with 30–40% of the total population shifting use to these areas in the present-day period. We found fecal-nitrogen levels of the present-day period significantly lower in the January–April and May–August seasons when compared to the same seasons of the historic time period. The long-term effects of habitat loss and lower forage quality are unknown. Artificially greater densities created by municipal areas may create conditions for increased disease transmission. The consequences of habituation to municipal food and water sources may be detrimental to translocation success if animals are unable to adjust to natural habitats.

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Bat Activity in Offshore Areas of Lake Michigan in the Context of Wind Energy Development

The Lake Michigan Offshore Wind Assessment Project is a joint effort whose principal objective is to develop a better understanding of offshore wind resources, as well as biological and environmental conditions offshore, as a precursor to development of offshore wind energy in the Great Lakes. The project employs an extended season offshore buoy featuring laser light pulse technology (LIDAR) to directly measure wind speeds at wind turbine hub heights, as well as serving as a research platform for a variety of other instrumentation. As bat mortality associated with wind turbines is a well-known concern at onshore wind farms, the buoy was used to conduct the 1st systematic assessment of bat activity in offshore areas of Lake Michigan via ultrasonic acoustic monitoring with subsequent call classification. The monitor/buoy was deployed at the mid-lake plateau of Lake Michigan, 56 km from the nearest shore, from April through November 2012. Preliminary analyses indicate that calls from 4 species were recorded: eastern red bat (*Lasiurus borealis*), hoary bat (*L. cinereus*), silver-haired bat (*Lasionycteris noctivagans*), and the eastern pipistrelle (*Perimyotis subflavus*), with calls from the first 3 species, all of which are long-distance migrants, being most frequent. To the best of our knowledge, these represent the 1st recordings of echolocation calls made in far offshore areas of the Great Lakes.

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Influence of Wind Turbines on Mammalian Mesocarnivore Occupancy Patterns

Wind energy is among the fastest growing industries in the United States. Although the industry strives to be environmentally friendly, the addition of infrastructure associated with wind farms alters ecosystems in novel ways. Numerous studies have shown the impacts turbines have on bird and bat mortality; however, far less attention has been given to responses of terrestrial organisms. Mammalian mesocarnivores are model organisms to document the alteration of communities surrounding wind turbines as they respond to addition of turbines and human activity, addition and improvement of roadways, and increases in turbine-induced carrion. In October of 2011, a yearlong study was established surrounding the Central Plains Wind Facility in western Kansas to model the occupancy dynamics of mesocarnivores within turbine and turbine-free habitats. We placed scent-baited trail cameras among turbine and control habitats, with a subset randomly placed along roadways. Detection histories during 28-day survey periods and habitat covariates were analyzed using PRESENCE. Coyote (*Canis latrans*) and swift fox (*Vulpes velox*) were the most abundant mesocarnivores detected with a 2.8% trap success. Turbines influence occupancy of mesocarnivores with coyote avoiding ($p = 0.75$) and swift fox preferring turbine areas ($p = 0.99$). Detection

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probabilities were influenced by weather and human activity. Species interactions also appear to play a role in occupancy dynamics surrounding wind farms. This research was supported by an ASM Grants-In-Aid of Research awarded to Brian P. Tanis in 2011.

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Small Mammals Exhibit Limited Spatiotemporal Structure in Sierra Nevada Forests

Western forests have been substantially altered over the past century and a half by human activities and are currently impacted by wildfire, climate change, urbanization, and invasive species. We monitored mammalian responses to 2 levels of canopy thinning in replicate plots over 8 years. Whereas forest structure was influenced by canopy treatments, small mammal numbers and assemblage composition were not. To better understand this pattern, we surveyed small mammals on 75 sampling transects established in a stratified random manner throughout the forest. We analyzed these data with constrained ordination. Ordination exposed significant associations between small mammals and underlying habitat metrics but explained remarkably little variation in these data, suggesting that small mammals are responding modestly to habitat variation as expressed by environmental variables measured at each plot. Finally, multiple regression explained little variation (12-36% across all "competitive models," e.g., those with $\Delta\text{AICc} \leq 2.0$) and regression coefficients were very low. Hence, both multivariate approaches suggest that the limited response by small mammals to canopy thinning reflects the generalist habits of the common species in this forest. We propose that anthropogenic influences have led to structural homogenization of these forests such that habitat specialists are unable to find productive habitat. The results presented here suggest that managers should strive to increase heterogeneity at multiple spatial scales and especially to promote the development of mature forest structure.

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Abundance and Distribution of Eastern Woodrats (*Neotoma floridana*) in Southern Illinois Following Genetic Augmentation and Reintroduction

Eastern woodrats (*Neotoma floridana*) historically occupied rock outcrops throughout the Shawnee Hills and Mississippi Bluffs regions in southern Illinois but were extirpated from most of this range during the last century. From 2003-2009, 422 eastern woodrats from Arkansas and Missouri were translocated to 5 historically occupied sites in southern Illinois to reestablish populations in the eastern Shawnee Hills. During 2004-2005, 47 woodrats were translocated to the Mississippi Bluffs to augment genetically depressed remnant populations. Although only 12.5% of the woodrats translocated to the Shawnee Hills were known to be alive approximately 1 month after release, sign surveys in 2011-2012 showed population persistence and dispersal up to 9 km from the nearest release site. During summer 2012, we live trapped at and around the release sites in the eastern Shawnee Hills capturing 260 woodrats (104 males, 154 females, 2 unsexed) in 911 trap nights with 109 recaptures (40% trapping success; on 4 occasions 2 woodrats were captured together in the same trap). Additionally, we trapped periodically at the largest remnant population in the Mississippi Bluffs during 2011-2013, capturing 209 woodrats (97 males, 110 females, 2 unsexed) in 643 trap nights with 90 recaptures (47% trapping success). Based on our trapping and sign-survey results, the southern Illinois woodrat reintroduction and population recovery appears to be the first of its kind to experience lengthy and widespread success.

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Post-release Survival of Captive-reared Allegheny Woodrats

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Allegheny woodrats (*Neotoma magister*) have experienced a severe range-wide decline over the past 40 years due to multiple demographic pressures that have caused a breakdown in metapopulation function. In Indiana, we developed a captive breeding program in response to steep declines in abundance and the onset of inbreeding depression in isolated subpopulations. A naïve captive-reared individual's capacity to transition successfully to the wild environment is critical for the program's efficacy. In 2011, we radio-marked and released 16 of these individuals directly into suitable dens and monitored post-release survival. For comparison, we radio-marked and monitored a parallel sample of resident young-of-the-year woodrats dispersing from maternal dens. We observed intense losses of captive-reared individuals through the initial 2-week settlement period with 50% perishing relative to 13% of residents. Consequently, we revised our approach in 2012 by releasing another 14 captive-reared woodrats into individual large wire-mesh enclosures constructed proximal to natural denning habitat. We provided food and water for 2 weeks, and finally opened enclosures to allow movement through the landscape. This procedure facilitated gradual adjustment to external challenges, and short-term survival improved by 54%. Captive propagation followed by hard releases may be ineffective for genetic supplementation; however, soft releases ease initial mortality and promote long-term survival, offering a positive outlook for future woodrat reintroductions. We recommend implementing similar conservation strategies in other programs managing small-bodied prey species.

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Demographic Response of Allegheny Woodrats to Habitat Conditions and Supplemental Feeding

Allegheny woodrat (*Neotoma magister*) populations are declining across their northern range. Multiple hypotheses have been proposed to explain these declines: 1) habitat fragmentation; 2) disease; and 3) food limitations. The purpose of our study was to relate demographic parameters to habitat characteristics and supplemental feeding. From May 2007–July 2010, we captured 328 woodrats (175 males and 153 females) on the Chestnut Ridge in Pennsylvania. We estimated population demographics using capture mark recapture methods. Estimates of apparent survival were highest between our first 2 years of sampling (0.552 ± 0.065 [females]), and lower for males (0.353 ± 0.082) and at our most disturbed study area (0.232 ± 0.076 [males]). Survival was higher at sites with greater hard mast tree diversity ($\beta = 0.115$, $SE = 0.029$) and lower at sites with greater pole timber density ($\beta = -0.110$, $SE = 0.030$). During supplemental feeding treatments, we saw evidence of earlier births at fed sites during 2009 following a year with an extremely low oak mast crop. We also observed greater numbers of new adult recruits ($p = 0.0007$, $F = 16.86$) and adult density ($p = 0.017$, $F = 6.96$) at fed sites compared to unfed sites.

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Factors Influencing Population Growth Rate of Virginia Opossums in North-central Florida

The Virginia opossum (*Didelphis virginiana*), the only marsupial occurring north of Mexico, is an important mesopredator with unique life history characteristics. Despite its wide distribution and potentially important role in southern ecosystems, little is known about its demography and population dynamics. We applied Pradel's temporal symmetry model to > 6 years of monthly capture-mark-recapture data and investigated factors influencing apparent survival, recruitment, and realized population growth rate of opossums at the Ordway-Swisher Biological Station in Florida. Apparent survival was dependent on sex, with a monthly probability of 0.86 ± 0.01 for females and 0.76 ± 0.02 for males. Recruitment rate varied seasonally with highest recruitment during the 1st mating season (January–February) and differed between sexes; estimates ranged from 0.07 ± 0.02 to 0.25 ± 0.05 for females and from 0.13 ± 0.04 to 0.44 ± 0.09 for males. Realized population growth rate varied monthly, with the lowest population growth rate in November (0.69 ± 0.05) and the highest in December (1.28 ± 0.18). Our study is the first to report realized population growth rate of opossums in the Southeast and represents a step toward understanding mesopredator population dynamics in a changing world where mesopredators are playing an increasingly significant role.

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Environmental Effects on Population Sensitivity to Reproduction

Survival and reproduction can vary in their impact on population growth rate. This variation can lead to changes in the reproductive strategy for individuals within the population. Previous studies indicate that the relative impact of adult

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survival and reproduction varies interannually in populations of small mammals and that some species vary reproductive effort in accordance to its influence on population growth. This suggests some reliable cue to the impact of reproduction. We tested for environmental cues associated with a greater relative impact of reproduction. We calculated elasticity of adult survival and reproduction for 3 species (*Sigmodon hispidus*, *Microtus ochrogaster*, and *Peromyscus leucopus*) for individual months from 1975-2003. We used environmental data and recursive partitioning analysis to determine if the elasticity of survival or reproduction varied with environment. We found no relationship between the environment and the elasticity of reproduction in *S. hispidus*. However, the elasticity of reproduction in *M. ochrogaster* and *P. leucopus* appeared to be higher in months with lower than average precipitation. These results suggest that environmental variation acts as a reliable cue to the impact of reproduction for these species and potentially allows individuals to modify reproductive effort accordingly.

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Hierarchical Modeling of Experimental Forest Harvest Effects on *Peromyscus*

The Missouri Ozark Forest Ecosystem Project (MOFEP) assesses ecological responses to even-aged, uneven-aged, and no-harvest forest management strategies in hardwood-pine forests of the Missouri Ozarks, USA. The MOFEP study evaluates harvest strategies applied at the scale of 300–500 ha sites, with only a portion of the forest patches (stands) within a site treated in any single harvest entry. The study uses a randomized block design, with 3 replicates per harvest strategy. *Peromyscus* abundance is measured on two 7.6-ha trap grids per site. We used multipopulation hierarchical mark-recapture models to estimate treatment effects on *Peromyscus* 2–14 years after the 1st round of harvest entries. Both even-aged and uneven-aged management strategies increased abundance compared to controls in the first 5 years after harvests. Overall, the estimated effect of even-aged treatments increased from years 2–5 after harvest [95% credible interval for log-scale even-aged treatment effect compared to controls in year 5: (0.412, 2.063)]. Uneven-aged treatment effects showed a similar pattern. In even-aged treatment sites, the positive treatment effect was localized in harvested stands 2–3 years after harvest. However, by years 4–5 after harvest, this treatment effect was a site-wide, not stand-level, effect. Effects of harvest treatments on abundance had partly dissipated 13–14 years after harvest. This likely reflects the rapid re-establishment of tree and tall shrub cover within the 1st decade after harvest in our study area.

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Spatial and Food Resource Partitioning in Two Sympatric Rabbit Populations in Southern Illinois

Resource partitioning is 1 way in which ecologically similar species may avoid competition. The Eastern cottontail (*Sylvilagus floridanus*), a generalist, and the swamp rabbit (*S. aquaticus*), a specialist, co-occur in early-successional bottomland hardwood forests in southern Illinois. We compared the extent of home range overlap within and between species for 17 cottontails and 47 swamp rabbits live trapped and radio collared at 3 sites between 2009 and 2012. Home range overlap was calculated as the volume of intersection (VOI) of the 95% utilization distributions for each rabbit. Both conspecific and heterospecific overlap was common, with mean VOIs of 0.18 (\pm 0.18) and 0.10 (\pm 0.09) respectively, however overlap varied considerably across sites. Using hair samples from a subset of rabbits, we examined differences in carbon and nitrogen stable isotope ratios. We modeled the effects of species and site on isotope ratios using repeated measures mixed-effects ANOVAs. Cottontails and swamp rabbits differed in their isotope ratios of both N ($p < 0.059$) and C ($p < 0.045$) at all sites, with cottontails consuming a greater variety of plants that included a greater proportion of C4 plants. Our results suggest that these species may be partitioning resources, but further research is needed to determine if competition drives resource use where they co-occur.

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Do Naïve Dispersers Rely on Natal Habitat Cues When Making Settlement Decisions? Evidence of Habitat Cueing and Potential Consequences in an Altered Forest Landscape

Mechanisms determining how naïve dispersers select areas to explore and settle remain poorly understood. Natal habitat preference induction (NHPI) may explain how dispersers select settlement locations, whereby natal habitat cues provide dispersers with a search image of quality habitat. If habitat imprinting occurs, forest structure in natal areas should be similar to settlement locations. We quantify forest structure and investigate the role of natal habitat cues in settlement of juvenile Mt. Graham red squirrels (*Tamiasciurus hudsonicus grahamensis*) dispersing within fragmented forest. We radiocollared 60 juveniles from 2010-2012, measured dispersal distance, quantified survival and food resources, and compared forest structure among natal areas, settlement locations, and random locations for each individual that successfully settled. Forest structure within 30 and 100 m of natal and settlement territory centers is similar. Intra-individual pairwise comparisons of natal versus settlement forest structure (collapsed via PCA) indicate immigrating individuals select structure similar to their own natal areas (mean individual natal PC score - settlement PC score 30 m = -0.75 ± 6.01 , $p = 0.8$). There is evidence for decreased survivorship in long distance dispersers. In fragmented forest, NHPI could serve as an adaptive strategy for identifying quality habitat in a matrix of poor quality or non-habitat. Conversely, NHPI could represent an ecological trap if habitat cues become decoupled from historically reliable fitness benefits. This research was supported by an ASM Grants-In-Aid of Research to Melissa J. Merrick in 2010.

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The Unseen Workers of the Fields: How Prairie Deer Mice are Helping Control Agricultural Weeds from Waste Grain

Agricultural land-use change and the increased reliance on glyphosate resistant corn varieties are growing ecological and economic problems in the Midwest. Our primary objectives are to determine how the patchiness of food resources affects the overwinter foraging of prairie deer mice (*Peromyscus maniculatus bairdii*) in these novel landscapes as well as determine the role that they play in controlling volunteer corn in intensively managed crop fields. Deer mice are one of the few year-round residents of Midwestern crop fields and have the potential to respond to small scale spatial variation within this larger simplified landscape. Deer mice also prefer eating corn waste grain over all other food types, thereby potentially providing an important ecosystem service in the form of volunteer corn pest control. While holding total seed resources constant, we predict that: 1) individual mice will functionally increase foraging in fields with many small patches; and 2) numerically, more mice will forage in fields with many small patches. To test these predictions we manipulate corn waste grain patches within tilled fields while controlling for total patch area and within-patch seed density. Preliminary results indicate that resource patchiness does influence the foraging behavior of mice (measured by giving-up densities) while numerical responses are equivocal. Our results suggest that deer mice living in corn fields can significantly reduce volunteer corn densities, potentially increasing farm profitability.

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Area and Distance Metrics Associated with Survival, Extinction and Re-Colonization of Black-tailed Prairie Dog Colonies (*Cynomys ludovicianus*) in Southwestern North Dakota

We surveyed 660 black-tailed prairie dog (*Cynomys ludovicianus*) colonies in southwestern North Dakota between May 2011 and September 2012. Black-tailed prairie dog colonies were ground surveyed by walking or driving colony perimeters. Data were collected from 611 total towns using Trimble Juno handheld GPS. These produced unique area polygons for each colony. Data from present surveys were compared to survey data collected in 2005–2006 to identify colonies that had become extinct and extinct colonies in 2005–2006 that had been recolonized. Mean area was computed for extinct and extant colonies in the present survey. Extinct and extant colony mean areas were compared using *t*-test. Mean distance of each colony from all other colonies (measured from the colony center) in the present survey was computed as a measure of relative isolation. Extinct and extant colony mean distances were compared using *t*-test as well. These analyses provide the opportunity to determine if minimum mean area and mean distance measurements can be used as indicators of susceptibility to extinction and therefore be used to assess long-term black-tailed prairie dog colony viability.

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164 (E, ST) Technical Session 14: Conservation Genetics, Salon E, Monday 17 June 2013

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Agricultural Intensification in a Neotropical Biological Corridor: Can Functional Connectivity for Frugivorous Bats Be Maintained?

As global human populations increase, the current trend of agricultural intensification in tropical landscapes is projected to continue. We use genetic approaches to investigate the impacts of agricultural intensification, specifically the recent expansion of pineapple plantations, on functional connectivity for frugivorous bat populations in the San Juan-La Selva (SJLS) biological corridor in Costa Rica. We focus on 2 frugivorous bats of differential size and mobility that are key dispersers of seeds: *Artibeus jamaicensis* and *Carollia castanea*. We hypothesize that populations of the larger, more mobile *A. jamaicensis* will retain higher functional connectivity in landscapes dominated by pineapple than populations of the smaller, more sedentary *C. castanea*. In 2012, we collected genetic samples from 109 *A. jamaicensis* and 197 *C. castanea* in 13 remnant primary forest patches in a matrix of pasture, annual crops, and pineapple in the SJLS. Using 10 microsatellite loci for *A. jamaicensis* and 8 microsatellite loci for *C. castanea*, we estimated genetic diversity within patches and gene flow between patches as functions of 1) patch size and isolation and 2) agriculture type in the matrix. Preliminary results indicate that *A. jamaicensis* retains higher functional connectivity through pineapple than *C. castanea*. Our research contributes to understanding of the impacts of habitat fragmentation and the conservation of frugivorous bats in the SJLS and in other Neotropical landscapes undergoing agricultural intensification.

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Broad-scale Patterns of Connectivity Among Black-tailed Prairie Dog Populations in a Heavily Managed Landscape

Habitat loss, persistent and pervasive poisoning, and the exotic disease sylvatic plague have substantially fragmented remaining populations of a keystone species of the prairie ecosystem: the black-tailed prairie dog (*Cynomys ludovicianus*). To understand how distance, land use practices, and grassland productivity affect individual dispersal and population connectivity, we conducted a population genetic analysis of black-tailed prairie dogs from the core of their distribution in the short grass prairie of Colorado to the eastern periphery of their distribution in the mixed grass prairie of Kansas. From this longitudinal gradient, we genotyped 1,096 individuals from 49 colonies at 19 microsatellite loci. Our estimates of gene flow and population isolation indicate that colonies throughout our study area are highly connected, although colonies on the eastern periphery are more isolated from one another than are colonies within the western core. We found that although isolation by distance predicts genetic distance between colonies at broad spatial scales, at finer scales, distance alone did not perform well, nor did models incorporating habitat features previously implicated as complete or semipermeable barriers to dispersal. Overall, our results suggest that black-tailed prairie dogs are not as sensitive to the effects of fragmentation as other grassland species, but that the magnitude of this effect depends on the scale of observation.

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Genetic Diversity vs. Genetic Distance: Reproduction, Growth and Survival in Captive Pygmy Rabbits

One-quarter of all lagomorph species worldwide are threatened with extinction. Although captive breeding programs sometimes are implemented as emergency conservation measures, such efforts often experience limited success. A better understanding of how tradeoffs between unique genotypes and genetic diversity affect successful breeding of captive lagomorphs is now an urgent conservation priority. We used regression models to explore the genetic, biological, and husbandry factors associated with pairing success, growth, and survival during the 10-year captive breeding program for Columbia Basin pygmy rabbits (*Brachylagus idahoensis*), an ecologically significant unit, at Washington State University. Pairing success increased, whereas juvenile survival decreased, over the years of the program. Pairing success and early juvenile growth declined with increasing Columbia Basin pedigree of the female, suggesting inbreeding depression among the small number of related founders. On the other hand, litter size, juvenile growth, and adult survival were unrelated to pedigree. Juveniles born at warmer ambient air temperatures had a higher survival to emergence from their natal burrow, and younger dams and dams bearing a previous litter were

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more successful than older ones and first litters of the season, respectively. Our study illustrates the complexity of using adaptive management to retain a unique genome for Columbia Basin pygmy rabbits while improving genetic diversity and simultaneously balancing intensive husbandry to improve survival with efforts to reduce artificial selection for the captive environment.

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Comparing Telemetry and Fecal DNA Sampling Methods to Quantify Survival and Dispersal of Juvenile Pygmy Rabbits

Understanding age-specific life history patterns can improve our knowledge of animal ecology and inform conservation strategies. Our goal was to compare telemetry and noninvasive genetic sampling (NGS) as methods for monitoring survival and dispersal of juvenile pygmy rabbits (*Brachylagus idahoensis*) reintroduced to central Washington. During summer 2012, we released 104 juvenile rabbits, 85 of which were fitted with glue-on radio transmitters and located 2-4 times per week while transmitters were retained. We tracked and recovered 64 transmitters, while signals were lost from 21. Most telemetered rabbits remained near the release site, with 11 dispersing > 1 km, and only 2 moving > 3 km. During winter, we surveyed 9.7 km² around the release site and collected 117 fecal samples for genetic analysis. Forty-two individuals were identified, 38 from the summer releases (37% survival) and 4 born in the wild from parents released 2 summers previously. Using NGS, we identified rabbits as: 1) released without transmitters; 2) with lost transmitter signals; 3) presumed dead; and 4) produced in the wild. Short-term dispersal behavior was best addressed with telemetry, but we were unable to estimate survival probabilities. The dispersal, survival, and reproduction trends provided by NGS allowed us to evaluate longer-term reintroduction success, without additional capture or handling. We review the costs, advantages, and limitations of each method for addressing specific monitoring objectives.

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Detection of Mitochondrial Pseudogenes in New England Cottontail (*Sylvilagus transitionalis*): Implications for Species Identification and Conservation

The New England cottontail (*Sylvilagus transitionalis*) is currently a candidate for endangered species listing under the Endangered Species Act of 1973. External characteristics do not allow New England cottontails to be distinguished accurately in the field from eastern cottontails (*S. floridanus*). Noninvasive techniques that allow sampling of large geographical areas with minimal cost require genetic identification to distinguish species. We sequenced the mitochondrial control region for 1,796 fecal and tissue samples from Connecticut, Massachusetts, New Hampshire, New York, and Rhode Island. We identified 12 New England cottontail, 101 eastern cottontail, and 8 snowshoe hare (*Lepus americanus*) haplotypes. We found 2 haplotypes that appeared to be non-mitochondrial in origin and could be preferentially amplified in some samples when a previously published method for identification was used. To provide an unambiguous and reliable identification method for species management, we created a barcode for the mitochondrial control region of these 3 species with 67 diagnostic nucleotides and developed a rabbit specific reverse primer. Phylogeographic analysis showed an extensive distribution of the majority of eastern cottontail haplotypes and minimal phylogeographic pattern across the 5 states sampled, which may be a result of the large number of introductions and provide eastern cottontail a competitive advantage in the form of hybrid vigor. New England cottontails showed low haplotype diversity across the landscape, which may be contributing to their decline.

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Hybrid Swarm Between Divergent Lineages of Mule Deer (*Odocoileus hemionus*)

Studies of hybrid zones reveal an array of evolutionary outcomes, yet the underlying structure is typically characterized as 1 of 3 types: a hybrid zone, a hybrid swarm, or a hybrid taxon. Our objective was to determine which structure best characterizes a zone of hybridization between 2 divergent lineages of mule deer. These lineages are morphologically, ecologically, and genetically distinct yet hybridize readily along a zone of secondary contact between

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the east and west slopes of the Cascade Mountains. Using microsatellite and mitochondrial DNA, we found clear evidence for extensive hybridization and introgression, with varying degrees of admixture across the zone of contact. The pattern of hybridization in the region closely resembles a hybrid swarm. Based on data from 10 microsatellite loci, we detected hybrids that extend well beyond the F1 generation, did not detect linkage disequilibrium at the center of the zone, and found that genotypes were associated randomly within the zone of contact. Introgression was characterized as bidirectional and symmetric, which is surprising given that the zone of contact occurs along a sharp ecotone and that the lineages are characterized by large differences in body size (a key component of mating success). Regardless of the underlying mechanisms promoting hybrid swarm maintenance, it is clear that the persistence of a hybrid swarm presents unique challenges for management in this region.

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Phylogeographic Inference of Insular Mule Deer (*Odocoileus hemionus*) Divergence in Baja California

Though mule deer (*Odocoileus hemionus*) persist in rather robust populations throughout most of their North American distribution, approximately one-half of their historic range in Mexico has declined due to habitat loss and unregulated hunting. Five subspecies inhabit northern Mexico's Sonoran and Chihuahuan deserts and the Baja California peninsula. Two of the 5 are of conservation concern, occurring on land bridge islands in the Pacific Ocean (*O. h. cerrosensis* on Cedros Island: threatened) and in the Sea of Cortés (*O. h. sheldoni* on Tiburón Island: endangered). The mitochondrial control region and cytochrome *b* were sequenced (totaling 1,405 base pairs) from museum specimens of Tiburón and Cedros deer. To assess regional intraspecific divergence, we compared insular sequences to peninsular (*O. h. fuliginatus* and *O. h. peninsulae*) and mainland deer (*O. h. crooki*) sequences. Estimated timing of expansion from mainland deer combined with maximum and statistical parsimony tree and haplotype reconstructions suggest that Tiburón and Cedros deer maintain genetic signatures of respective mainland lineages to varying degrees. Both Cedros and Tiburón deer match divergence patterns of estimated expansion events during the late Pleistocene (estimated 19,000-30,000 ybp) inferred from previously identified haplogroups. This study provides the 1st phylogeographic analysis of insular deer in Baja California. Future conservation priorities require consideration of the evolutionary and biogeographic histories of these insular deer for informed management.

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Evaluation of Alternative Culling Strategies on Maintenance of Genetic Variation in Bison

Bison (*Bison bison*) once numbered in the millions and roamed across much of the lower 48 states. By the late 1800s, overhunting had reduced the population to around 1,000 individuals. Strong efforts to establish managed herds have resulted in a steady bison population increase. Currently, 6 herds are maintained by the US Fish and Wildlife Service (FWS) at National Wildlife Refuges (NWRs) and are intensively managed through annual culling to keep herds at targeted levels. Although various criteria have historically been used to select individuals for culling, the FWS currently employs an "all allele conservation" strategy, with the goal of keeping at least a few individuals that represent each element of genetic variation. Other bison management entities such as the National Park Service often use random culling or slight variations thereof. We have developed an individual-based model to test the all "allele conservation" and "random" culling strategies to a proposed "pedigree-based" strategy based on the field of zoo biology to cull individuals based on kinship. The model is parameterized using existing long-term demographic and genetic data from the herd located in the Fort Niobrara NWR, Nebraska. Variation among culling strategies in heterozygosity and allele frequencies was detected at 100, 200, and 500 year marks. The model will aid the long-term management of bison and provides a useful tool for other intensively managed mammal species.

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Variability at MHC-DQB Gene in the Population of *Balaenoptera musculus* in the Gulf of California, Mexico

The Major Histocompatibility Complex (MHC) plays an important role in vertebrate immune system response against pathogens, therefore it is one of the most polymorphic genes in vertebrates. Because the MHC is under adaptive

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selection pressure against parasites, its genetic variation is maintained by balancing selection. However not all vertebrates have shown high polymorphism at the MHC; for example, cetaceans have shown low polymorphism compared with terrestrial mammals. MHC class II DQB exon 2 genotypes were analyzed in the Gulf of California population of blue whale (*Balaenoptera musculus*). Sequences from 80 individuals were analyzed; we obtained 8 sequences of 172 bp per individual by cloning. We identified 23 functional haplotypes and 1 pseudogene. One to 5 haplotypes were found in unique individuals suggesting gene duplication; no deletions or insertions were detected. We found 20 polymorphic sites and 24 mutations. The haplotype diversity was considerably high ($h = 0.869$) and the average nucleotide diversity ($\pi = 0.029$) was greater than that reported in other cetaceans. The number of nonsynonymous substitutions (128.05, $\pi = 0.034$) per site was greater than synonymous substitutions (42.95, $\pi = 0.01$). The peptide-binding region showed the highest polymorphism. These results support the hypothesis that balancing selection is acting on MHC genes.

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Bridging the Gap: Communication Between Scientists and Policy-makers

We live in an era of unprecedented technological sophistication and power. Our capacity to shape the environment at a global scale must be matched by an understanding of the far reaching and often elusive consequences of our actions. Basic science research is the foundation for understanding dynamics of populations and communities, how ecosystems function and when they cease to do so, and the scale and impact of climate change, among many other topics of immediate import. Without scientific knowledge, rational discussion and good decision-making is impossible. Correspondingly, for science to have any impact, there must be communication between scientists and the public, particularly policymakers. It is thus increasingly urgent that scientists and lawmakers effectively communicate their discoveries and needs; yet, it is often challenging to do so. Here, I outline some of the avenues by which scientists can connect with policy-makers, using as illustrations experiences from three months working as a Public Policy Fellow at the American Institute of Biological Sciences. This research was supported by ASM-AIBS Public Policy Fellowship awarded to Eve S. McCulloch in 2012.

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Incorporating Natural History Collections into Undergraduate Education

Natural history collections provide an invaluable resource for research on many aspects of mammalian biology including studies related to environmental change and public health. Similarly, natural history collections have been integral to a number of educational efforts in mammalogy, including classroom instruction. Ongoing efforts to digitize information associated with mammalian specimens and serve these data via the web have provided new opportunities to engage students in mammalogy. Access to digitized information on mammalian diversity provides new opportunities in education at a critical time. The Research Coordinating Network called Advancing the Integration of Museums into Undergraduate Programs (AIM-UP!) is developing educational modules for undergraduate courses that utilize collections and databases. These inquiry-based activities promote critical thinking, provide place-based experiences, integrate across diverse sets of data, and encourage students to take a broad view of the scientific process. We provide examples of successful incorporation of natural history collection data into an undergraduate mammalogy course. Students were able to access and utilize mammal collections data as they developed a semester-long project. The projects presented many challenges for the students; however they self-reported a better understanding of mammalogy after completing the project. We are incorporating student feedback and what we learned through this experience to develop more inquiry-based modules in mammalogy and other disciplines that utilize natural history collections and databases.

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Correcting Spatial Bias in Wildlife Citizen-Surveys: Integrating Manatee Sighting Reports with GPS Tag Data

Species occurrence data collected by citizen volunteers or mined from historic records can supplement species distribution studies by adding dimensions of spatial and temporal survey coverage. In the absence of rigorous survey

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or quality assurance methods, most citizen-collected or historic occurrence data may be biased, favoring human population centers; species in areas of high human activity may be oversampled, while species in unpopulated areas may be undersampled. We gathered citizen-reported occurrence data for the West Indian manatee (*Trichechus manatus*) in coastal Alabama, United States, from 2007 to 2012. We found significant differences in spatial distribution between citizen-reported sightings and reference locations derived from GPS tag data from 6 manatees in the study area. To correct for potential spatial biases in the citizen-reported dataset, we weighted each sighting report using: 1) population density of closest U. S. Census block (2010); and 2) aquatic distance to closest boat ramp. After correcting for spatial bias, spatial distribution of citizen-reported sightings was nearly homogenous with reference GPS locations. These results provided a foundation to enhance our knowledge of manatee distribution in AL by supplementing GPS tag data with unbiased data not explicitly detected by GPS tags (manatee group size and behavior). These results demonstrate that species occurrence data collected under different methodologies may be corrected and integrated to form a more robust depiction of location and movement patterns for the species.

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From the Retired Boomer to the Young Professional: Volunteers in Mammal Collections can be a Powerful Force

In 2011, The Collection of Mammals (OMNH) at the Sam Noble Museum of Natural History increased its size by over 50% with the addition of the mammal collection from the University of Memphis. In striving to meet the goals of the project while maintaining normal operations, the staff at OMNH modified its management culture and began recruiting large numbers of volunteers. Through outreach efforts, the OMNH collection has had over 50 volunteers since 2012 and the program continues to grow. This talk will discuss assessing collection needs, volunteer recruitment and retention efforts, challenges in quality control, and generational motivation tools. Theories exist regarding the benefits of volunteering; that is, it makes one feel part of a community and helps people stay connected and part of a bigger picture, an opportunity mammalogists can use to educate people of the importance of natural history collections, conservation, etc. In this economic climate, volunteers can be the key to continued productivity.

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Citizen Mammalogy: How Should the ASM be Involved in Citizen Science?

Fueled by a general human fascination with the natural world, many wildlife and taxon-based research initiatives are now benefiting from engaging citizen scientist volunteers in data collection. Volunteers benefit by direct participation in scientific research and by learning about their natural world in a local context. In turn, scientists gain valuable low cost monitoring or distribution data, particularly across broad spatial or temporal scales (e.g., Cornell Lab of Ornithology's eBird or Project BudBurst). Although a number of mammal focused labs and projects embrace the use of citizen scientists, mammalogy is lagging behind in capitalizing on public interest, which can facilitate research and monitoring efforts. A Web of Science search using the term citizen science returned 2058 articles; refining the search with the term "bird*" resulted in 59 articles, and with "butterfly*" 18. However, refining with "mammal*" returned only 7 articles. Here we explore the state of citizen science in mammalogy, with comparisons to other taxon-based efforts. We also address the question of how the ASM and its members can combine citizen science and public education with quality research. To heighten awareness of the mammals that share our neighborhoods and landscapes, we suggest ways to tap into existing naturalist networks. We also discuss ways to make mammalogy, mammal tracking, and track and sign identification more accessible and engaging for the general public.

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Porcupines: The Animal Answer Guide

"Porcupines" is written for nature lovers and interested laymen/women, with topics treated in depth and supported by an up-to-date bibliography. Two porcupine families, the Old World Hystricidae and New World Erethizontidae, encompass 26 species worldwide. Descriptions, and where possible, photo images are provided. The topics are covered in question and answer format. The North American porcupine is by far the best-studied porcupine species in

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the world; hence it receives greater coverage than other species. Treated in a comparative perspective, this species emerges as a highly divergent form.

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Project Passenger Pigeon: Building Sustainable Relationships with Other Species

Anthropocentric activity is the most significant cause of decline and extinction of mammals throughout the world. Although not a mammal, the passenger pigeon is an icon of extinction. The year 2014 marks the centenary of the extinction of the passenger pigeon. Numbering in the billions in 1800, the last bird died on September 1, 1914, driven to extinction by human activity. Project Passenger Pigeon (P3) is an international effort to commemorate this anniversary and use it not only as an opportunity to familiarize people with this remarkable species, but also to raise awareness of current issues related to human-caused extinction, explore connections between humans and the natural world, and inspire people to become more involved in building a sustainable relationship with other species. Individuals and institutions alike are encouraged to use P3 resources to prepare activities that highlight these goals on a local level. From species that are imperiled, such as bats or black-footed ferrets, to those that have made remarkable recoveries, like deer and beaver, the story of the passenger pigeon is one that can be utilized to unify the conservation efforts of all biologists in 2014.

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Habitat and Dietary Preferences in a Nocturnal Primate, the Thick-tailed Greater Galago (*Otolemur crassicaudatus*)

The thick-tailed greater galago (*Otolemur crassicaudatus*) is a widespread and relatively common primate in wooded habitats of eastern and central sub-Saharan Africa. It has shown the ability to adapt to human disturbance, including tree plantations but, like most primates, little is understood about how it uses specific microhabitats. Using the principles of giving up densities (GUDs), we examined the nocturnal microhabitat and foraging preferences of a galago population in a natural South African woodland with a full suite of predators. While tree density and size are relatively uniform throughout this habitat, approximately half of the forest grows on a talus and boulder-covered slope, while the rest is on level ground. As would be expected in an arboreal species, galagos preferentially foraged above the ground. However, they foraged more extensively in the areas with a steep slope and rocky substrate. This seems to show sensitivity to predation risk and use of rocky ground as additional protection from terrestrial predators. In addition to differences in microhabitat use, we documented dietary preferences of experimentally useful food items including cat food, raisins, alfalfa pellets, and peanuts. Cat food is significantly preferred while, unlike many species, galagos in this population rejected peanuts almost completely. The techniques presented here could be used to elucidate microhabitat preferences and foraging patterns in wide range of primate species, both diurnal and nocturnal.

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Bobcat (*Lynx rufus*) Home Range and Habitat Selection at Multiple Spatial Scales in New Hampshire

In New Hampshire, bobcats (*Lynx rufus*) have experienced dramatic population declines largely precipitated by changes in land use and forest succession. Evidence suggests that populations are rebounding and expanding into habitats that previously supported few bobcats. We initiated an investigation to understand bobcat habitat associations as one method of estimating their potential population in New Hampshire. Many methods have been developed to determine species-specific habitat suitability; however, resource selection functions (RSF) are one of the most popular methods due to their application within a geographic information system. We investigated habitat use at 2 spatial scales using bobcat locations obtained from incident sightings collected statewide and more intensive telemetry data from bobcats in 2 study areas. Second-order selection (home range composition) was investigated by comparing incidental bobcat sightings that were buffered by estimated home range sizes to random "available" home ranges. We attempted to correct for sampling bias associated with these data by modeling the probability of detection as a function of temporal, environmental, and human demographic variables at a township level. Locations from bobcats equipped with GPS-equipped telemetry collars were then used to describe 3rd-order habitat selection (within available home ranges). The resulting RSFs were compared and combined in an effort to generate a

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comprehensive description of bobcat habitat associations. Combined with estimates of area requirements, we estimated statewide bobcat abundance.

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Characteristics of Reproductive Dens Used by Fishers (*Martes pennanti*) in the Southern Sierra Nevada

The fisher (*Martes pennanti*) is a medium-sized carnivore commonly associated with features of older forests such as dense canopy cover, large trees, and cavities. Over the last 2 centuries, the impacts of fur trapping, loss of mature forest habitat, and other human disturbance have led to range reductions and extirpations of fisher populations in the western United States. Although efforts are underway to conserve remaining populations by protecting suitable habitat, little baseline data are available on habitat required by reproductive females, particularly in the southern Sierra Nevada. Between 2008 and 2012, we located 165 fisher reproductive dens associated with 27 radio-collared females, including 50 natal dens, 109 maternal dens, and 6 unsuccessful dens. We documented 8 cases of structure reuse; 4 trees were reused by the same individual and 4 by different individuals. Black oaks (*Quercus kelloggii*) were selected by females as dens more than other tree species (48% natal, 50% maternal), followed by white fir (*Abies concolor*; 20% natal, 24% maternal), and incense cedar (*Calocedrus decurrens*; 20% natal, 16.5% maternal). Mean canopy cover at dens (73.7%) was high and did not differ from that at available trees (74.1%) in the same stand. Mean understory (0-3 m) cover at dens (56%) did not differ from cover at nearby available trees (56%). We describe additional characteristics of fisher reproductive dens with implications for conservation and management.

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Seasonal and Spatial Variation in Diet Recorded by $\delta^{13}\text{C}$ of Incisor Enamel of Free-ranging Thirteen-lined Ground Squirrels (*Ictidomys tridecemlineatus*)

We tested the hypothesis that $\delta^{13}\text{C}$ profiles of incisor enamel from free-ranging thirteen-lined ground squirrels (*Ictidomys tridecemlineatus*) record seasonality in diet. We used laser ablation to densely sample lower incisor enamel (on average, one sample per 3 days of tooth growth) from 20 squirrels collected in SW Michigan, and analyzed samples using GC-IRMS. The basal ~20-35 increments of record always displayed a negative trend in $\delta^{13}\text{C}$, probably reflecting contamination by organic carbon in developing enamel; we excluded these values. At one colony, squirrels collected within 25 m of a cornfield displayed significantly higher and more variable $\delta^{13}\text{C}$ (variable C4-rich diet; mean = -5.03, SD = 2.38, n = 6) than did squirrels from mowed lawn distant from the cornfield (C3-rich diet; mean = -13.92, SD = 0.61, n = 6); this pattern persisted from early May-late August and was confirmed to reflect dietary differences ($\delta^{13}\text{C}$ of fecal pellets). Both groups displayed a positive excursion in $\delta^{13}\text{C}$ in late August. Late-season use of C4-rich vegetation was also documented at a second colony (n = 8) without access to a cornfield, studied in late summer through hibernation. Isotope values peaked rapidly from mid-August to mid-September and subsequently dropped precipitously to hibernation. We suggest rodent incisors as possible recorders of fine-scale seasonal variation of interest to paleoecologists.

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Reproductive Phenologies of Phyllostomid Bats from Costa Rica

Reproductive phenologies of populations are strongly molded by environmental variation, because natural selection favors individuals that time energetically demanding portions of their life cycle to correspond with periods of high resource availability. A variety of reproductive phenologies are known for species depending of their size, foraging strategy, or environmental context. Global change may alter these patterns by modifying the timing of resource availability or the timing of proximate cues that signal the initiation of reproductive behavior. We quantified reproductive phenologies of frugivores (*Artibeus jamaicensis*, *A. watsoni*, *Carollia castanea*, *C. perspicillata*, and *C. sowelli*) and a nectarivore (*Glossophaga soricina*), as well as, 3 feeding ensembles of phyllostomid bats that assist in seed dispersal and pollination. Additionally, we explored the roles of precipitation and resource availability in relation

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to reproductive phenologies. Reproductive classifications were based on peaks in frequency of pregnancy or lactation in adult females. All 6 species exhibited bimodal phenologies (2 peaks). Each of the 3 ensembles exhibited different phenologies (i.e., frugivores: bimodal; nectarivores: polymodal (3 peaks); gleaning animalivores: unimodal (1 peak)). Bat species that consume plant material evinced pregnancy peaks in the late dry season and mid wet season, with a 4 to 5 month hiatus between peaks. Conversely, gleaning animalivores exhibited a single peak in the mid to late dry season. These guild-specific differences in phenology exemplify how reproductive strategies relate to resource use. This research was supported by 2 Grants-in-Aid of Research awarded to Laura M. Cisneros in 2009 and 2010.

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Modeling Raccoon Removals and Recolonization of Woodlots Using Animal Dispersal Model SEARCH

Raccoons (*Procyon lotor*) are a prevalent North American mesopredator that serve as a vector for zoonotic diseases, including rabies and roundworm. Consequently, raccoons are often viewed as a threat to native wildlife, as well as a pest in agricultural and urban environments. Localized reductions are a common management tactic to control raccoon populations. However, the long-term effectiveness of raccoon trapping is not well understood. Some evidence suggests that localized trapping favors an increase in juvenile male dispersal, facilitating the spread of raccoons throughout the landscape. Thus, a better understanding of raccoon dispersal will help to inform management efforts. SEARCH (Spatially Explicit Animal Response to Composition of Habitat) is an individual-based, spatially explicit population model built to simulate animal dispersal through realistic habitats. We applied SEARCH to a population of raccoons in the Upper Wabash Basin (UWB) of north-central Indiana, where removal experiments were carried out. We created realistic virtual raccoons and habitat maps corresponding to the landscape of the UWB. We calibrated these inputs by running pre-removal simulations at several woodlots and comparing model output to field data (i.e., raccoon weights and dispersal success). We then simulated raccoon removals at several additional woodlots to explore long-term trends in population demographics and dispersal. This predictive use of SEARCH allowed us to virtually explore the viability of raccoon removal management scenarios.

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Patterns of Transience in Four Species of Oldfield Herbivorous Rodents in the United States

The dogma of population sub-structure assumes that rodents live their lives in circumscribed (natal) areas, with males and juveniles being more prone to disperse than females or adults. To test these assumptions, we examined records of geographic populations of hispid cotton rat, meadow vole, prairie vole, and marsh rice rat obtained through capture-mark-recapture methods from long-term studies in Kansas and Illinois and studies in Virginia. We evaluated proportions of residents and transients (1 capture), adults and juveniles, and males and females for differences among seasons, years, and geographic locations. Hispid cotton rats exhibited seasonally density-independent transience, with adults comprising the greatest proportions of initial captures and no differences in body mass between residents and transients. Meadow and prairie vole populations had seasonally significant transience, with geographic variation in the density dependence of transience and differences in body mass between residents and transients. The marsh rice rat had seasonal transience and no differences in body of residents and transients. All populations had seasonally significant transience and 6 of 7 populations had >50% transients, i.e., rodents never seen again after initial capture. In brief, none of these populations fulfilled the expectations of the current model of population sub-structure; perhaps a new model is needed.

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Demography of the Meadow Vole, *Microtus pennsylvanicus*, in Southeastern Virginia

We conducted a mark-capture-release (MCR) monitoring program of meadow voles, *Microtus pennsylvanicus*, on 2 separate old field restoration sites owned by The Nature Conservancy, in the Northwest River basin, formerly a part of the Great Dismal Swamp in Chesapeake, Virginia. We established an 8 x 8 research grid, at 12.5 m intervals, and with 2 modified Fitch traps per station on the Su Tract from 2002 to 2005 and on the Stephens Tract from 2005 to 2012. Both grids were trapped for 3 days each month, averaging 4,600 trap nights per year. The life history traits for these 2 populations were analyzed and compared with data throughout their range for yearly and seasonal changes in density, individual, survival and growth rates, mean body mass, sex ratios, transient/resident ratios, periods of reproduction, as well as lifespans.

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Detecting the Signal of Climate Change in Small Mammal Populations of Eastern Kansas

Changes in climate are expected to have variable impacts on populations. Many studies have projected the effects of climate change over the next century, but the effect of changes in climate may already be apparent in some populations. Our goal was to determine if we could detect the signal of climate change in populations of *Microtus ochrogaster*, *Sigmodon hispidus*, and *Peromyscus leucopus* using long-term mark-recapture data. We predicted population response based on previous studies of the populations and models that project the populations in a changing climate. We used a robust model in program MARK to estimate monthly population size of each species. We assessed population trends and stability using time series trend analysis. *Peromyscus leucopus* increased in abundance over time, which did not conform to our expectations. *Sigmodon hispidus* increased in abundance and the population became less variable over the 28 years of data collection, whereas *M. ochrogaster* declined in abundance although only slightly. The trends for *S. hispidus* and *M. ochrogaster* conform to our expectations of population response to a warming climate in eastern Kansas and suggest that the effects of climate change are already apparent in some populations of small mammal.

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Population Ecology and Dynamics of Nine-banded Armadillos

We used 15 years (1992-2006) of capture-mark-recapture data to examine the population ecology and dynamics of a population of nine-banded armadillos (*Dasypus novemcinctus*) inhabiting Tall Timbers Research Station, near Tallahassee, Florida. Conditional on survival, the annual transition probability for reproductive adult females to remain reproductive was high, but the estimate for non-reproductive adult females to become reproductive was low. Annual apparent survival was lowest for juveniles and highest for reproductive adult females. Annual apparent survival was lower for all animals during an extensive hardwood removal that occurred from 1998-2000 than in either preceding or subsequent years. Modeling across a range of values for γ , the probability of juveniles surviving in the population until first capture, we found that population growth rates only approached 1.0 when $\gamma \geq 0.80$, a situation that might not occur commonly because of the high rate of disappearance of juveniles. Growth rates were lower during the period of hardwood removal than in the years preceding or following. Life-table response experiment (LTRE) analysis indicated that the decrease in growth rate during logging was primarily due to changes in survival rates of adults. Likewise, elasticity analyses of both deterministic and stochastic population growth rates revealed that survival parameters were more influential on population growth than were those related to reproduction.

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Noninvasive Genetics Versus Camera Trapping: Estimating Population Density of an Elusive Carnivore, *Leopardus pardalis*

Knowledge of population density is imperative for effective species conservation; however, estimating density by traditional capture or re-sight methods is prohibitively difficult for many elusive carnivore species. Camera trapping has become a commonly used noninvasive approach for estimating density; however it has limitations such as the inability to estimate density from species that cannot be individually identified from photographs. Density estimation using noninvasively collected fecal DNA in conjunction with capture-recapture models may provide an effective alternative. Few studies have critically evaluated the reliability of noninvasive DNA-based approaches to provide robust estimates of population density through comparisons with more established estimation methods. In 2012, we conducted a study on Barro Colorado Island in Panama to estimate population density of ocelots (*Leopardus pardalis*) using noninvasive genetic samples and camera trapping, simultaneously. We collected 56 genetically identified ocelot scats from 20 ocelot latrines. We also captured >600 ocelot records from 34 camera traps deployed

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during the study. We used traditional and spatially-explicit capture-recapture models to estimate population density from both camera trapping and noninvasive genetic samples. We discuss the accuracy and precision of both methods and make recommendations for their future use in estimation of population density of elusive carnivores. This research was supported by an ASM Grants-In-Aid of Research awarded to Torrey W. Rodgers in 2012

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Factors Influencing the Occurrence of the Endangered Baird's Tapir *Tapirus bairdii*: Potential Flagship Species for a Costa Rican Biological Corridor

Baird's tapir (*Tapirus bairdii*) is classified as an endangered species and is considered rare and locally extirpated from most of its historic range within Costa Rica. We conducted camera trap and track surveys at 38 forested sites in and around the San Juan-La Selva Biological Corridor in the northern zone of Costa Rica. Cameras were set along established game trails and natural funnels and operated for 14-38 days per site. Additionally, we documented tapir tracks during our visits to cameras at many sites. We used survey photos and track presence to create detection histories to estimate the habitat and survey-specific variables that influence the probability of detection (\hat{p}) and the probability of occurrence (ψ) for Baird's tapir. Protected areas had a strong positive relationship with tapir occurrence, while forest cover and tree plantations also presented positive influences. Though the Baird's tapir is still rare, our findings suggest that tapirs are more resilient and able to use available habitat in the fragmented corridor than previously suggested. This is most likely a consequence of increased forest cover from reforestation and tree plantations and limited hunting pressure. Given its charismatic status, we recommend that this species would serve the San Juan-La Selva Biological Corridor as an excellent flagship species to increase local awareness about conservation and increase economic growth from ecotourism.

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The Feeding Ecology of Non-native Red Fox (*Vulpes vulpes*) on an Atlantic Barrier Island

The red fox (*Vulpes vulpes*) is a non-native predator inhabiting most of North America and fragile ecosystems, such as Fire Island National Seashore (FINS), New York. Fire Island is an Atlantic Barrier Island with more than 330 species of birds that are both migratory and resident. FINS is also located along the Atlantic Migratory Flyway and is a prime nesting site for Piping Plover (*Charadrius melodus*). While Red Fox are known to prey on ground nesting birds and small mammals elsewhere, almost nothing is known about fox food habits on Atlantic Barrier islands, such as FINS, that are likely home to important migratory and resident species. We proposed a red fox diet study on FINS to look at differences in diet within residential areas and wilderness areas and to detect seasonal differences within the red fox diet. Fox feces were collected from February 2011 to October 2012. There were 90 red fox feces samples collected. Mammalian bones and hair were identified to species. Avian bones and feathers were identified to order and family. Fish bones were identified to class. Plants were identified to kingdom, and crustaceans were identified to subphylum. This study is the first complete study on the diet of red fox inhabiting a fragile barrier island and will be a valuable tool in creating a management plan for sensitive island ecosystems.

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Using Camera Traps to Evaluate Placement of Artificial Water Sources at Fort Carson, Colorado

Artificial water sources can be used effectively in semi-arid regions to support wildlife populations. We monitored 14 guzzlers with camera traps in all seasons on Fort Carson Military Reservation, Colorado. The objective of the study was to examine wildlife usage patterns. To determine species and frequency of use at the guzzlers, we used five

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cameras and rotated them among the guzzlers from February 2011 to February 2013. Frequency of use for mule deer (*Odocoileus hemionus*) and elk (*Cervus elaphus*) increased during the hotter, drier, summer months and during drought conditions in any season. Predators such as coyotes (*Canis latrans*), badgers (*Taxidea taxus*) and bobcats (*Lynx rufus*) were observed year round at several different guzzlers. In addition, 1 grey fox (*Urocyon cinereoargenteus*) and a mountain lion (*Felis concolor*) were observed at only 1 guzzler each, but for multiple visits. Small songbirds of several species and ravens (*Corvus corax*) were also observed throughout the year, but large birds of prey, such as red-tailed hawks (*Buteo jamaicensis*) and golden eagles (*Aquila chryseotus*), were observed during the spring and summer. Guzzler locations closer to military training sites were frequented less often. Other factors affecting guzzler usage were guzzler size and frequency of refilling during times of drought.

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Investigating Fine-scale Genetic Structure in Female Mule Deer (*Odocoileus hemionus*) Through Spatial Analysis of Microsatellite-derived Relatedness Estimates

Genetic structure can often be seen at many spatial scales in free-living species. Fine-scale structure is seen at the smallest scales, both demographically and spatially. Genetic comparisons between individuals in a population are usually made in terms of relatedness, the relative measure of alleles shared by individuals due to shared ancestry. Because the distribution of individuals in natural populations is rarely random, spatial autocorrelation of relatedness between individuals may be observed. This study investigated the spatial autocorrelation of relatedness between individual female mule deer on Fort Carson Military Reservation in the central Front Range of Colorado. Thirty-four deer were fitted with GPS collars, and fecal samples were collected for subsequent genetic analyses. GPS data were used to identify an average position for each animal. To estimate relatedness, DNA was extracted from the fecal samples and amplified using primers for seven microsatellite loci. Genotype scores were combined with the position data for autocorrelation analysis. We found significant genetic structure only at relatively small scales, which would correspond to related individuals with overlapping or adjacent home ranges.

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Phylogeography, Demographic History, and Molecular Diversity of Two Neotropical Species of Family Procyonidae (Mammalia, Carnivora): *Nasua nasua* and *Procyon cancrivorus*

Comparative phylogeographic analyses are useful to shed light on common historical processes affecting regional faunas, as well as to identify species-specific life history features that may influence their genetic legacy. Here, we performed phylogeographic analysis of 2 medium-sized Neotropical carnivores, the brown-nosed coati (*Nasua nasua*) and the crab-eating raccoon (*Procyon cancrivorus*), using mitochondrial DNA and microsatellite markers, in order to characterize and compare their patterns of genetic diversity and underlying evolutionary history. Mitochondrial DNA analyses showed levels of diversity that were up to 10-fold higher for *N. nasua* relative to *P. cancrivorus*. Six reciprocally monophyletic mtDNA phylogroups were recognized for *N. nasua*, which were also supported as distinct populations by the microsatellite analyses. In contrast, the mtDNA data set for *P. cancrivorus* indicated the existence of 3 recognizable population units, but the magnitude of their differentiation was much less pronounced than that observed in *N. nasua*. Moreover, the microsatellite data did not support any genetic subdivision in this species. These results demonstrate that these species have very distinct evolutionary histories, which may at least in part be a consequence of differences in social structure and dispersal patterns. These results highlight the evolutionary complexity of the Neotropical biota and underscore the need for multi-species analyses employing comparable data sets so that common and contrasting patterns can be adequately investigated.

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Non-invasive Approach to River Otter (*Lontra canadensis*) Monitoring and Population Estimation in the Finger Lakes Region of New York

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River otters (*Lontra canadensis*) were once abundant in western and central New York but were extirpated early in the 20th century after decades of unregulated trapping and habitat loss. Between 1995 and 2001, approximately 300 otters were released throughout the region in an effort to restore populations to their former range. Though generally accepted as successful, there have been few published reports or systematic effort to document otter population status since the reintroduction. We applied non-invasive methods to estimate abundance and document behavior at latrine sites in the Finger Lakes Region of upstate New York. Using microsatellite multilocus genotyping, we will identify individuals via scat samples collected from June to August 2012 and 2013 and estimate abundance using closed population mark and recapture modeling. We will also analyze visitation behavior and group composition at active latrine sites using camera traps deployed from May 2012 to May 2013. We found 32 latrine sites on 3 Finger Lakes and collected 126 scat samples in 2012. We documented 178 visits to latrines by river otters from May to December 2012. With these results, we can better understand the behavior and status of this newly established population and, more importantly, establish a baseline condition of the population before the emerging threats of shale oil and natural gas extraction and climate change affect wetland ecosystems in New York.

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Bighorn Sheep at the Edge of the Translocated Range: Genetic and Environmental Variation

Understanding geographic variation across the distribution of species can provide important insights for management and conservation. Management is often focused on the re-establishment of previously extirpated populations to restore ecological function, augment genetic variation, and conserve historical diversity. The mountain sheep of North America (*Ovis canadensis*) faced significant declines during the late 19th and early 20th centuries, but conservation efforts have re-established many extirpated populations through translocation efforts. Our goal is to quantify genetic variation across the translocated range of bighorn sheep in Nevada and to assess the distribution of this variation in relation to environmental variables (niche space) and current taxonomy. We quantify variation at 20 microsatellite loci in approximately 400 individuals that include the 3 recognized subspecies whose translocated ranges meet in Nevada. To better understand the niche structure of bighorn sheep, we sample 22 (biotic and abiotic) variables across the historical distribution of *O. canadensis* using multivariate ordination and correlative modeling. We test hypotheses of niche identity and background similarity to assess consistency with intraspecific taxonomy. We find substantial genetic subdivision across the translocated range that reflects both recognized taxonomic units and differences in niche space. Our results emphasize the importance of considering both genetic and environmental variation in designing successful translocations.

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Population Genetics and Transcriptomics of Bowhead Whales (*Balaena mysticetus*)

Multiple mitochondrial DNA markers were sequenced to monitor genetic diversity, and RNA sequences were obtained from multiple tissues and multiple individuals to assess gene expression and genetic diversity in coding regions across the genome of bowhead whales (*Balaena mysticetus*). These data will be used to estimate effective population size and historical demography of this species for conservation and management purposes. We further report on the construction of a genetic database for bowhead whales to be used by the Scientific Committee of the International Whaling Commission, which is tasked with making recommendations about harvest quotas for this species.

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Short-tailed Shrews (*Blarina*) in Arkansas and Oklahoma

Short-tailed shrews (*Blarina*) have not been well studied in Oklahoma and Arkansas. Previous research identified two species (*B. carolinensis* and *B. hylophaga*) as occurring in these states, but information on their distribution is incomplete and identification has been based primarily on morphology. Using molecular analyses of the mitochondrial cytochrome *b* gene and AFLP analysis, the identification and distribution of these species has been clarified and the presence of a third species, *B. brevicauda*, confirmed in both states. Specimens of *Blarina* found at sites in the Ozark Plateau and Boston Mountains of Arkansas and in 2 counties in Oklahoma, previously thought to be *B. hylophaga*, were identified as *B. brevicauda* based on molecular data. Further study is required to clarify: 1) the presence of *B. hylophaga*, particularly in areas of western Arkansas bordering Oklahoma; and 2) the distribution of *B. brevicauda* in eastern Oklahoma and in Arkansas south and east of the Ozarks.

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Phylogeny of Holarctic Ground Squirrel Genus *Urocitellus*

Holarctic ground squirrels (*Urocitellus*) comprise a unique genus found predominately in higher latitudes and altitudes of North America and Asia, including Alaska, Canada, and Siberia. This study aims to increase resolution of both the patterns and rates of speciation within the genus. Despite decades of research on both the biogeography and socioecology of the group, phylogenetic resolution within *U. undulates* and *U. parryii* remains unresolved. We present a preliminary phylogenetic analysis consisting of nearly 40 samples of various species gathered from collections at the Museum of Southwestern Biology and combined with additional specimens previously archived in GenBank. In the future, we will expand our phylogenetic reconstruction using both mitochondrial and nuclear loci to better understand the dynamics of diversification of this genus and also clarify temporal estimates of its divergence from closely related ground squirrel genera. Molecular data will also be related directly to biogeography of modern *Urocitellus* in an attempt to reconstruct patterns of Beringian immigration and diversification.

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Reconstructing the Biogeography of Hawaiian Hoary Bats (*Lasiurus cinereus*)

The Hawaiian hoary bat is a subspecies of the species *Lasiurus cinereus*, which is primarily located in North and South America. The current population in Hawaii most probably descended from the North American population but now has a great number of morphological differences from that population. This study sought to investigate the genetic relationships between hoary bats from the Hawaiian Islands and hoary bats from mainland North America in order to reconstruct the biogeographic history of this species. Nuclear intron and mitochondrial DNA sequences from the Hawaiian bats and the North American bats were analyzed to estimate effective population sizes, rates of gene flow, and the time of dispersal separating the two populations. These parameters are of critical importance in assessing the conservation status of this unique Hawaiian population, and evaluating the frequency of long-distance dispersal events in populating isolated oceanic islands.

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Conservation of *Sigmodon* Along the Lower Colorado River: Past, Present, and Future

The lower Colorado River Multi-Species Conservation Program (MSCP) is a regionally coordinated conservation program, established to balance water use with the conservation and recovery of native species and their habitats. The lower Colorado River includes the drainage system of the Colorado River in Nevada, California, and Arizona, beginning at the full pool elevation of Lake Mead and extending south to the international border with Mexico. Within this managed area of the lower Colorado River, and of special interest to the MSCP, are isolated populations of 2 species of cotton rats (*Sigmodon*). Herein, I highlight the last 5 years of research I have conducted in cooperation with the MSCP on these populations including the biogeography of the area (past), a mark-recapture analysis (present), and species conservation through the design and construction of viable habitat along the largest river system in the western United States (future).

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Neotoma Species Turnover Identified by Ancient DNA from Paleomidden Feces

Our best way of understanding how taxa respond demographically and distributionally to environmental changes is by examining what has occurred in the past. The Great Basin holds a prodigious amount of information on ecological dynamics through the late Pleistocene and Holocene, thanks to the dry climate and middens of *Neotoma* species, which often last tens of thousands of years. While much good research has been conducted based on just the identification of subfossil materials, we have barely scratched the surface of what questions may be possible to answer through molecular analyses. Here, we report amplification and sequencing of ancient DNA (cytochrome *b*) from *Neotoma* fecal pellets over 9,500 years old from a paleomidden near Pyramid Lake, Nevada, capturing a Holocene turn-over of *Neotoma* species occupancy at that site. Our technique allows us to identify subfossils to species but also clade, holds the promise of improved temporal demographic reconstruction, and makes use of the copious fecal pellets that are ideal for destructive sampling.

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Spots on Trees: Examining the Phylogeography of the Western Spotted Skunk (*Spilogale gracilis*)

One major limitation to addressing species diversity within spotted skunks (*Spilogale*) is the lack of detailed assessments of intraspecific genetic diversity, which can provide evolutionary context for recognizing species limits. Herein, we present a detailed assessment of the genetic diversity of the western spotted skunk (*Spilogale gracilis*) using DNA sequence data from 2 mitochondrial genes (cytochrome *b* and D-loop) and Amplified Fragment Length Polymorphisms (AFLP). Bayesian and maximum likelihood analyses of the full cytochrome *b* dataset (705 bp, 71 individuals) revealed 2 statistically supported clades of *S. gracilis*, a western (CA, NM, NV, OR, and Baja Peninsula) and eastern (NM, TX, Chihuahua, Durango, and Sonora, Mexico). A 3rd, yet statistically unsupported monophyletic clade from the Sonoran Desert (AZ, Sonora and W Chihuahua Mexico) was also recovered. Pairwise genetic distances between western and eastern clades of *S. gracilis* was 4.3%. The Sonoran Desert clade was 4.2% different from the western clade and 3.2% from the eastern clade. The concatenated cytochrome *b* and D-loop dataset (1560 bp, 38 individuals) recovered the same clades as cytochrome *b* alone. Principal coordinate analysis of AFLPs (190 loci, 8 individuals) also supported the western and eastern clade split. Interestingly, the geographic break between western and eastern clades appears to differ between the mtDNA and AFLP datasets, occurring in central NM and southwestern AZ, respectively.

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A Taxonomic Revision of *Phyllotis andium* Thomas 1912 (Rodentia: Cricetidae)

Phyllotis andium is a medium-sized phyllotine rodent that occurs from Tungurahua Department, Ecuador, through the Andes to Lima Department, Peru. Pearson (1958) and Hershkovitz (1962) observed some morphological variation; however they treated the species as monophyletic, with the taxa *P. fruticicolus*, *P. melanius*, *P. stenops*, and *P. tamborum* as synonyms. These arguments have not been supported or rejected by modern studies. In this study, we carried out a taxonomic revision of *P. andium* based on a morphological and morphometric approach. To start, specimens were lumped in populations (OTUs), delimited by potential geographical barriers such as large rivers, high mountains, depressions, etc. For morphology, we examined 176 external and cranial-dental morphological characters commonly used in sigmodontine rodents. For the morphometric approach, 20 cranio-dental measurements were taken from 323 specimens to develop a non-geographical and a geographical analysis. We found that *Phyllotis andium* is a complex group of 5 different taxa, each one supported by synapomorphies and morphometry. *Phyllotis andium* (sensu stricto) is restricted to the population ranging from Tungurahua, Ecuador, to Northern Peru. *Phyllotis stenops* and *P. tamborum* are considered valid species, and both are apparently restricted to the east side of the Marañón River, Amazonas Department. *Phyllotis andium* "center" occurs from Cajamarca, south of the

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Huancabamba depression, to Huánuco Department, and *P. andium* “south” is restricted to Ancash and Lima Departments, on the Western slope of the Andes.

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Phylogenetic Position of *Phyllotis definitus* Osgood 1915 (Rodentia: Cricetidae)

Phyllotis (Rodentia: Cricetidae) is considered a monophyletic genus, with 17 species grouped in 3 clades: *P. andium* group, *P. darwini* group, and *P. osilae* group. The objective of this study was to clarify the phylogenetic position of *P. definitus*, which is distributed only in the “Cordillera Negra”, Ancash Department, Peru, and listed as endangered by the IUCN. The phylogenetic position of this species is controversial, and it has been considered related to *P. magister*, *P. xanthopygus*, or *P. andium* by several authors. Stepan et al. (2007) provided a molecular phylogeny of the genus, however, *P. definitus* was not included; therefore, its position is still uncertain. We developed a phylogeny of *Phyllotis* in order to test the position of *P. definitus* based on 98 morphological characters and 1184 base pairs of cytochrome *b* sequences. Fourteen recognized species of *Phyllotis* genus were included in the ingroup, and *Calomys sorellus*, *Graomys griseoflavus*, *Akodon boliviensis*, *Oxymycterus hispidus*, and *Thomasomys baeops* were used as outgroups. The matrix was subjected to parsimony and maximum likelihood analysis. Our results indicate that *P. definitus* is a member of the *Phyllotis andium* group, and it is closely related to a new species from Northern Peru, followed by *P. andium*, *P. amicus*, and *P. gerbillus*.

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Zelotomys hildegardae (Thomas, 1902): A Detailed Record of the Elusive African Sink Rat

Despite a large distribution across south, central and east Africa, the East African stink mouse or broad-headed mouse, *Zelotomys hildegardae*, is rarely observed or collected and is known from very few specimens in museum collections. Part of our research in the Laikipia region of Kenya has focused on identifying the full complement of small mammal species present in the region’s savanna habitats and compiling as much information as possible on species’ habitats and life history. Here, we present basic information on the natural history and biology of *Z. hildegardae*, including the 1st living images of this little-known species.

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Species Boundaries of Brushtail Possums in the Queensland Wet Tropics

To elucidate any morphological differences between *Trichosurus vulpecula* and *Trichosurus johnstonii*, A total of 45 skulls and pelts were measured from *Trichosurus* specimens collected in Queensland, Australia. Specimens were obtained from the National Museum of Natural History and the American Museum of Natural History. For each skull, a series of 21 measurements was taken, and three measurements were gathered from the pelts of specimens. Females of both species tended to be similar in skull morphology, but males of *T. johnstonii* had significantly larger tooth measurements than males of *T. vulpecula*. Both male and female *T. johnstonii* specimens had longer tails than *T. vulpecula*. A discriminant function analysis of skull measurements suggests not only clear grouping of individuals based on species but also more skull dimorphism among *T. vulpecula* than *T. johnstonii*. The results lend support for the hypothesis that *Trichosurus vulpecula* and *Trichosurus johnstonii* are, in fact, two distinct species. A larger sample size and molecular analysis are recommended as future steps in this experimental process.

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***Thomomys nayarensis*, a New Species of Pocket Gopher from the Sierra del Nayar, Nayarit, Mexico**

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The southern pocket gopher, *Thomomys umbrinus*, traditionally has been divided into as many as 5 genetically defined subclades based on chromosomal and allozymic data. Recent molecular analyses have resurrected 2 species from within these clades: 1 from the Pacific coastal lowlands (*T. atrovarius*), and another from the highlands of the Sierra Madre Occidental (*T. sheldoni*). In this study, multi-locus genetic analyses of 3 mitochondrial and 5 nuclear genes reveal a previously undescribed 3rd species apparently restricted to the Sierra del Nayar of northeastern Nayarit. In addition to molecular and chromosomal studies of this new species, cranial morphology is analyzed to help distinguish it from its congeners. This taxon, *T. nayarensis*, is described.

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First Assessment of the Medium and Large Mammal Diversity in the Pacific Tropical Rainforest of Peru using Line Transect Census and Camera Traps

The Pacific Tropical rainforest is one of the lesser known ecosystems of South America and is represented in Peru in only a small area of the Department of Tumbes where it is protected in the Cerros de Amotape National Park (CANP). Unfortunately habitat loss for farming and agriculture is leaving this tropical forest isolated. The aim of this study was to determine the richness and abundance of medium and large mammals and to identify priority areas of conservation. Line transect censuses were conducted, and 32 camera stations were placed in a 90 km² area in three localities of CANP from August to December of 2012. Mammal abundance was calculated with captured frequency (number of photos/1000 trap nights). The sampling effort was 120 km and 2102 camera days. As result, 18 species were registered with camera trapping and 10 with line transect censuses (21 in total). Camera traps proved to be more effective, because they registered elusive species that could not be sighted in line transect census. The accumulation curve using camera traps shows the asymptote at 19 species, suggesting adequate sampling effort. *Mazama americana* was the most frequent species (98.61) followed by *Pecari tajacu* (33.5), and *Eira barbara* was the least frequent (3.2). The presence of a diverse community of large and medium-sized mammals in CANP should move authorities to give the area the highest priority in conservation.

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Natural History of Small Mammals Sampled by Pitfall Arrays in Southeastern Oklahoma

Despite more than 100 years of collecting, few regions of Oklahoma have been well surveyed, and there is a paucity of taxonomic, distributional, and natural history information for most species. Between August 2008-July 2010, we surveyed an old-field habitat adjacent to a mixed-hardwood forest in Le Flore County in the Ouachita Mountains ecoregion of southeastern Oklahoma. Removal trapping using pitfall trap arrays resulted in captures of 521 individuals of 14 species of rodents, shrews, chipmunks, and rabbits, including 4 new records of mammals for the county. Four species were abundant (*Reithrodontomys fulvescens*, *Blarina carolinensis*, *Mictorus pinetorum*, and *Sigmodon hispidus*), 4 species were uncommon (*Peromyscus maniculatus*, *P. gossypinus*, *Oryzomys palustris*, and *Ochrotomys nuttalli*), 4 species were rare (*Cryptotis parva*, *P. leucopus*, *Sorex longirostris*, *R. humulis*), and 2 species were accidental captures (*Sylvilagus floridanus* and *Tamias striatus*). We present information on the natural history, reproduction, and population ecology of these species. These data are critical to understand those species that are known to play important roles in ecological processes, are environmental indicators, or have been designated as species of special concern by the state of Oklahoma.

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Recent Holocene Paleoecology of Terrestrial Vertebrates on Guam

Ritidian Point Cave (13° 39' 01.26" N, 144° 51' 43.28" E) in Guam, a US Territory, contains abundant sedimentary deposits that likely date from several thousand years prior to present times. From 3-1x1 m squares randomly placed on the cave floor, the 1st 10 cm of sediment were collected and later sorted under controlled laboratory conditions. Specimens were identified to the most specific taxonomic grouping possible via comparison with reference material. A total of 1,761 subfossil elements were recovered, of which 716 were too fragmented for identification. Of the remaining 1,045 identifiable elements, 371 were found on the surface while 674 were recovered from deeper sediments. The sample provides a preliminary representation of both native and introduced terrestrial species in the

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late Holocene. A minimum of 72 individuals were recovered, representing the classes Aves, Reptilia, Osteichthyes, Amphibia, and Mammalia. Within mammals, the orders Chiroptera, Artiodactyla and Rodentia were present, and we suspect elements of Soricomorpha as well. A minimum of 2 Chiropteran species were present, representing now-extirpated *Emballonura semicaudata* and *Pteropus tokudae*. Our data significantly deviate from previous surveys of older nearby cave sediments on northern Guam, which found few mammals and higher percentages of native species, perhaps reflecting a major shift in faunal composition following the introduction of non-native species paired with increasing human activity during the last several hundred years.

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Small Mammals from an Isolated, Remnant Cloud Forest in Guatemala

As part of a long-term effort to better determine the community structure of small mammals inhabiting highland habitats in Guatemala, we surveyed a remnant, isolated mixed hardwood cloud forest (2640 m elevation) at Finca El Pilar, 11 km SE of La Antigua, Sacatepequez, Guatemala. Removal trapping using a combination of live traps, snap traps, and pit fall traps for 5 nights (4-9 January 2013) with a total of 968 trap nights and 620 pit fall nights resulted in 46 captures representing ten species of marsupials, shrews, and rodents. This diversity of small mammals is about what we would expect for cloud forest habitats in Guatemala. Similar to other studies in cloud forests of Central America, one species dominated the small mammal community, *Peromyscus guatemalensis* ($n = 20$, 44%). Other species were much less abundant: *Cryptotis goodwini* ($n = 6$), *Sorex veraepacis* ($n = 5$), *Reithrodontomys sumichrasti* ($n = 4$), *Handleyomys rhabdops* ($n = 3$), *Heteromys desmarestianus* ($n = 2$), *P. beatae* ($n = 2$), *R. mexicanus* ($n = 2$), *Marmosa mexicana* ($n = 1$), and *Nyctomys sumichrasti* ($n = 1$). We discuss reproductive activity of these small mammals. While the habitat in this cloud forest has been disturbed, the species diversity for this small mammal community remains relatively high as indicated by the presence of ten species.

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New Records of Small Mammals from Prairie Dog (*Cynomys ludovicianus*) Towns in Southwest North Dakota

We surveyed small mammals in 2011 at prairie dog towns (*Cynomys ludovicianus*) in southwest North Dakota. Small mammals were sampled using Y-shaped pitfall arrays with drift fencing. Pitfalls were operated for five consecutive nights over four sampling periods during July 2011 and July 2012. Thirty-four small mammals were collected over four trapping periods between 2011 and 2012. These included 22 rodents and 12 insectivores. There were no significant associations between capture rates of small mammals and rainfall over the 2-year sampling period. Eight species (14 specimens) serve as new county records in 4 counties in southwest North Dakota. In addition, 2 specimens of Merriam's shrew (*Sorex merriami*) were captured. Merriam's shrew was known previously from North Dakota by only a single specimen collected in 1913 near Medora, North Dakota. These new records highlight the importance of periodic sampling towards our understanding of small mammal ecology and natural history.

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Paradiso Found — Mammals of Maryland Revised

In 1969, the US Department of the Interior, Bureau of Sports Fisheries and Wildlife, published *Mammals of Maryland* by John L. Paradiso. Number 66 in the series North American Fauna, it provided the first comprehensive review of the known mammals of the state. Sixteen years later, in 1985, Wm. David Webster, James F. Parnell, and Walter C. Biggs, Jr. updated most of the species in their book on *Mammals of the Carolinas, Virginia, and Maryland*. In the almost 30 years since then, some species have been extirpated and others have expanded their ranges. We are revising and updating Paradiso's publication to provide a modern scientific inventory of the mammals of Maryland. The book will include a wealth of information on Maryland mammals, including their habitats (physiographic regions descriptions), the human population and its impacts in the state, protected areas in Maryland, the best places to see

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wild mammals, mammalian diversity in the state, species accounts for all 75 species of terrestrial mammals, and 30 species of marine mammals occurring in the state, information on recent extirpations of mammals from the state, taxonomic keys for each of the 10 orders and 105 species of mammals, and records of Maryland mammals found in a wide variety of collections in natural history museums.

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How Much Do We Actually Know about Mammals of the Southeastern U.S.?

The southeastern United States is home to diverse ecosystems and associated mammalian fauna (>130 native and introduced species). We assessed the relative scientific knowledge of southeastern United States mammals through a literature search of electronically abstracted scientific publications. From these results, we estimated the number of scientific publications for each mammal species in individual states within the region. The average publication frequency for mammals was low with zero being the most common number of publications per species found in every southeastern state. States within the region differed widely in frequency and focus of published knowledge of resident mammals. There were also inequalities in the published literature based on taxonomic group with a disproportionately larger number of publications than expected on Order Artiodactyla and Carnivora. Smaller than expected number of publications were found on species rich groups such as Orders Rodentia and Chiroptera. Our results indicate that the general knowledge of mammals in the southeastern US is far from complete. These results suggest that large-bodied mammal species of social or economic importance are likely to receive more study than smaller-bodied mammal species. Variations between states in publication frequency appear to be caused by differences in land area, economic prosperity, and identity of federally endangered species. We recommend states prioritize funding towards study of neglected species and promote publication of “gray” literature in peer-reviewed journals.

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Climate Warming Effects on a Keystone Vertebrate

A multi-disciplinary team of scientists addresses effects of anthropogenic climate warming on the dusky-footed woodrat (*Neotoma fuscipes*), a keystone vertebrate in habitats ranging from desert, to woodland, to forestland. Current field data for climate-change analyses includes capture-recapture records (~31,500) from the live trapping of dusky-footed woodrats each spring and fall since 1993 in California oak woodland. Woodrat demographic histories, including reproductive output (juveniles/adult female) and seasonal survival, will assess the influences on woodrat demography of analogs of climate warming, including annual variation in temperature and precipitation, El Niño Southern Oscillations and North Atlantic Oscillations that have occurred during the two decades of measurement. Population Viability Analysis (PVA) will link woodrat demographic attributes to climate-warming predictions. Desert woodrat (*N. lepida*) ancestral range shifts and extinctions known from paleo (ancient) climate and paleo midden data, which date from the late Quaternary Period (40,000 to 5,000 years BP), will test the models. If models accurately hind cast paleo distributions, they will accurately future cast climate impacts.

217 Thematic Session II: Mammalian Predator Control, Salon E, Tuesday 18 June 2013

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Coexisting with Carnivores in the United States: Overcoming Prejudice and Persecution

Perhaps at no other time in United States history has predator management been more controversial. Increasing numbers of lawsuits, ballot measures, legislation, and federal petitions reflect a growing discontent with conventional predator management practices and policies and raise questions about what it means to coexist with carnivores. Resolution of human-wildlife conflicts have historically been the purview of the US Department of Agriculture's Wildlife Services program under the federal “Animal Damage Control Act” through taxpayer subsidized programs that emphasize lethal control through trapping, poisoning, and aerial-gunning. This program has been criticized for: 1) being unaccountable to the public; 2) lacking transparency and failing to incorporate ethical review of its processes, policies, and practices; and 3) failing to integrate modern science and shifting public values toward wildlife. Public opposition to the federal predator control program and greater understanding of the ecological importance of large carnivores has led to increased demand for humane and ecologically sound solutions to conflicts that integrate

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current science, ethics, and animal welfare considerations. Modes of civic processes that foster inclusion, transparency, and public involvement in community-based problem solving are needed. This presentation will discuss “practice-based improvements” using actual experience and adaptive management practices to address site-specific conflicts as the basis for solving human-wildlife conflicts. Key findings of an analysis of a community-based model adopted in Marin County, California will be presented as a case study.

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Stewart W. Breck

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Review of Non-lethal Methods for Predator Control

I will present a review of past, ongoing, and planned nonlethal research focused on minimizing human-carnivore conflict that I have conducted over 11 years and that is the result of support, funding and encouragement of USDA-Wildlife Services. I will define and review primary, secondary, and adaptive repellents developed to work on carnivores, briefly highlighting their efficacy or lack thereof and the importance of considering the social-ecological fabric and economic factors that contribute to their use and efficacy. I will also present past and ongoing research I am conducting focused on understanding and changing human behavior for decreasing human-carnivore conflict and my beliefs on the importance of this arena for future research. Case studies will include work from agricultural, urban, and natural systems and include research on wolves, black bears, and coyotes. I will stress the importance of good science and share my beliefs on the best allocation of limited resources for future work.

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The Intricacy of Wolf Control in Areas with Domestic and Wild Prey or with Threatened Caribou

In Canada, where livestock and wolves overlap, wolf control by government personnel typically takes place after calls for action by livestock producers. Control is also applied when hunters claim that wild prey populations are numerically depressed by wolves. However, such programs do not seem effective in diminishing wolf depredation occurrence or at increasing wild prey densities at a regional level or in the long-term. Control can extirpate wolf populations locally (an outcome opposed by many citizens), and then wolves recolonize such regions. Finally, aerial shooting and sometimes poisoning are also applied to diminish wolf predation and halt decline of threatened caribou. Such programs demonstrated some effectiveness (e.g., a caribou population not declining in the last year, but after 7 years of control), at the cost of wolf near-eradication, some poisoning of non-target species, and with use of significant taxpayers funds. For example, in a small 40 by 40-km area 500+ wolves may be killed by spending approximately \$1 million dollars in 5 years. Without accompanying efforts to address underlying systemic issues of caribou decline (e.g., habitat loss), wolf control efforts remain an expensive, band-aid, short term approach to treat the symptom not the problem. Ecological evaluations of wolf control programs are ongoing. However, social, economic, and ethical evaluations should also be conducted with the objective to inform the public and to avoid settling on controversial management options.

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The Western Wolf Conflict Deconstructed

Few issues in conservation receive as much attention as the management and conservation of gray wolves (*Canis lupus*). Despite recent successes in restoration efforts, tolerance for wolves remains elusive. Upon their removal from Endangered Species Act (ESA) protections, states in the American West quickly enacted aggressive management policies designed to reduce wolf populations. These actions were met with outrage from a variety of interested groups who oppose population reductions. Herein, I attempt to deconstruct the wolf conflict. Drawing on social science theory, I examine psychological, social, and institutional factors that perpetuate the conflict and prevent meaningful political compromise. Supporters and opponents of wolves show widely divergent perceptions about the risks and benefits of wolf populations, factors that parsimoniously explain intolerant actions. Perceptions of risks and benefits, in turn, are explained by social identification with relevant interest groups (e.g., hunters, environmentalists) who promote dramatically different visions of wolves' role in ecosystems. At the institutional level, authority over wildlife resides with state governments absent federal protections. Yet state game agencies in the West exhibit signs of regulatory “capture,” that is, undue influence by the interests most impacted by that agency (i.e., hunting, ranching). Thus, several interested organizations promote relisting of wolves as a means of ensuring their continued conservation. In this way, the conflict is reduced to win-lose scenarios, with the outcome determined by federal courts.

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221 Technical Session 15: Systematics and Biogeography: Old World Mammals, Salon E, Tuesday 18 June 2013

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Comparative Phylogeography of Three Sympatric Macropodid from Huon Peninsula, Papua New Guinea: Implications for Conservation and Management

The analysis of sympatric species can greatly enhance the identification of habitat variables that are potentially important barriers to gene flow and a comparative phylogeographic approach can detect patterns that may not be apparent by analyzing a single taxon. Three macropodid taxa with sympatric distributions inhabit the 4 mountain ranges on the Huon Peninsula, Papua New Guinea. Matschie's tree kangaroo (*Dendrolagus matschiei*) is a unique arboreal marsupial endemic to the Huon that is classified as endangered. Two additional macropodid marsupials on the Huon, New Guinea pademelon (*Thylogale browni*) and small dorcopsis (*Dorcopsulus vanheurni*), are both terrestrial. *Thylogale browni* is classified as vulnerable and is distributed on northern and eastern New Guinea in montane forest, savannah, and grasslands from sea level to an elevation of about 2,100 m. *Dorcopsulus vanheurni* is classified as near threatened and is distributed widely in montane forest on New Guinea's Central Cordillera and the Huon from 800 to 3,100 m. We sequenced 3 partial mitochondrial DNA (mtDNA) genes to: 1) investigate phylogeographic structure; 2) identify conservation units; and 3) detect common environmental variables that may have influenced the distribution of each taxon's maternal gene flow. All 3 macropodid taxa displayed a similar pattern in the spatial distribution of their mtDNA haplotypes. Our results will be used to inform management decisions for these species of conservation concern.

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Phylogenetics of Tribe Planigalini (Marsupialia, Dasyuridae) Using a Multigene Approach

Relationships within Planigalini have not been fully resolved by previous studies of morphological and molecular data. We employ a multigene approach that has proven robust for the dasyurid tribes, Sminthopsini and Phascogalini. An analysis of 26 *Planigale* sequences was undertaken to assess relationships among currently recognized species as well as 2 potentially new species from the Pilbara and Mount Tom Price (MTP) regions of Western Australia. This study uses 7 loci (7,292 nucleotides) for phylogenetic estimation. Maximum likelihood and Bayesian analyses of exemplar sequences showed that each locus implies a different topology. Concatenated results show 3 clades: *P. maculata*-*P. novaequinae*, *P. ingrami*-MTP planigale, *P. gilesi*-*P. tenuirostris*-Pilbara planigale supported with high posterior probabilities (0.71-0.98) and moderate ML bootstrapping (61-63). *BEAST was employed to generate a species tree that shows 2 distinct clades: one of *P. tenuirostris*-*P. gilesi* and the other including *P. maculata*-*P. novaequinae*-*P. ingrami* along with Pilbara and MTP specimens, however the support values are lower (0.42-0.45) compared to the individual gene trees or concatenated tree. Future work will involve hypothesis testing to better decipher relationships between species and to understand the discrepancies between the *BEAST species tree and the concatenated results. Fossil data will also be incorporated for more accurate divergence dates and to put into a historical context. This work also lends support to collecting and describing more specimens from Western Australia.

223 Technical Session 15: Systematics and Biogeography: Old World Mammals, Salon E, Tuesday 18 June 2013

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Genomic Evidence for Extensive Admixture in African Golden Jackals (*Canis aureus*) from Gray Wolves (*Canis lupus*)

Recent studies using mitochondrial DNA sequences have shown that golden jackals (*Canis aureus*) found in northern and western Africa actually represent a distinct lineage of African gray wolves (*C. lupus lupaster*), which appear to be an ancient and cryptic lineage within the gray wolf complex. To further clarify the genetic history of golden jackals and gray wolves in Africa, we collected genome-wide data from multiple populations of each species, including putative golden jackals from sub-Saharan Africa and Israel. Our results show that the genomes of golden jackals in Africa are extensively admixed with those of gray wolves, suggesting an ancient introgression event. Overall, our data suggest that golden jackals and gray wolves have a complex genetic history, similar to other canid populations and we discuss scenarios that may account for these genetic patterns.

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Plio-Pleistocene History of the Southern African Savanna: Diversification of Southern African Rodents of the Genus *Gerbilliscus*

The murid rodent genus *Gerbilliscus* is widespread and abundant throughout sub-Saharan Africa. Several molecular and morphological studies have examined the evolutionary relationships of this genus in eastern and western Africa. However, no study has produced a complete phylogeny for the southern African forms. The most recent checklist for this group suggests that the genus contains at least 6 species in the southern subregion. We estimate the number of species and the evolutionary relationships of the southern African *Gerbilliscus* using sequence data from multiple transmission elements including mitochondrial cytochrome *b* and cytochrome oxidase I, sequences from nuclear Y-chromosome markers, and nuclear AFLPs. Coalescent modeling indicates that the southern African forms originated from east Africa ~3 MYA with a subsequent radiation into southern Africa at times that correspond to African savanna expansion during the Pleistocene. Our data also indicate that diversity within southern African *Gerbilliscus* is currently underrepresented with at least 4 unrecognized species and therefore warrants specific taxonomic attention to accurately define species boundaries within this group and region.

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Cryptic Species Delimitation and Long-term Persistence Among Small Mammal Lineages in the Eastern Afromontane Biodiversity Hotspot

The Eastern Afromontane region of Africa is characterized by striking levels of endemism and species richness accompanied by significant conservation threat, a pattern typical across biodiversity hotspots. Using multilocus molecular data under a coalescent species tree framework, we identify major cryptic biogeographic patterns within and between 2 endemic montane small mammal species complexes, *Hylomyscus* mice and *Sylvisorex* shrews, codistributed across the Albertine Rift and Kenya Highlands of the Eastern Afromontane biodiversity hotspot. Putative independently evolving lineages are inferred using a combination of distribution data, coalescent species delimitation, and historical demographic inference. Hypotheses put forward to account for the high diversity of the region include both retention of older palaeo-endemic lineages across major regions in climatically stable refugia, as well as the accumulation of lineages associated with more recent differentiation between allopatric populations separated by unsuitable habitat at the Last Glacial Maximum. Populations have persisted since the Pliocene to mid-Pleistocene across a climatic gradient from the Albertine Rift in the west to the Kenya Highlands in the east for both focal taxa. Multiple recently differentiated populations are identified within both groups. Furthermore, deeply divergent and sympatric cryptic lineages, previously unidentified, are strongly supported in both mice and shrews, highlighting the broad temporal scale at which cyclical climatic changes over the last 5 Ma may have contributed to high species diversity and endemism in the Eastern Afromontane Hotspot.

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Evolutionary Relationships and Divergence Timing of Oryzoricline Tenrecs

Malagasy tenrecs, 1 of only 4 extant mammal radiations on the island continent of Madagascar, include 3 recognized subfamilies, the most diverse of which is Oryzoricinae. Oryzoricines have evolved a variety of unique adaptations and include terrestrial, semifossorial, scansorial, and semiaquatic ecomorphologies. Research interest in oryzoricines has surged in the past 20 years, and the number of recognized species has risen from 16 to 26 as a result of extensive collecting efforts and commensurate molecular and morphological phylogenetic studies. Although most higher-level studies support oryzoricline monophyly, few hypotheses have been proposed to explain their in situ diversification on Madagascar. Debate also surrounds oryzoricline phylogeny, specifically the position of the semiaquatic and monotypic *Limnogale* and its effect on the monophyly of shrew tenrecs (*Microgale*), the most speciose genus of terrestrial Malagasy mammals alive today. We analyzed DNA sequence variation from 10 unlinked nuclear and mitochondrial loci to estimate phylogenetic relationships and divergence timing. These analyses improve our understanding of tenrec diversification on Madagascar.

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Assessing Niche Evolution and Population Connectivity Over Glacial Cycles for Two Malagasy Small Mammals

We use ecological niche models (ENMs) to test for niche evolution and assess past and present population connectivity of 2 Malagasy small mammals, *Eliurus majori* and *Oryzoricetes hova*. Phylogeographic studies have identified 2 lineages within each of these tropical montane species. Pleistocene climatic oscillations may have affected population connectivity, with allopatric isolation likely during the warmer interglacials. For each species, we first use ENMs to test for niche conservatism between lineages. We then model each species' niche and predict the suitable areas in the present and at the Last Glacial Maximum (LGM; 21 KYA), proxies for past interglacial and glacial maxima, respectively. We calibrated models using occurrence records, 19 bioclimatic variables, and MaxEnt. To make high-quality models, we reduced the effects of sampling biases (via spatial filtering), implemented principles of study-region selection, and tuned model settings (to approximate optimal complexity). Tests of interpredictivity between lineages showed moderate (*O. hova*) to high (*E. majori*) levels of niche conservatism. Present-day predictions for *E. majori* indicated several disjunct areas of suitable conditions, whereas projections to the LGM suggested more extensive areas and higher connectivity. Results for *O. hova* were similar, but with larger areas of suitable conditions during both time periods. Overall, the results match the prediction of range contraction during interglacials and expansion at glacial maxima.

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Biogeographic Transitions in Extant Murinae (Rodentia: Muridae) of the Indo-Australian Archipelago

The Indo-Australian Archipelago (IAA) spans the Asian (Sunda) and Australian (Sahul) continental shelves, the Philippines, and Wallacea. Each of these 4 regions is home to endemic communities of murine rodents that together comprise nearly 70% of murine species. Sulawesi Island is the largest landmass in Wallacea, which forms a biogeographic bridge between the biotas of Sunda and Sahul. Previous phylogenetic studies showed that extant murine rodents of the Philippines and Sahul resulted from 5 and 2 colonizations, respectively. However, the diverse rodent fauna of Sulawesi was largely absent from these analyses. Here we present a phylogeny of 200 murine species and nearly complete sampling of genera from Sulawesi and the IAA. We use a 5-locus dataset to reconstruct a well-resolved phylogeny of Murinae. We modeled biogeographic transitions among the 4 biogeographic regions on

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the resulting phylogeny and used a fossil-calibrated, relaxed molecular clock to estimate transition dates. We infer at least 7 transitions between Sunda and Wallacea and at least 2 from Sulawesi to the Philippines and Sahul. The repeated colonization of Sulawesi by murines emphasizes the importance of isolation and in situ diversification in generating the modern murine fauna.

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Molecular Phylogenetics of Southeast Asian Squirrels Based on Mitochondrial DNA Reveals Paraphyly in the Genus *Dremomys*

The sciurid subfamily Nannosciurinae encompasses 14 genera and > 60 species, which range from India to Sulawesi. This group is largely understudied and species limits are often difficult to discriminate. Previous molecular phylogenetic studies of plain long-nosed squirrels of the genus *Dremomys* from mainland Southeast Asia revealed a strongly supported monophyletic group. However, the phylogenetic placement of the Bornean mountain squirrel *Dremomys everetti* with respect to other members of the genus has not been evaluated. In this study, we re-evaluated the cytochrome *b* phylogeny of 2 genera, *Dremomys* and *Sundasciurus*, with all representative species within the *Sundasciurus* subgenus *Atelosciurus* and all 6 species of the genus *Dremomys*. Likelihood and Bayesian analyses provided support for the placement of *Dremomys everetti* within the diversity of the subgenus *Atelosciurus* (genus *Sundasciurus*). We also analyzed a concatenated dataset for representative taxa with whole mitochondrial genomes and cytochrome *b* sequences for additional resolution and support for the paraphyly of *Dremomys*. Cranial morphometrics did not reliably separate these species. Additional morphological analyses as well as sequencing nuclear DNA will be needed to determine whether the Bornean mountain ground squirrel requires taxonomic revision and to rule out the possibility that historic mitochondrial introgression from *Sundasciurus* may be responsible for the genetic signature that we observed. This research was supported by an ASM Grants-In-Aid of Research awarded to Melissa T. Roberts in 2012.

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Morphological Distinctiveness of Javan *Tupaia hypochrysa* (Scandentia, Tupaiidae)

Treeshrews (Scandentia) are small-bodied mammals from South and Southeast Asia. The last comprehensive taxonomic review of this group was published a century ago, and species-level diversity remains uncertain. *Tupaia glis*, which included 27 synonyms as of 2005, is a taxonomically problematic species complex that is mostly distributed south of the Isthmus of Kra on the Malay Peninsula and surrounding islands. In our ongoing revision of this species complex, we recognized *T. ferruginea* from Sumatra as a distinct species, though we could not adequately assess the population from Java (*T. "glis" hypochrysa*) because only a single specimen was available. We expanded our sample and re-analyzed its hand proportions, using principal components and cluster analyses of 38 variables from 64 specimens, as well as 22 craniodental measurements from 132 skulls, of *T. "glis" hypochrysa*, *T. glis*, *T. ferruginea*, and *T. chrysogaster* from the Mentawai Islands. The manus and skull of Javan *T. "glis" hypochrysa* are most similar to those of *T. chrysogaster* and distinct from those of *T. glis* and *T. ferruginea*. The Javan population can be differentiated from *T. chrysogaster* based on differences in mammae counts, supporting recognition of *T. hypochrysa* as a distinct species. The change in taxonomic status of *T. hypochrysa* has important conservation implications for *T. glis* and this rare Javan endemic.

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The Biochemistry and Physiology of the Resistance to WNS by *Eptesicus fuscus*

White-nose Syndrome (WNS) causes severe over-winter mortality in little brown (*Myotis lucifugus*), Indiana (*Myotis sodalis*), northern (*Myotis septentrionalis*), and tricolored (*Perimyotis subflavus*) bats in North America. It is caused by

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cutaneous infection with the fungus *Geomyces destructans*. The infection causes bats to die during hibernation by disrupting their normal torpor patterns, which leads to the premature depletion of body fat reserves. The results of 2 studies suggest that big brown bats (*Eptesicus fuscus*) are resistant to cutaneous infection with *G. destructans*. Field studies were conducted during the winters of 2011–2012 and 2012–2013 on the torpor patterns of *E. fuscus* hibernating at a site where *G. destructans* is found. The torpor bouts of both male and female big brown bats during hibernation at this site were well within the normal range of lengths previously reported for this species. Annual counts also revealed no decline in the number of *E. fuscus* hibernating at this site since *G. destructans* 1st appeared. There was also no evidence of fungal growth on the skin of the 26 big brown bats examined. The mean body fat content of *E. fuscus* in February was nearly twice that of *M. lucifugus* hibernating in the same area during this period. These findings demonstrate that big brown bats are resistant to WNS.

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Potential Influence of White-nose Syndrome on Summer Bat Distribution in Pennsylvania

White-nose Syndrome (WNS) is a fatal fungal infection affecting bats in North America, having caused the death of > 1 million bats since its discovery in 2006 and threatening at least 1 species with regional extinction. The spread of WNS through Pennsylvania has been staggered; eastern hibernacula have experienced longer exposure than in the west. It is unclear if mortality observed in these areas translates to lowered summer bat activity. We used maximum entropy modeling and treated WNS as a habitat variable to determine how exposure to WNS has changed summer bat communities. Using a combination of mist netting and acoustic sampling in 12 sites spanning the state, total bat activity appeared greater in the west (1,458 call minutes) versus the east (1,093 call minutes). Species-specific distribution models indicated that greater bat activity was associated with types of bedrock geology and greater forest area within a 10 km² landscape. Among cave bats, activity of little brown and Indiana bats had the greatest negative relationship to WNS risk. We demonstrated the utility of using standardized methods and ecological niche modeling to identify variables relevant to summer bat activity. As WNS continues to infect hibernacula, focus on improving survivorship in the active season is increasingly imperative.

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Regional Extinction Risks of the Eastern Pipistrelle Bat

Recent conservation concerns have surfaced for migratory and hibernating bat species in North America. White-nose Syndrome (WNS) has resulted in regional population declines in hibernating bat species. Eastern pipistrelles, *Perimyotis subflavus*, have experienced mortality rates of 85% in affected hibernacula. In addition to declines by WNS, *P. subflavus* is 1 of the 4 migratory bat species predominately affected by wind turbines, accounting for about 25% of turbine mortalities within the species' geographic range. If *P. subflavus* populations are to remain viable, they must survive both of these conservation threats. Here, we address the following questions: What are the population-specific extirpation risks from WNS and turbine mortality? What rates of decline from WNS and turbines can *P. subflavus* populations sustain? Using genetic data to parameterize migration rates and effective population sizes, we present a range of risk scenarios designed to investigate the limits of population viability in *P. subflavus*. This research represents a novel approach in which the combined effects of both WNS and wind turbine mortality rates are assessed.

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Does *Geomyces destructans* Infection Impair Reproductive Capacity in the Little Brown Bat (*Myotis lucifugus*)?

White-nose Syndrome (WNS) is a disease caused by a cold-adapted fungus, *Geomyces destructans* (Gd), which results in devastating population declines of North American cave-hibernating bats. Rates of decline at most sites are estimated by annual counts, so it is uncertain whether declines are due entirely to increased mortality or if reduced fecundity also occurs. Female little brown bats (*Myotis lucifugus*) store sperm and a single Graafian follicle throughout hibernation and will not produce any offspring if storage fails before spring emergence. Bats with WNS become emaciated and dehydrated, which could compromise their ability to maintain the stored follicle and sperm. We collected reproductive tissues from hibernating female *M. lucifugus*, including both Gd-positive and Gd-negative

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individuals. We hypothesized that Gd-positive females would be less likely than Gd-negative females to maintain a mature ovarian follicle and stored sperm. Our results will indicate whether Gd infection reduces reproductive capacity of hibernating females. Additional studies of reproductive capacity of females at maternal colonies will determine if Gd infection reduces the probability of maintaining pregnancy in the post-hibernation season.

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Large Herbivore Removal Increases Rodent-borne Disease Prevalence in East Africa

Understanding the effects of wildlife loss on zoonotic disease is important both for public health and conservation initiatives. For rodent-borne diseases, there is strong conceptual support, but little empirical evidence, for the hypothesis that the loss of large wildlife tends to increase rodent-borne disease risk by removing controls on rodent density - either by removing predators or competitors of rodents. To examine this question, we experimentally excluded large wildlife and then examined the prevalence of *Bartonella* infection in rodents and their ectoparasite vectors and the total density of infected rodents and vectors. We found no significant effect of wildlife removal on prevalence of infection in either rodents or vectors. However, because rodent and vector abundance roughly doubles following the removal of large wildlife, we found that the density of infected hosts and infected vectors was more than 2 times higher in sites where wildlife was present. As the fleas in this study system also parasitize humans and are known to transmit *Bartonella*, this work strongly suggests that wildlife loss will greatly increase human risk for *Bartonella* transmission.

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Management of Raccoon Roundworm in Free-ranging Raccoon Populations Via Anthelmintic Baiting

Raccoon roundworm (*Baylisascaris procyonis*), a common gastrointestinal parasite of raccoons (*Procyon lotor*), has been implicated in population declines of Allegheny woodrats (*Neotoma magister*). Medicinal baiting is a viable tool in wildlife disease management, although unique challenges exist for pathogenic systems in which the host can be immediately reinfected following treatment. Our goals were to evaluate the efficacy of using anthelmintic baits to reduce the prevalence of roundworm infection in raccoons and to quantify patterns of bait acceptance among populations repeatedly exposed to medicinal baits. We distributed baits monthly throughout areas surrounding woodrat habitats in Indiana. We conducted raccoon latrine surveys annually to quantify the effect of treatment on roundworm prevalence and used remote cameras to identify the species contacting baits and rate at which baits were removed. Among treatment sites, roundworm prevalence declined in response to treatment. Baits were removed rapidly from camera stations with 60% taken within 24 hours, 80% within 48 hours, and 90% within 72 hours. Virginia opossums (*Didelphis virginiana*) removed 51% of baits whereas raccoons removed 44%. Identification of opossums as the predominant consumer of baits emphasizes the limitations imposed by nontarget bait consumption for mitigation of roundworm and other wildlife diseases. Similar treatment measures may facilitate conservation of Allegheny woodrats in habitats with high rates of roundworm-related mortality and could be used to reduce human exposure to this zoonotic parasite.

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Mitigation Efforts to Conserve Black-footed Ferrets During a Plague Epizootic

Black-footed ferrets (*Mustela nigripes*) are endangered obligate carnivores of prairie dogs (*Cynomys*), and both species are highly susceptible to sylvatic plague. The reintroduced population of ferrets at Conata Basin, South Dakota, was once the largest black-footed ferret population in the world partly due to a lack of plague. In 2008, plague entered Conata Basin and has since affected 20,000+ acres of prairie dogs and ferrets. Dusting prairie dog

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burrows with an insecticide to kill fleas, a vector of plague, has been successful in maintaining approximately 10,000 acres of habitat. Past studies suggested that dusting alone may be enough to preserve prairie dogs and ferrets in the presence of plague, but we also vaccinated many ferrets against plague. We analyzed data from annual ferret population surveys using logistic regression to compare re-encounter rates of ferrets pre-/post-plague and to assess vaccine effect on dusted colonies. Re-encounter rates were lower in the presence of plague ($P < 0.001$) and males were more susceptible than females ($P = 0.039$). On dusted colonies during a plague epizootic re-encounter rates were higher for vaccinated than nonvaccinated ferrets ($P = 0.078$), with a trend towards even higher survival for vaccinates receiving more than 1 dose of vaccine. The combination of dusting and vaccine is needed for plague mitigation at Conata Basin and without both the population might have perished.

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Devil Disease Before DFTD: Museum Specimen Insight into Marsupial Carnivore Declines

The Tasmanian devil (*Sarcophilus harrisii*), the largest living carnivorous marsupial, is currently endangered by the spread of a naturally-occurring fatal contagious cancer (Devil Facial Tumor Disease, DFTD). Historical reports suggest that at the start of the 20th century, Tasmanian devils also underwent a precipitous disease decline, which may have also affected other large marsupial carnivores in Tasmania at the same time, including quolls (*Dasyurus*), as well as the Tasmanian tiger or thylacine (*Thylacinus cynocephalus*), which never recovered from this decline and subsequently became extinct. Examination of historical accounts and specimens suggests that this century-old disease event, from which Tasmanian devil populations eventually recovered, was not a contagious cancer like the current epidemic, but an infectious disease that has not previously been identified. A Tasmanian devil that was captured in Tasmania at the time of the epidemic, exhibited at the National Zoo, and deposited upon its death at the National Museum of Natural History allows us to explore links between the pathology associated with this disease, archived necropsy information, and data derived from molecular biological (ancient DNA) approaches. These comparisons enable us to identify for the first time a candidate pathogen for Tasmania's historical disease declines.

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Modeling the Distribution of Feral Swine in the United States

Feral swine are the most abundant nonnative, free-ranging ungulate in North America. Feral swine carry over 30 viral and bacterial pathogens that affect humans or livestock and cause about \$1.5 billion in annual damage to agricultural ecosystems. Although feral swine were once primarily found in the southern United States, they have spread northward and are now reported in at least 39 states and 3 Canadian provinces. Despite their impact on socio-ecological systems, little is known about the environmental factors that influence the macro-scale distribution or invasive potential of feral swine in the US. We addressed this deficiency by developing a species-distribution model for feral swine in the conterminous US. We compiled occurrence data from databases maintained by the Southern Cooperative Wildlife Disease Study and the US Department of Agriculture, Animal and Plant Health Inspection Service, Wildlife Services. We used these occurrence data in a model that correlated the known distribution of feral swine to covariates like climate, land cover, hydrology, and elevation. Due to the biogeographic scale of this analysis, climatic covariates, such as temperature, were found to strongly influence the distribution of feral swine in the US. However, land-cover classes like cropland and forest were also important. We evaluate our results relative to factors that complicate our understanding of invasive species distributions, such as generalized habitat requirements, expanding range margins, and anthropogenic dispersal.

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Interactions Between Small Mammals and Ticks in Successional Wetlands in Virginia

Rodents and other small mammals play an important role in the enzootic maintenance of tick-borne diseases. It is known, for example, that the white-footed mouse (*Peromyscus leucopus*) is integral to the enzootic cycle of *Borrelia burgdorferi*, the agent of Lyme disease, in the northeastern United States. Tick diversity is higher in the southeastern

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U. S., and the warmer climate results in faster succession and a different suite of small mammal hosts than in the northeast. These differences in the makeup of the small mammal community may have implications for the ecology of ticks and tick-borne diseases. We explore the relationships between ticks and their small mammal hosts in successional wetlands in southeastern Virginia through monthly live trapping at one site from 2010 to 2013, and another site from 2012 to 2013. We find that the meadow vole (*Microtus pennsylvanicus*), the marsh rice rat (*Oryzomys palustris*), and the southern short-tailed shrew (*Blarina carolinensis*) have the highest tick load per animal, and that the cotton rat (*Sigmodon hispidus*) and *B. carolinensis* may play an important role in the life cycle of *Ixodes* ticks and in the southeastern cycle of *B. burgdorferi*.

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Pathways to Ecological Generalism in a Savanna Small-Mammal Community: An Experimental Test of a Macroecological Pattern

The correlation between the abundance and distribution of species is one of the most pervasive in macroecology. This pattern has been attributed to variation in the breadth of resource requirements among species, and, alternatively, differences in landscape connectivity that affect the colonization-extinction dynamic underlying species occupancy at different localities. In central Kenya, we combined a large-scale ungulate exclusion experiment with repeated sampling of individuals for carbon isotopes to test the prediction that purported generalists (i.e., common, widely-distributed species) display greater diet breadth compared to their rare, narrowly distributed counterparts. For 18 sites arranged along a pronounced rainfall gradient (480 to 715 mm/year), abundance and distribution were strongly correlated across an assemblage of 16 species of small mammals. We show that diet composition for the most widely distributed and numerically-dominant species (the fringe-tailed gerbil) was more strongly related to availability of grasses than those of 2 rarer, more restricted co-occurring species (Harrington's tateril and the rufous elephant shrew). Given this, we then sought to understand the relative contribution of between- and within-individual variation for dietary generalists, and the degree to which generalism is driven by dietary plasticity of individuals versus a population comprised of a broad spectrum of individual dietary specialists. We discuss the results of our work in the context of shifting rainfall regimes and ungulate extinctions throughout East Africa.

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Bison-mediated Seed Dispersal in a Tallgrass Prairie Reconstruction

Bison have the potential to be significant seed dispersers in prairie ecosystems. We report the seed composition found in bison dung and shed hair collected from the Neal Smith National Wildlife Refuge in Iowa. We hypothesized that seed species composition found in bison dung would be dominated by graminoid species. Shed hair was expected to contain a higher proportion of forb species than found in dung. Seeds were extracted and identified from 131 fecal samples and 40 shed hair samples collected monthly from May 2011 through April 2012. Bison dung contained a greater percentage of non-native species than native species. Greater numbers of grass seeds per gram of dung were found than forbs, sedges or rushes, but over one-half of the grass seeds extracted from bison dung were damaged by the digestive processes. Shed hair contained more native than non-native seed species and a greater proportion of forb species than was found in dung. These data will be used to create predictive models of seed dispersal by bison. Models will be used to assess the role bison may have had in the establishment and maintenance of post-glacial plant communities in the central United States, to inform current management and reconstruction of grasslands, and to evaluate the effect of bison removal from grasslands on current plant community dynamics and their ability to respond to climate change.

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Influence of an Exotic Ungulate on Community Dynamics of Wildlife at Water Sources in the Great Basin Desert

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Exotic species can have negative direct and indirect impacts on communities of wildlife. Exotic species may directly compete with native wildlife for resources or indirectly alter structure and quality of habitat for native species. These direct and indirect effects would be most apparent in areas of high community overlap or use where the potential for interspecific interactions is greatest. In arid regions, water is limiting and locations with water are likely areas of communal aggregation that may become flash points for interspecific interactions. Our objective was to compare species richness and diversity of wildlife communities at water sources with and without feral horses (*Equus caballus*) in the Great Basin Desert, Utah. We predicted that the exotic horse would negatively influence species richness and diversity of native communities using water sources. From July 2010 to August 2011, we used infrared-triggered cameras to detect mammalian and avian species at 32 water sources. We obtained 67,458 photographs of mammals (16 species) and 34,038 photographs of birds (60 species). Species richness and diversity were nearly double at water sources where horses were absent than at water sources where horses were present. Water sources and the immediate surroundings that were used by horses were typically degraded and denuded of natural vegetation (due to trampling). Our results indicate that exotic species may exclude native species from access to a limited resource.

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Mammalian Consumers Mediate the Effect of Mycorrhizae on the Establishment and Growth of a Native Perennial Bunchgrass

Mammalian herbivores can have significant effects on plant establishment, growth, and persistence. Plants that form symbiotic mycorrhizal associations may be more buffered from the effects of mammalian herbivores because mycorrhizae can increase plant nutrient uptake. We planted seedlings of a perennial native bunchgrass, *Nassella pulchra*, that were or were not inoculated with mycorrhizal fungi. Seedlings were planted within 4 enclosure treatments that allowed access by different guilds of mammalian herbivores: 1) access by all mammalian herbivores (deer, squirrels, rabbits, and voles); 2) access by squirrels, rabbits, and voles; 3) access by voles; and 4) no mammalian herbivore access. We found that mycorrhizal plants exhibited significant increases in initial size at the start of the experiment, but that differences in growth over the course of the field experiment were only apparent when plants were protected from a subset of the herbivore community. Specifically, when only voles had access to plants, mycorrhizal plants were significantly larger than non-mycorrhizal plants. Mycorrhizae did not alter plant biomass when herbivore pressure was high (treatments that allowed voles, squirrels, rabbits, and deer); that is, strong herbivore pressure eliminated the beneficial effects of mycorrhizae on plant growth. Our results illustrate how understanding the effect of herbivores on plants requires knowledge not only of which herbivores are likely to attack the aboveground portions of the plant but also knowledge of important belowground mutualisms.

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Impact of Rodents on Composition and Chemistry of Transitional Plant Communities

Rodents are often key drivers of species composition in transitional ecosystems. However, little is known about how rodents influence the chemical characteristics of plant communities. We hypothesize that rodents, through selective herbivory, can influence the composition of plant functional groups in grasslands, and subsequently, the chemical nature of plant communities. During fall 2010, we collected standing plant biomass and litter from 9 fenced and 10 unfenced plots that were established in a conservation grassland during spring 2008 at Oak Ridge Environmental Research Park, Oak Ridge, Tennessee. Distance-based multivariate analysis indicated that fenced plots have distinct and less variable plant functional group composition than unfenced plots. The functional group contributing most to these differences was C3 grasses, whose average biomass was 673% higher in fenced, relative to unfenced plots. This difference was due primarily to the selective suppression of the native C3 grass, *Tridens flavus*, by the most abundant rodent, *Sigmodon hispidus*. We predict that the substantial control imposed by rodents on community composition will lead to plant communities with enhanced recalcitrance, because the chemical attributes of unpalatable and slowly decomposing plants are similar (e.g., high C:N ratios and lignin concentrations). To test that prediction, chemical analysis of biomass is underway. If our prediction is supported, future work should focus on understanding potential indirect effects of rodent herbivory on energy and material cycling in transitional systems. This research was supported by an ASM Grants-In-Aid of Research awarded to Christopher W. Habeck in 2009.

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Habitat Associations and Assemblages of Small Mammals in Natural Plant Communities of Wisconsin

Determining habitat associations of small mammal species and environmental characteristics important for site occupancy are central to understanding species biology, community organization, and the impact of changing environmental conditions due to management treatments or climate-induced changes. Most studies of small mammal communities are conducted on a local scale and often in one habitat type, overlooking patterns manifested over a heterogeneous landscape. During the summers of 2009 and 2010, we trapped small mammals throughout Wisconsin at 180 sites among 13 natural habitats, capturing 3,261 individuals of 23 taxa. We modeled site occupancy using habitat characteristics for 16 of the most commonly caught taxa while incorporating imperfect detection and compared small mammal community similarity among habitats. Regional variation of tree density, soil moisture regimes, and winter temperatures were the most important variables in describing site occupancy of species. With the exception of *Zapus hudsonius* and *Sorex hoyi*, occupancy rates of species varied across habitats. Species-specific responses to habitat characteristics created distinct natural habitat associations leading to unique and predictable small mammal assemblages. This study demonstrates the importance of sampling across the full range of environmental and habitat gradients when determining how species are distributed and communities organized at the landscape scale.

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Habitat Characteristics Within a Zone of Separation Between the Ranges of Two Species of Pocket Gophers

Distributions of the Plains pocket gopher (*Geomys bursarius*) and the yellow-faced pocket gopher (*Cratogeomys castanops*) generally are described as parapatric. Often times as the distributions of both species approach one another a narrow gap forms where no species occur creating a zone of separation. This gap could exist because of the lack of resources in that area. The purpose of this study is to determine if habitat conditions are unsuitable within the zone of separation. Field surveys for pocket gophers took place in southwestern Kansas where both *G. bursarius* and *C. castanops* exist. Digitized maps of soil characteristics were downloaded and habitat suitability maps were produced for each species using MaxEnt (3.3.2). Soil variables that were important in predicting habitat suitability for each species was obtained from the MaxEnt output. Student *t*-tests were used to determine if habitat suitability and soil characteristics were different in the zone of separation compared to presence locations of pocket gophers. Percent sand was the most important variable in predicting habitat suitability for *G. bursarius*, while percent sand and clay were important for *C. castanops*. Habitat suitability and soil characteristics were significantly different ($p < 0.001$) between presence localities for each species and the zone of separation. These results suggest the declining habitat conditions are maintaining the zone of separation between *G. bursarius* and *C. castanops*.

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Mesocosms Designed to Investigate Ecological Facilitation Between *Ochrotomys nuttalli* and *Peromyscus leucopus*

We investigated ecological facilitation between the golden mouse (*Ochrotomys nuttalli*) and white-footed mouse (*Peromyscus leucopus*) under seminatural field conditions. Two components of facilitation were considered; activity was determined by pattern of behavior, and aggregation by determinants of animal associations. The research design encompassed duplicate enclosed mesocosms (3 by 6 by 6 m). Sheets of 20-gauge galvanized steel were anchored approximately 50 centimeters into the ground, secured with angle-iron posts, to prevent mice from escaping. Each enclosure was covered with seamless wire mesh to protect mice from predation. Each of 2 live red cedars supported 2 nest boxes 1 m and 1.5 m aboveground. Four black nest tubes were positioned midway along interior walls. A platform feeder was centered between the red cedar trees (1.25 m aboveground). Seasoned sweetgum tree trunks and wild grapevine linked each tree to the platform feeder. Two pairs of adult *O. nuttalli* and *P. leucopus* were released into each enclosure. Three Foscam IP infrared cameras digitally recorded nocturnal feeding behavior and social interaction within each enclosure. ReflectAll® coded ear tags designated species. Location and reproductive condition of each mouse were documented weekly. Combative markings were noted on individuals of both species. *O. nuttalli* circulated as a group among nesting structures within each enclosure. No *O. nuttalli* reproduced. Nesting associations and patterns of interactions will be monitored throughout spring 2013.

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Community Structure, Population Demographics, and Biomarkers in Chiroptera from Tar Creek Superfund Site, Oklahoma, USA

Bat communities within the contaminated Tar Creek Superfund Site were compared to uncontaminated sites within Oologah Wildlife Management Area for: 1) community composition and population structure; 2) behavioral impacts using a flight cage and thermographic camera; 3) levels of lead, zinc, and cadmium in fur, liver, and kidney tissues; and 4) enzyme ALA-d inhibition in response to lead accumulation. We are focusing on common species such as the red bat (*Lasiurus borealis*) and hoary bat (*L. cinereus*), which may serve as surrogates for federally listed species occurring in the same area: gray bat (*Myotis grisescens*), Indiana bat (*M. sodalis*) and Ozark big-eared bat (*Corynorhinus townsendii*). Our total of 24 bats was composed of 4 different species, including 21 red bats, and a single hoary bat, tri-colored bat (*Perimyotis subflavus*), and little brown bat (*M. lucifugus*). We are already seeing unexpected results in that 67% of animals were collected from the contaminated sites, suggesting that bat communities in these areas may be more successful than previously expected. This project will give us a better understanding of the anthropogenic impacts on bats living within a Superfund site and will inform decisions on remediation/reclamation of contaminated habitats for conservation of bats.

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Exposure and Effects of Heavy Pesticide Application on Small Mammals Inhabiting an Arid Agroecosystem in Xinjiang Province, China

Small mammals have proven to be reliable bioindicators of environmental conditions and serve as useful models in predicting possible ecological and human impacts. We conducted a field study using small mammals naturally occurring in grape vineyards to examine possible exposure and effects of heavy pesticide application. Four grape vineyards with heavy pesticide application, and 2 control sites without any pesticide application, were trapped for 5 nights, and 133 small mammals of 6 species were captured. Triplicate soil and plant samples were taken at each small mammal capture site for pesticide residue analysis. Small mammals were returned to the lab and standard data were taken for each animal. The herb field mouse (*Apodemus uralensis*) was the only species caught in large enough numbers for statistical analysis. Results indicated that significantly more males than females were captured from both grape vineyards and control sites. Mice of both sexes from grape vineyards had greater body mass than those from control sites. Further, mice of both sexes from the grape vineyards were significantly less reproductively active compared to those from control sites, particularly the males. Pesticides used in grape vineyards included at least 16 different fungicides and several insecticides and herbicides, many of which are banned in the US and Canada. Pesticide residue analysis currently is ongoing. Available data indicate that pesticides exerted sublethal effects on exposed small mammals.

251 Capstone Symposium: Ungulates Today, Salon E, Tuesday 18 June 2013

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Evolution of Ungulate Mating Systems: Sociality, Resources, and Terrain

Quality and distribution of resources likely shape mating systems of ungulates. Further, sociality, and hence the ability of males to sequester mating opportunities from females, may be limited by steep or broken terrain. We developed a model to explore pathways of evolution for diverse ungulate mating systems based on environmental attributes. The model begins with habitat structure shaping degree of sociality for ungulates via mechanisms associated with predation risk. If habitat structure is closed (forested), and if resources are of sufficient quality and can be defended, we predict the evolution of a pair territory; where defense is less practical, a tending bond should evolve. In more open habitats with sufficient resource quality and defensibility, population density may be a critical factor. Where density is comparatively low, a polygynous resource territory is predicted; where density is high, a lek

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may evolve, although that system does not require defense of resources. In open habitats with low resource quality, rugged terrain may promote a tending bond, whereas in level areas the size of groups may be critical; extremely large groups, which cannot be monopolized by a single male should exhibit a tending bond, and smaller groups are expected to evolve a harem mating system. In level terrain and at high density, leks also may evolve. We provide examples that illustrate these pathways among and within species of ungulates.

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Conservation Genetics of Ungulates: How Far We've Come

Before “conservation genetics” was a term in our lexicon, Smith et al. (1976) published a review of the nascent field of genetic applications in wildlife management, focusing on, among other topics, allozyme variation in white-tailed deer (*Odocoileus virginianus*). Since then, massive leaps forward in genetic technology and theory have increased the power of our inference and the subjects we can address in ungulate ecology and evolution. Nonetheless, we continue to be intrigued by the effects of harvest on populations, use of genetics in identification of management units and in endangered species management, and what spatial variation in genetic markers tells us about population processes. Heterozygosity-fitness correlations have given way to examination of harvest-mediated changes in quantitative characters, which indicates that selectively targeting harvest on trophy males can alter phenotypes for fitness-related traits. Phylogenetic relationships within and among threatened and endangered species have been clarified by DNA sequencing and taxonomy has subsequently been revised but taxonomic inflation remains a major concern for conservation. Population-level processes can now more easily be probed by application of coalescent theory, which connects phylogeny and demography, and Bayesian approaches allow population assignment and detection of hybridization with other native species, exotics, or domestics. New spatial analytical approaches reveal social behavior, and genomic and metagenomic approaches provide promise for the future.

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From Rhetoric to Results: Making Captive Ungulate Populations Relevant to Conservation Efforts

Captive breeding programs can play an important role in the conservation of hoofed mammals; indeed, several ungulate species would otherwise now be extinct. However, sustaining viable *ex situ* hoofstock populations is a challenge for modern zoos. Changing business models and public expectations have resulted in fewer ungulate exhibits and smaller populations. Simultaneously, taxonomic revisions have cast doubt on the intrinsic conservation value of many existing breeding programs. To stay relevant, the zoo community is responding with a multifaceted approach to ungulate stewardship. Internal campaigns seek to increase the space in zoos for conservation-dependent species, and trials with innovative husbandry and genetic management practices aim to maximize breeding success with the limited resources available. Other initiatives pursue links between zoos and *in situ* research and stewardship projects, recognizing that funding and expertise can extend the impact of captive ungulate populations (even those of low genetic value) beyond the zoo community. The recent recovery program for the critically endangered Visayan warty pig (*Sus cebifrons*) exemplifies this holistic approach to ungulate conservation, with taxonomically-robust *ex situ* populations, direct connections to projects on the Visayan Islands, and strong institutional support for both. This paradigm shift is increasingly prominent as modern zoos accept the limitations of captive breeding and embrace these new initiatives, exchanging assumptions of conservation value for meaningful contributions to global ungulate stewardship.

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Colin P. Groves Keynote Speaker

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Carl Meets Karl: The Case for Testability in Ungulate Taxonomy

For the founder of systematics, Carl Linnaeus, species were a “given,” with Aristotelian essences. Since the general acceptance of evolution as the basic principle of biology, a new characterization of species has had to be sought. In the 1930s and 1940s, Theodosius Dobzhansky and Ernst Mayr proposed the so-called Biological Species Concept (BSC), whereby species are “actually or potentially interbreeding natural populations which are reproductively isolated from other such populations.” G. G. Simpson in 1963 proposed the Evolutionary Species Concept (ESC), under which species are regarded as having their own evolutionary roles and tendencies. From about the 1970s onward, systematic biologists became more and more dissatisfied with the BSC and many of them, feeling that the ESC is close to the crux of what a species actually is, began to search for a way to operationalize it. And so was born the Phylogenetic Species Concept (PSC), in which a species is characterized above all by its diagnosability.

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The philosopher Karl Popper maintained that, to be truly scientific, a proposition must be testable. I have argued elsewhere, for example in *Primate Taxonomy* (Groves, 2001), that the PSC is the only “species concept” under which species are truly testable. In *Ungulate Taxonomy* (Groves and Grubb 2011), the PSC was for the 1st time applied to the Perissodactyla and Artiodactyla, and we reiterated arguments that testability is essential to alpha taxonomy. Our resulting taxonomic scheme just about doubled the number of species recognized in ungulates, and this has proved unwelcome to quite a number of mammalogists (see, for example, Zachos et al. 2012 in *Mammalian Biology*), although no argument against the general principle has been advanced: rather, detractors have promoted the merits of the sort of untestable schema dignified only by time (approximately since 1951, when Ellerman and Morrison-Scott’s *Checklist of Palaearctic and Indian Mammals* was published). In this presentation, I will outline some of the arguments and present some key case studies in ungulate alpha taxonomy.

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LOCAL RESTAURANTS

The following is a list of superb and diverse array of restaurants that are within a 6-block walking radius of the Philadelphia Marriott Downtown Hotel. While there are many incredible restaurants covering all types of ethnicities beyond the 6-block radius, if you choose to stay within the 6-block walking radius of the hotel, feel free to utilize this list. If there is a cuisine that you do not see here, or would like reservations secured for a restaurant that is on the list (or for one not on the list and/or beyond the 6-block radius), please feel free to email the director of concierge services prior to your arrival – Matt.Harris@marriott.com. Thank you for choosing the Philadelphia Marriott Downtown as your home away from home while you are in Philadelphia, one of America's most walk-able, historic cities, and forever known as "The City of Brotherly Love."

Steak

Morton's
1411 Walnut St. – 4 ½ blocks away

Capital Grille
1338 Chestnut St. – 2 blocks away

Butcher & Singer
1500 Walnut St. – 5 blocks away

The Palm
200 S. Broad St. – 4 blocks away

Del Frisco's
1426 Chestnut St. – 3 blocks away

Fogo de Chao (Brazilian)
1337 Chestnut St. – 2 blocks away

Italian

Amis
412 S. 13th St. – 6 blocks away

Table 31 (Italian/Steakhouse)
1701 JFK Blvd. – 5 blocks away

Davio's (Italian/Steakhouse)
111 S. 17th St. – 6 blocks

Maggiano's
1201 Filbert St. – across the street

LaScala's
615 Chestnut St. – 6 blocks away

Mercato (Bring Own Bottle – cash)
1216 Spruce St – 6 blocks away

Varalli
231 S. Broad St. – 6 blocks away

Walnut St. Supper Club
1227 Walnut St. – 3 ¼ blocks away

Mediterranean/Greek

Estia (Greek)
1407 Locust St. – 5 blocks away

Barbuzzo (Mediterranean)
110 S. 13th St – 2 ½ blocks away

Opa (Greek)
1311 Sansom St. – 3 blocks away

Kanella (Greek – Bring Own Bottle)
1001 Spruce St. – 6 blocks away

Spanish/Latin/Mexican

El Vez (Contemporary Mexican)
121-23 S. 13th St. – 2 blocks away

Tequila's (Traditional Mexican)
1602 Locust St. – 6 blocks away

Lolita (Mexican – Bring Own Bottle – cash)
106 S. 13th St. – 2 blocks away
Reservations are Sunday – Thursday; no reservations accepted for Friday or Saturday nights; for Friday or Saturday days, reservations only for parties less than 6 persons.

Alma De Cuba (Cuban)
1623 Walnut St. – 6 blocks away

Jamonera (Spanish)
105 S. 13th St. – 2 blocks away

Seafood

McCormick & Schmick's
1 S. Broad St. – 2 blocks away

Oyster House
1516 Sansom St. – 5 blocks away

Fish
1234 Locust St. – 4 blocks away

The Farm and the Fisherman (Bring Your Own Bottle)
1120 Pine St. – 6 blocks away

Asian/Japanese/Chinese

Sampan (Asian/Pan-Asian)
122 S. 13th St. – 2 ½ blocks away

Tazia (Asian/Asian Tapas)
101 N. 11th St. – 2 blocks away

Morimoto (Japanese)
723 Chestnut St. – 6 blocks away

Raw (Japanese Sushi/Sake)
1225 Sansom St. – 2 ½ blocks away

Makiman Sushi (Japanese)
1326 Spruce St. – 5 blocks away

Erawan (Thai)
925 Arch St. – 4 blocks away

Aqua (Thai)
705 Chestnut St. – 6 blocks away

Penang (Malaysian)
117 N. 10th St. – 3 blocks away

Rangoon (Burmese)
112 N. 9th St. – 3 ½ blocks away

Joy Tsin Lau
1026 Race St. – 4 blocks away

Banana Leaf (Malaysian)
1009 Arch St. – 3 blocks away

Chifa (Cantonese/Peruvian/Latin Am.)
707 Chestnut St. – 6 blocks away

Spice 28 (Chinese)
1228 Chestnut St. – 2 blocks away

French

Caribou Cafe
1126 Walnut St. – 3 blocks away

Zinc
246 S. 11th St. – 4 blocks away

Amuse (Meridian Hotel)
1426 Arch St. – 2 ½ blocks away

Le Bec Fin
1523 Walnut St. – 5 blocks away

Vegetarian

Vedge
1221 Locust St. – 4 blocks away

Indian

Palace at the Ben
834 Chestnut St. – 4 blocks away

American

10 Arts
10 Avenue of the Republic – 2 blocks away

Bliss
220 S. Broad St. – 3 ½ blocks away

The Corner
102 S. 13th St. – 2 blocks away

Marathon Grill
121 S. 16th St. – 6 blocks away

Nineteen
200 S. Broad St. – 5 blocks away

R2L – Two Liberty Place 37th Floor
50 S. 16th St. – 3 ½ blocks away

Time
1315 Sansom St. – 2 ½ blocks away

Smokin Betty's
1113 Walnut St. – 4 blocks away

The Farmer's Cabinet
116 S. 11th St. – 3 blocks away



Inspiring the World through Green Meetings

Marriott International aspires to be the global leader that demonstrates how responsible hospitality management can be a positive force for the environment and create economic opportunities around the world, in the communities where we work and live!

Marriott Hotels and Resorts

- Replaced light bulbs with energy-efficient bulbs
- Installed low-flow showerheads and toilets
- Introduced water/energy saving linen program
- Operates the most ENERGY STAR® certified properties in the industry, as part of Marriott's portfolio of brands
- Involves its global workforce in eco-volunteerism

Meetings and Events

- 100% Recycled Note Pads
- Pens made from Recycled materials
- Eco-Friendly Water Service
- Meeting Room Recycling, where available
- On-Line Event Menus
- Organic Flowers (upon request)
- America's Second Harvest, where available
- Recyclable Box Lunch Program
- Paperless billing
- Linen-free buffet tables
- Green Meeting Room Level

Philadelphia Marriott

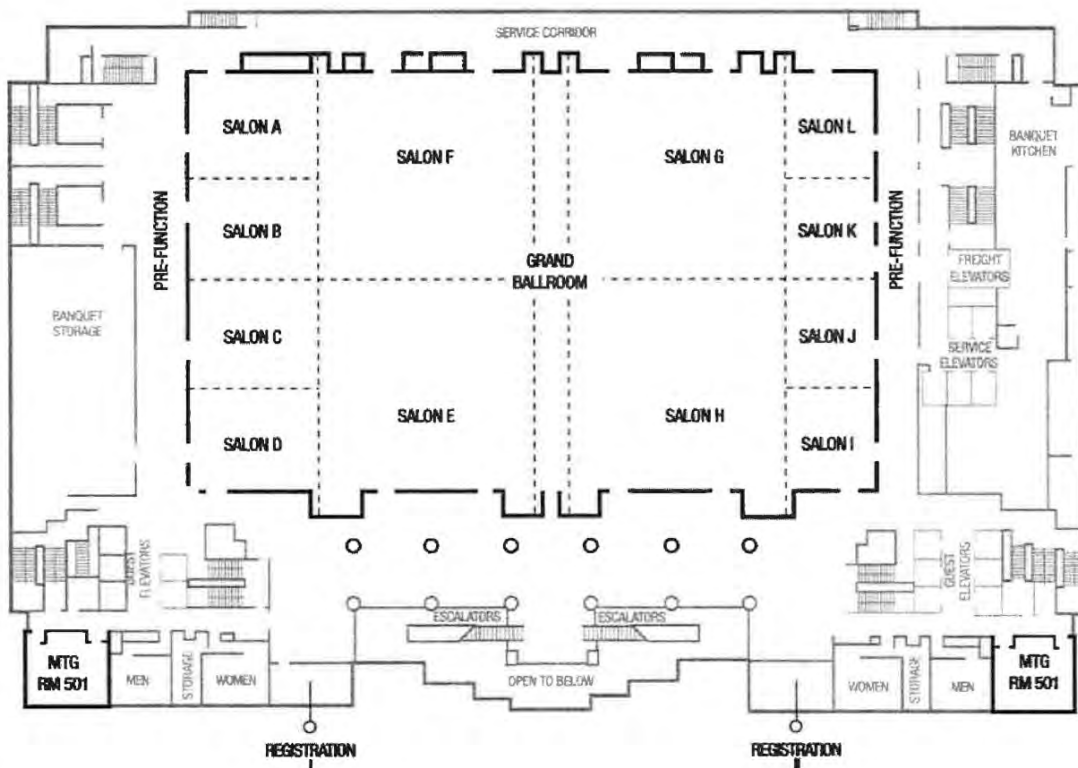
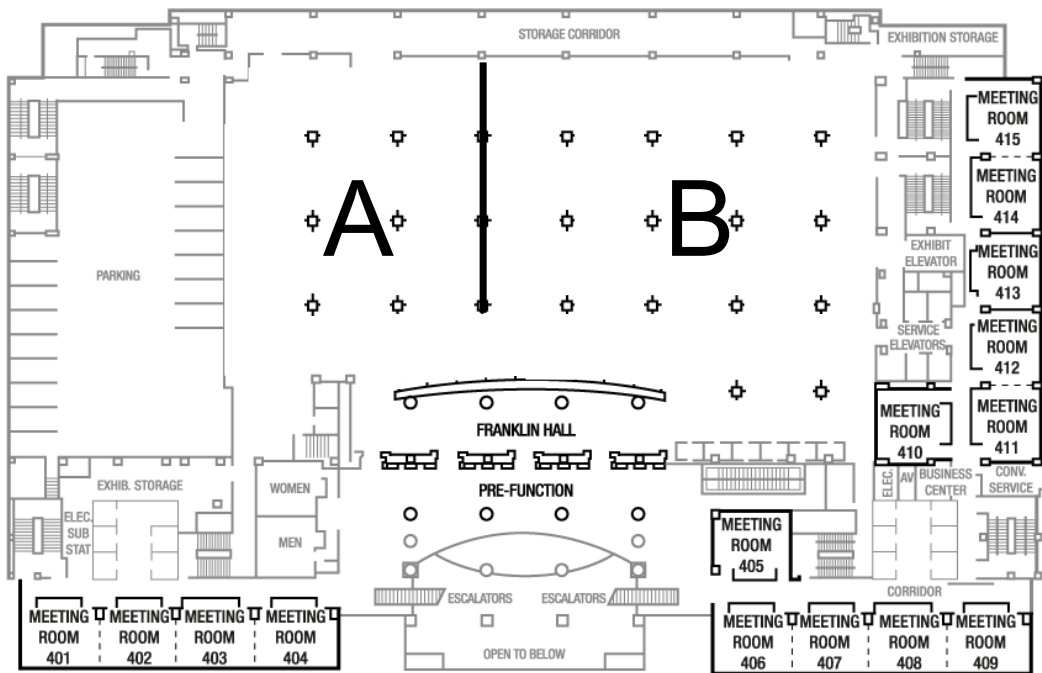
- Hotel is located within 1 block of public transportation
- Bed Linen replaced on as needed basis for stay over guests
- Recycle all batteries, oils, paints and refrigerants
- Recycle all used fluorescent light bulbs
- Uses only post-consumer paper
- 100% Smoke free environment
- Maintain permanent, reusable "pre-filters"
- Use only eco-friendly cleaning supplies throughout the hotel
- Water saving showers heads in all guest rooms
- Water conserving 1.6pgf toilets in all guest rooms
- Vending machines utilize motion sensors for energy reduction
- Motion sensor and timed light switches in all offices and storage rooms
- Sensors and water conserving faucets in all public restrooms
- Florescent lighting throughout meeting areas
- Starbucks uses recyclable cups from post consumer paper

Learn about Marriott's green programs by visiting marriott.com/environment

Contact us to make your next meeting green.



Following the conclusion of the meeting, be sure to stop by ASM's Registration Desk to drop off your badge and lanyard—ASM is striving to recycle as many meeting materials as possible.



2014 Meeting Announcement

Annual Meeting of the
American Society of Mammalogists
6-10 June 2014

Oklahoma City Renaissance Hotel and Cox Convention Center
Oklahoma City, Oklahoma



The 2014 American Society of Mammalogists Annual Meeting logo features a Pronghorn (symbol of the ASM) with an abstracted Oklahoma City skyline, and water representing the Oklahoma River and Bricktown Canal. The arrangement suggests OKC's historic Art Deco architecture and new architecture like the Devon Tower, Scissortail Bridge, and Oklahoma River bathhouses. The logo was designed by Hadley Jerman, Graphic Designer at the Sam Noble Museum in Norman, Oklahoma.



Scan the QR Code above for a preview of all the 2014 meeting will have to offer!

