18th **IBRC**

28 JULY - 1 AUGUST 2019

THE SLATE, PHUKET, THAILAND

PRINCESS MAHA CHAKRI SIRINDHORN PSU NATURAL HISTORY MUSEUM PRINCE OF SONGKLA UNIVERSITY

PSU PRINCE OF SONGKLA UNIVERSITY

Harrison Institute

18th International BAT RESEARCH CONFERENCE

IBRC 2019

PRINCESS MAHA CHAKRI SIRINDHORN NATURAL HISTORY MUSEUM
PRINCE OF SONGKLA UNIVERSITY

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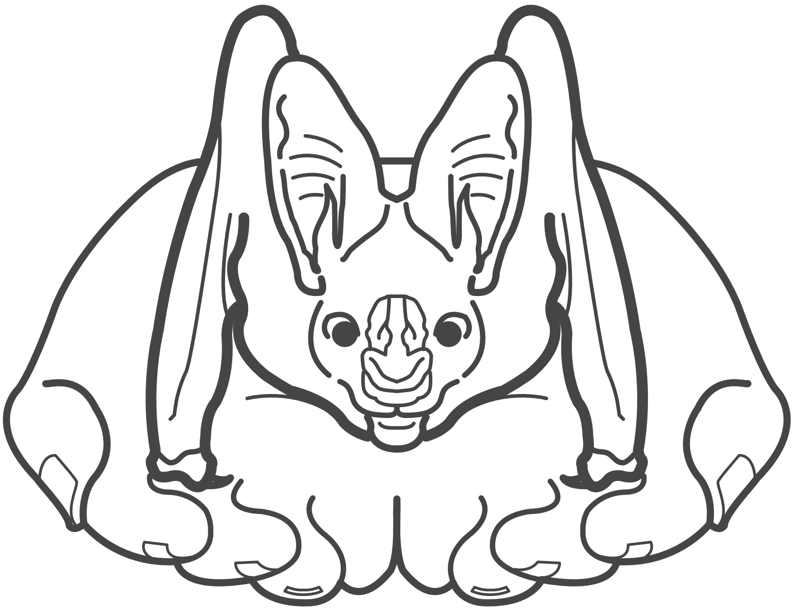

18th IBRC

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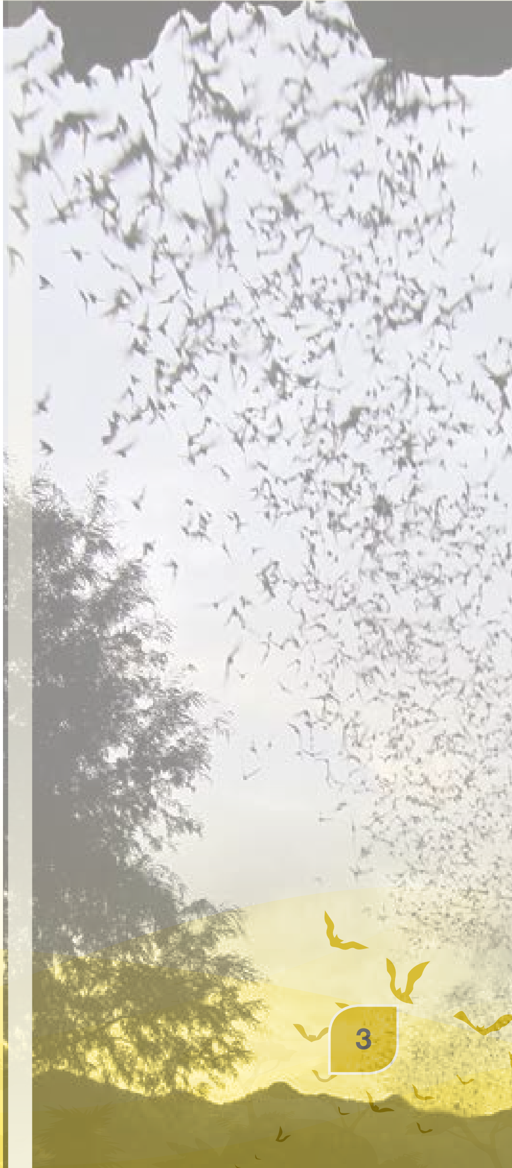


WELCOME MESSAGE

On behalf of the 18th IBRC organising committee, it gives me great pleasure to welcome you all to Phuket and to this international conference on bat research and conservation. I hope it will prove to be a fascinating week of talks, discussions, and workshops.

Thailand has always prided itself on its hospitality and therefore I am extremely pleased to learn that the organising committee of the Prince of Songkla University has extended its hand of friendship to delegates from all over the world. With scientists and students coming from North, Central and South America, Africa, Australia/Oceania, Europe and Asia, it will indeed be a fertile melting pot of ideas and one that will hopefully lead to diverse and fruitful research in the future.

For sure, research in the 21st century can never be carried out in isolation. We cannot, and should not, work in our little 'ivory towers', whether it be within our own universities or even our own countries. Today, research and especially scientific research, is a thing of joint endeavour, where through mutually beneficial collaboration, the smartest of brains and the richest of cultures meet and work together for the common good.

All here at the Prince of Songkla University are happy to be part of this global network of smart people, smart ideas, smart projects and smart on-going programmes of research. I am therefore extremely pleased to see that the Faculty of Science, and particularly the Princess Maha Chakri Sirindhorn Natural History Museum, is the lead organiser of this international conference. I am proud that this museum, which hosted the first 'Southeast Asian Bat Conference' in 2007 and the first 'Ornithological Congress of Southeast Asia' in 2012, is reinforcing the on-going message that the Prince of Songkla University is actively participating in the world of science and is open to international collaboration.

And what of the bats themselves? Many here in Thailand know relatively little about them. Too little, it seems, as I have already learnt what amazing creatures they are. To me, it seems extraordinary that something so small, and with its nocturnal habits almost invisible to humans, should have such a wonderful natural history, such a rich evolutionary history, and should play such a key role in helping man and nature through its 'ecosystem services' of pollination, seed dispersal and pest control.

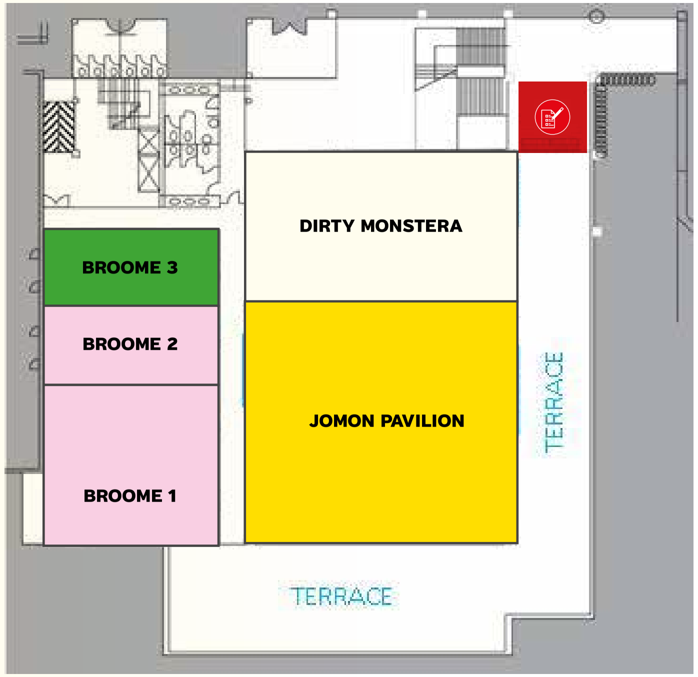
In Thailand, we have a strong tradition of studying bats. Dr. Kitti Thonglongya (1928-1974) was one of our most famous naturalists and did so much to teach about the birds and mammals of our country. He discovered the world's smallest mammal and it was in his honour that is named Kitti's hog-nosed bat (*Craseonycteris thonglongyai*). In the Prince of Songkla University, we too have an expanding team of international bat specialists. Two have already won global awards in North America for the quality of their research – both ecological and taxonomic. And, in the tradition of the great Kitti, scientists from our Natural History Museum are not only describing the biodiversity of our country but are also discovering new species, including 11 species and one new genus of bat from Thailand and its neighbouring countries.

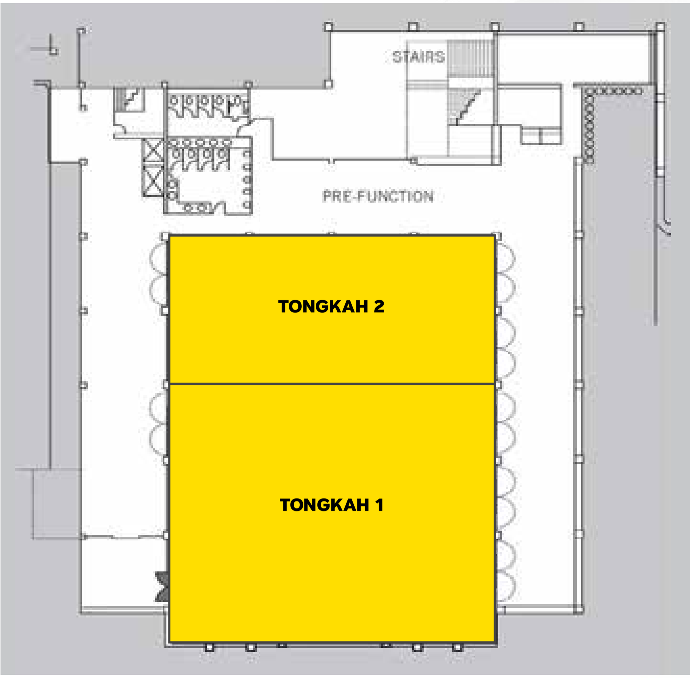
I wish you a very pleasant stay in Phuket. I hope that the 18th IBRC will be interesting and invigorating but also a little relaxing. I hope you will leave with new friendships and inspired with a desire to do yet more collaborative research of the highest quality. For those of you who have not been to Thailand before, I hope you will leave with a love of our beautiful country and its culture and an enhanced understanding of the hospitality of its people. I hope we will see you again in the Prince of Songkla University and, in the future, we can work together on a range of new and exciting projects.

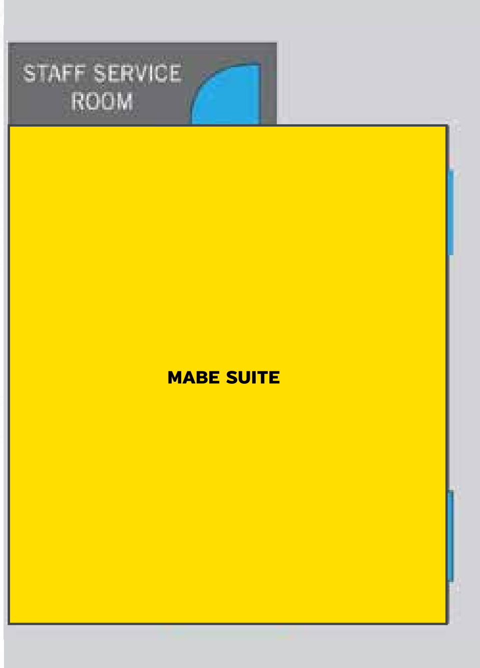
N. Keawpradub

Asst. Prof. Dr. Niwat Keawpradub
President, Prince of Songkla University

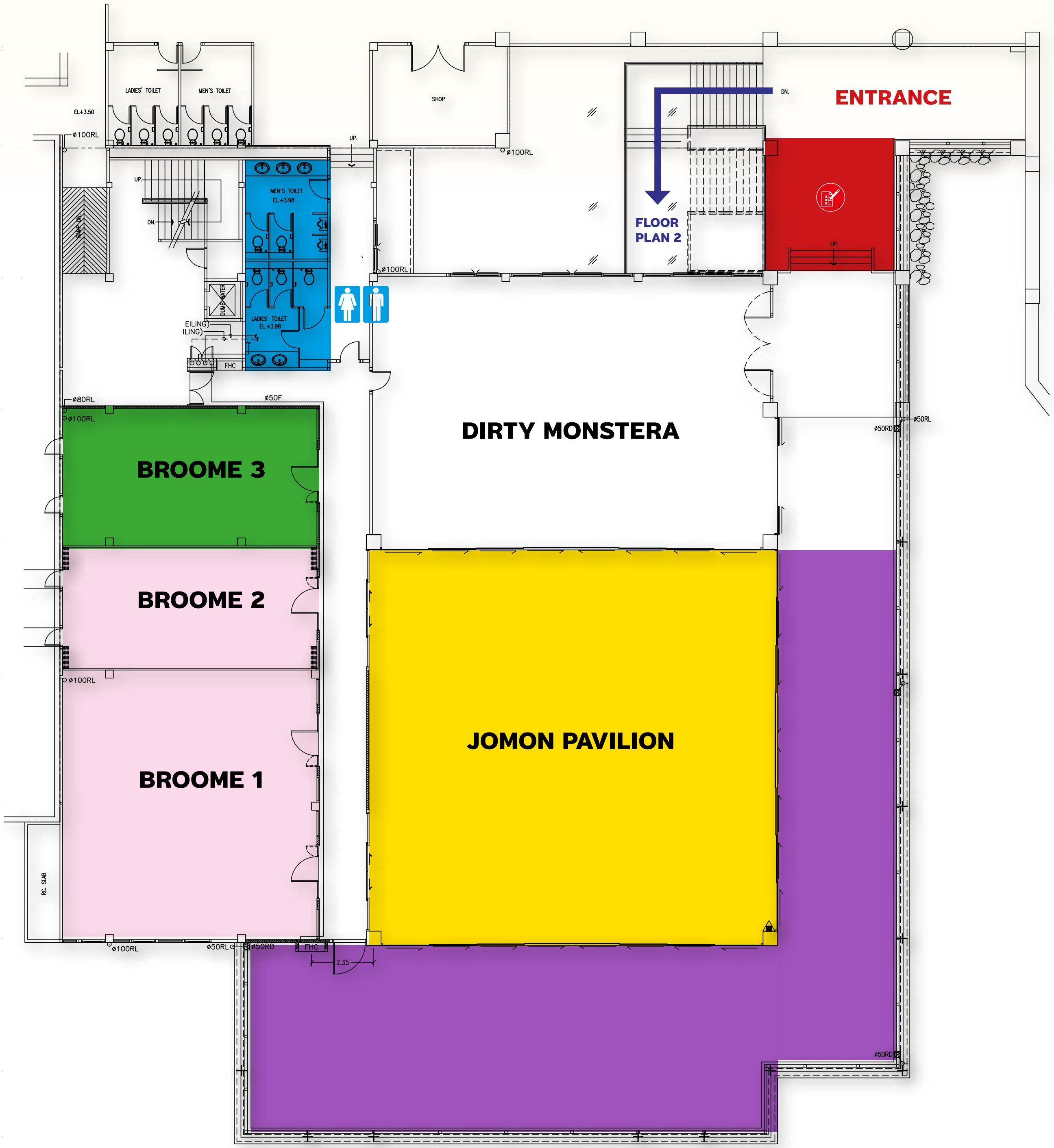
FLOOR PLANS


DIRTY MONSTERA
BROOME 3
BROOME 2
JOMON PAVILION
TERRACE
BROOME 1
TERRACE


STAIRS
PRE-FUNCTION
TONGKAH 2
TONGKAH 1


STAFF SERVICE ROOM
MABE SUITE

FLOOR PLAN 1



REGISTRATION
INFORMATION COUNTER

TOILET

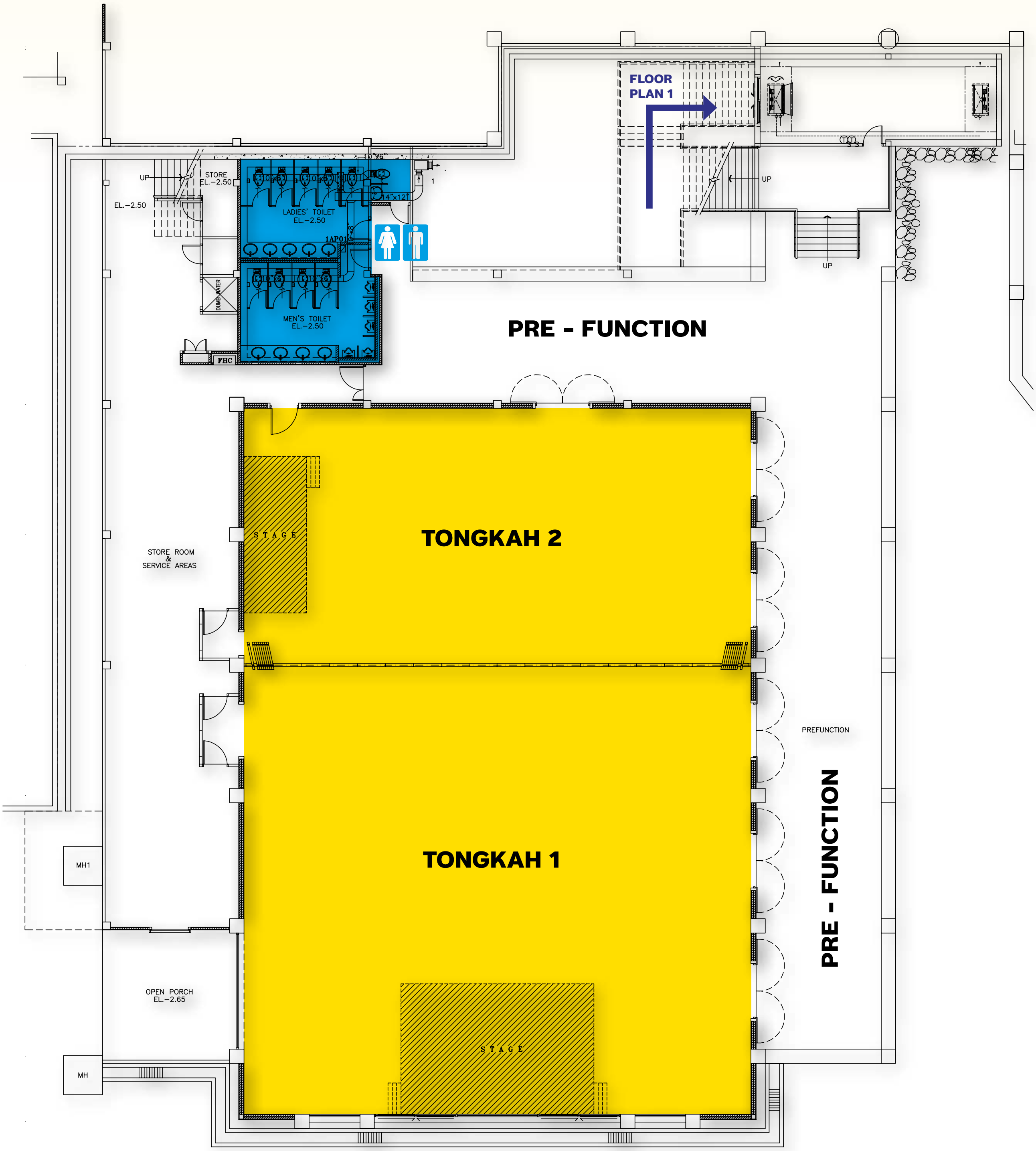
🟨 **POSTER AND SPONSOR BOOTHS**

🟩 **STAFF ROOM**

🟪 **REFRESHMENT / COFFEE BREAK**

■ **WORKSHOPS & PARALLEL SESSIONS**

FLOOR PLAN 2



🚻 TOILET

🟨 CONVENTION HALL & PARALLEL SESSIONS

ABOUT THE CONFERENCE

from the IBRC organising committee
18th International Bat Research Conference (IBRC) 2019

Every three years, some of the best and brightest scientists and students in bat research and conservation come together for the IBRC. The 18th IBRC in Phuket is no exception and we are delighted to host 400 delegates who will, over the course of the week, deliver some 230 oral presentations and 70 poster presentations.

Through the kindness and generosity of the owner of The Slate, a long-term supporter of the Prince of Songkla University, we have been able to meet in a place of great serenity and beauty. In addition, we are just a stones-throw from the waters of the Andaman Sea and adjacent to the Sirinat National Park, which includes forest, an extensive marine area, and Phuket's longest beach. We hope all of this will contribute to your enjoyment and to the quality of the experience. We therefore thank all at The Slate and all our sponsors for making this possible. We also thank those in the Prince of Songkla University and especially the Princess Maha Chakri Sirindhorn Natural History Museum for their tireless work in helping to make the conference come together.

Having read the abstracts, it is clearly apparent that the scope of the research to be discussed is more than impressive. The breadth of the topics is remarkable, and the quality of the abstracts is exceptional. In addition, we have four key-note speakers who are world experts in their fields and whose topics are fascinating and relevant. For sure, bat research is in a very healthy place.

It is also certain that for all delegates the overriding problem will not be – is there enough to keep me interested? But rather, how do I get to see all the presentations that fascinate me/or might fascinate me, especially those in different parallel sessions? And, for the presenters, it will be – how can I say everything I want to say in such a tiny slither of time (12 minutes). As organisers, we sympathise with all of you and have been no easy answers – a longer conference is too expensive – significantly reducing the number of speakers is less inclusive and less of a forum for the exchange of ideas. For presenters, we thank you in advance for your discipline. Your presentation is your 'marketing slot'. Your 12 minutes is your moment to advertise and to summarise the key points of your study in front of a global audience. It can be no more. For everyone, we rely on your discipline. Without good, disciplined timekeeping, this conference will struggle.

Finally, as organisers with a love of bats, we ask all of you to join forces once again to promote their conservation. Future generations will look back at us and say 'When nature was so clearly under threat, what did the bat researchers do to help protect it? What did they study? How did they communicate to the public and to the decision-makers about the wonders of nature and about the extraordinary things that bats do every day? Did they help enthuse the young; did they involve local communities in their studies; did they explain adequately and appropriately to decision makers, farmers and the general public about the ecosystem services that bats perform for the natural environment and for humans? Did they highlight the threats to such a diverse group of mammals?'

As bat researchers, we know that those of us who study nature have a duty to help conserve nature. The future of bats is in our hands. Together we can embrace this responsibility and share the wonderful world of bats with the broader public.

We wish you a great stay in Phuket and hope that the 18th IBRC is both valuable and enjoyable for you all.

The 18th IBRC Organising Committee
Prince of Songkla University, Thailand / Harrison Institute, UK

DATE AND VENUE:

28 July – 1 August 2019 at The Slate, Phuket, Thailand

Organised by:

Princess Maha Chakri Sirindhorn Natural History Museum, Prince of Songkla University, Thailand

Harrison Institute, United Kingdom

Supported by:

Prince of Songkla University

Faculty of Science, Prince of Songkla University

The Slate, Phuket, Thailand

Event location:

EVENT	LOCATION
Main conference	Tongkah 1+2
Parallel sessions	Tongkah 1, Tongkah 2, Broome 1, Broome 2
Workshop	Tongkah 1, Tongkah 2, Broome 1, Broome 2
Presentation file uploading	via Google Drive
Poster and sponsor booths	Jomon Pavilion
Registration counter	Dirty Monstera Hall
Staff room	Broome 3
Refreshment	Jomon Pavilion - foyer
Lunch	Tin Mine exclusive Mabe Suite
Welcome Dinner	Coliseum Lawn BU: Tin Mine

Name badges:

All participants are requested to wear the name badge at all times in order to enter the conference area and to participate in all arranged events, i.e. lunch, dinner.

For participants who stay at Nai Yang Beach Resort and all other hotels, please also wear your name badge at all time to make sure the security of the Slate can identify you and allow you to enter the hotel.

Social Programs:

All participants are welcome to join the Opening Ceremony, Welcome Dinner, Student Award Announcement and Closing Remark.

Opening Ceremony

Date: **July 29, 2019**
Time: 09.00 - 09.30
Location: Tongkah 1+2

Welcome Dinner

Date: **July 29, 2019**
Time: 18.45 - 21.30
Location: Coliseum Lawn
(BU: Tin Mine)
(Cultural show: Khon Performance,
performed by students from
Prince of Songkla University,
Trang Campus)

Student Presentation Awards Announcement and Closing Remark

Date: **August 1, 2019**
Time: 11.15 - 12.30
Location: Tongkah 1

SCIENTIFIC COMMITTEES

Pipat Soisook	Prince of Songkla University	Thailand
Paul J. J. Bates	Harrison Institute	UK
Paul A. Racey	University of Exeter	UK
Nancy B. Simmons	American Museum of Natural History	USA
Tigga Kingston	Texas Tech University	USA
Tanja Straka	Leibniz Institute for Zoo and Wildlife Research	Germany
Rodrigo Medellin	Universidad Nacional Autónoma de México	Mexico
Kyle Armstrong	South Australian Museum	Australia
Neil Furey	Independent	Cambodia
Joe Chun-Chia Huang	Southeast Asian Bat Conservation and Research Unit, Taiwan	Taiwan
Juliana Senawi	Universiti Kebangsaan Malaysia	Malaysia
Faisal Anwar Anwarali Khan	Universiti Malaysia Sarawak	Malaysia
Thong Vu Dinh	Vietnam Academy of Science and Technology	Vietnam

LOCAL ORGANISING COMMITTEES

Assoc. Prof. Dr. Chutamas Satasook
Dr. Pipat Soisook
Dr. Phannee Sa-ardrit
Dr. Abdulloh Samoh
Mrs. Natrada Mitpuangchon
Miss Awatsaya Pimsai
Mr. Rueangrit Promdam
Mr. Natjadee Dorloh
Mr. Monrach Intarasiri
Miss Chiraporn Tepchinda
Miss Sakeenah Ha-u-ra
Miss Pemika Thongpeng

PROGRAM AT A GLANCE

Day 1: **Sunday, 28 July 2019**

Time	Venue & Session	
13.30 - 16.30	Broome 1	Wildlife Acoustics Workshop: Hands-on training on Song Meter SM4BAT FS
	Broome 2	SEABCRU Call Library Workshop-Implementation of acoustics to fill the gaps of bat biodiversity information for Southeast Asia
14.30 - 17.30	Dirty Monstera Hall	Registration
	Jomon Pavilion	Poster set up

PROGRAM AT A GLANCE

Day 2: **Monday, 29 July 2019**

Time	Venue & Session			
08.00 - 09.00	Dirty Monstera Hall	Registration		
09.00 - 09.30	Tongkah 1+2	Opening & welcome remarks + group photo		
09.30 - 10.10	Tongkah 1+2	Keynote speaker 1: ***Emma Teeling*** 'Growing old yet staying young: do bats hold the secret of extended longevity?'		
10.10 - 10.40	Jomon Pavilion	Refreshment & Poster		
10.40 - 12.40	Tongkah 1	Tongkah 2	Broome 1+2	
	Molecules and Morphology Reveal the Basis of Bat Evolutionary History and Unique Adaptations	Old World Fruit Bat Ecology and Conservation	Taxonomy, Diversity and Monitoring	
12.40 - 13.45	Lunch & Poster			
13.45 - 15.45	Tongkah 1	Tongkah 2	Broome 1+2	
	Phylogeny and Evolution	Old World Fruit Bat Ecology and Conservation	Taxonomy, Diversity and Monitoring	
15.45 - 16.05	Jomon Pavilion	Refreshment & Poster session*		
16.05 - 17.35	Tongkah 1	Tongkah 2	Broome 1+2	
	Phylogeny and Evolution (*17.00 - 18.30 Prep for dinner*)	Conservation	Taxonomy, Diversity and Monitoring	
18.45 - 21.30	Coliseum Lawn (BU: Tin Mine)	-Welcome dinner -Fund raising for student researches on bat conservation in SE Asia		

* Students should be presented at their posters during this session.

PROGRAM AT A GLANCE

Day 3: **Tuesday, 30 July 2019**

Time	Venue & Session			
08.30 - 09.10	Tongkah 1	Keynote speaker 2: ***Kevin Olival*** ‘Bat viral ecology: past, present, and future’ (+5 min transition)		
09.15 - 10.15	Tongkah 1	Tongkah 2	Broome 1	Broome 2
	Win-win Solutions for Emerging Infectious Disease Surveillance and Bat Conservation	Human Dimensions of Bat Conservation: Conflict, Drivers and Solutions	Diet and Foraging Ecology	Phylogeny and Evolution 2
10.15 - 10.30	Jomon Pavilion	Refreshment & Poster		
10.30 - 12.30	Tongkah 1	Tongkah 2	Broome 1	Broome 2
	Win-win Solutions for Emerging Infectious Disease Surveillance and Bat Conservation	Flying Foxes Hunting and Conservation in SE Asia	Diet and Foraging Ecology	Phylogeny and Evolution 2
12.30 - 13.30	Lunch & Poster			
13.30 - 14.00	Tongkah 1	Special lecture: ***Hans-Urich Schnitzler*** ‘Burst Echolocation: Another strategy of bats to detect fluttering insects in clutter’		
14.00 - 16.00	Tongkah 1	Tongkah 2	Broome 1	Broome 2
	Disease Ecology and Parasitology	Bioacoustics 1	Diet and Foraging Ecology	Behaviour and Community Ecology
16.00 - 16.20	Jomon Pavilion	Refreshment & Poster session*		
16.20 - 19.00	Tongkah 1	Tongkah 2	Broome 1	
	Workshop:Bat1K-Initiative to Sequence to Chromosome Level Assembly the Genome of Every Species of Living Bat	Titley Scientific Acoustic Workshop	Workshop: Bat House DIY	

* Students should be presented at their posters during this session.

PROGRAM AT A GLANCE

Day 4: **Wednesday, 31 July 2019**

Time	Venue & Session		
08.30 - 09.10	Tongkah 1	Keynote speaker 3: ***Tanja Straka*** 'All Eyes on Bats: Why Understanding People benefits Bat Conservation' (+5 min transition)	
09.15 - 10.15	Tongkah 1	Tongkah 2	Broome 1+2
	White-nose Syndrome and Disease Ecology	Bioacoustics 2	Roosting Ecology
10.15 - 10.30	Jomon Pavilion	Refreshment & Poster	
10.30 - 12.30	Tongkah 1	Tongkah 2	Broome 1+2
	White-nose Syndrome and Disease Ecology	Bioacoustics 2	Roosting Ecology
12.30 - 13.30	Lunch & Poster		
13.30 - 15.30	Tongkah 1	Tongkah 2	Broome 1+2
	Microbiome and Ectoparasite	Bioacoustics 2	Movement, Activity and Reproductive Biology
15.30 - 15.50	Jomon Pavilion	Refreshment & Poster	
15.50 - 17.50	Tongkah 1	Tongkah 2	Broome 1+2
	Wildlife Acoustics Workshop 2: Hands-on Training on Song Meter SM4BAT FS	Workshop: Student and Early Career Scientist Mental Health	Movement, Activity and Reproductive Biology
17.50 - 20.00	Bat Walk + Equipment demonstration (brought to you by Wildlife Acoustics)		

PROGRAM AT A GLANCE

Day 5: **Thursday, 1 August 2019**

Time	Venue & Session		
08.30 - 09.10	Tongkah 1	Keynote speaker 4: ***Sara Bumrungsri*** 'Ecosystem services of insectivorous bats in Southeast Asia' (+5 min transition)	
09.15 - 11.00	Tongkah 1	Tongkah 2	Broome 1+2
	Ecosystem Services	Bats Mortality and Conservation Solutions	Adaptation and Climate/Environmental Change
11.00 - 11.15	Jomon Pavilion	Refreshment	
11.15 - 12.30	Tongkah 1	Student awards and Closing remark	
12.30 - 13.40	Lunch		

Post conference activities:

1) 2-5 August 2019: 'Post conference trip' at Ratchaburi and Kanchanaburi provinces, Thailand

2) 2-6 August 2019: 'Paleotropical Bat Ecology and Conservation' at Prince of Songkla University, Hat Yai, Songkhla Province, Thailand

PROGRAM

Monday, 29 July 2019

Room: Tongkah 1

Parallel session: Molecules and Morphology Reveal the Basis of Bat Evolutionary History and Unique Adaptations		
Chair: Emma Teeling, University College Dublin		
Co-chair: Stephen Rossiter, Queen Mary University of London		
10.40 - 10.55	**AO7-101**	**Molecular Adaptations Underpin Dietary Diversification and Specialization in New World Bats**
		Stephen Rossiter
		Queen Mary University of London, UK
10.55 - 11.10	**AO2-105**	**Genomic signatures of evolutionary divergence among Hawaiian hoary bat populations**
		Frank Bonaccorso
		US Geological Survey, USA
11.10 - 11.25	**AO2-101**	**Collagen fiber orientation within the bones of long-lived big brown bats (*Eptesicus fuscus*) relative to mice**
		Lisa Noelle Cooper
		Northeast Ohio Medical University, USA
11.25 - 11.40	**AO2-112**	**Limiting the damage: longitudinal comparative transcriptomics reveals novel mechanisms underlying extended healthspan in bats**
		Zixia Huang
		University College Dublin, Ireland
11.40 - 11.55	**AO2-104**	**Population genetic structure of island flying fox *Pteropus hypomelanus* Temminck, 1853 in Thailand**
		Patcharapon Jumsri
		Chulalongkorn University, Thailand
11.55 - 12.10	**AO2-124**	**Diversification Rates Have No Effect on the Convergent Evolution of Foraging Strategies of *Myotis***
		Ariadna E. Morales
		American Museum of Natural History, USA
12.10 - 12.25	**AO2-127**	**Comparative Transcriptome Sequencing Among Natural *Rhinolophus ferrumequinum* Populations with Different Acoustic Phenotypes**
		Hanbo Zhao
		Northeast Normal University, China
12.25 - 12.40	**AO2-103**	**Transcriptome Assembly and Functional Annotation in Five Tropical Bat Species by Using High-Throughput RNA Sequencing**
		Jorge Ortega
		Instituto Politécnico Nacional, Mexico
12.40 - 13.45	Lunch & Poster	

PROGRAM

Monday, 29 July 2019

Room: Tongkah 1

Parallel session: Phylogeny and Evolution 1		
Chair: Nancy Simmons, American Museum of Natural History		
Co-chair: Frank Bonaccorso, US Geological Survey		
13.45 - 14.00	**AO2-119**	**Evolution and Ontogeny of the Bat Calcar**
		Kathryn Stanchak
		University of Washington, USA
14.00 - 14.15	**AO2-106**	**Phylogenetic Analyses Show Bat Communities in Baja California Harbour a High Diversity of Cryptic Ectoparasite Species**
		Laura Alejandra Najera Cortazar
		University of Leeds, UK
14.15 - 14.30	**AO2-107**	**Is Stress Management a Key Factor in the LRS of Female Greater Horseshoe Bats?**
		Roger D. Ransome
		University of Bristol, UK
14.30 - 14.45	**AO2-118**	**Diversification of the Indo-Australasian bent-winged bats**
		Sigit Wiantoro
		The University of Adelaide, Australia
14.45 - 15.00	**AO2-109**	**Evolution of skull diversity across the bat radiation**
		Sharlene E. Santana
		University of Washington, USA
15.00 - 15.15	**AO5-143**	**Ecology Outweighs Evolutionary History in Shaping the Bat Microbiome**
		Holly L. Lutz
		Field Museum of Natural History, USA
15.15 - 15.30	**AO2-111**	**Evolution of developmental sequence in bats and its peculiarity among mammals**
		Daisuke Koyabu
		Musashino Art University/ Kyoto University, Japan
15.30 - 15.45	**AO2-114**	**Penis size and sperm quality, are all bats grey in the dark?**
		Ireneusz Ruczyński
		Polish Academy of Sciences, Poland
15.45 - 16.05	Refreshment & Poster session	
16.05 - 16.20	**AO2-115**	**Aerial Righting in Response to Flight Perturbation in *Carollia perspicillata***
		Sharon Swartz
		Brown University, USA
16.20 - 16.35	**AO2-116**	**Biomechanics and not ecology describe variation in cross-sectional shape of the humerus in bats**
		Camilo Lopez-Aguirre
		University of New South Wales, Australia
16.35 - 16.50	**AO6-101**	**Burning Fat by Inducing Beige Adipocytes: Insights from a Bat Study**
		Zhe Wang
		Shenyang Agricultural University, China

PROGRAM

Monday, 29 July 2019

Room: Tongkah 2

Parallel Session: Old World Fruit Bat Ecology and Conservation		
Chair: Tammy Mildenstein, Cornell College,		
Co-chair: Sheema Abdul Aziz, Rimba		
10.40 - 10.55	**AO14-104**	**Bats and Typhoons: What Do Stronger and More Frequent Storms Mean for Large Fruit Bats?**
		Tammy Mildenstein
		Cornell College, USA
10.55 - 11.10	**AO14-103**	**Extreme Nomadism of Fruit bats Poses Key Challenges for Management and Conservation**
		Justin Arno Welbergen
		Western Sydney University, Australia
11.10 - 11.25	**AO14-108**	**Managing human/flying-fox conflict in Australia**
		Emily Sara Hatfield
		Ecosure Pty Ltd, Australia
11.25 - 11.40	**AO14-109**	**How to Get an Endangered Ecological Keystone Flying Fox Species Mass-Culled: the Mauritius Example**
		F. B. Vincent Florens
		Tropical Island Biodiversity, Ecology and Conservation Pole of Research, University of Mauritius, Mauritius
11.40 - 11.55	**AO14-110**	**Bats roles in pollination networks were driven by plantation and urban landscape**
		Tuanjit Sritongchuay
		Xishuangbanna Tropical Botanical Garden, CAS, China/Thailand
11.55 - 12.10	**AO10-107**	**Severe decline in *Pteropus* spp. sightings across peninsular Malaysia - an effect of intense hunting and persecution?**
		Sheema Abdul Aziz
		Rimba, Malaysia
12.10 - 12.25	**AO14-105**	**Fruit bats in Singapore – What have they done for us lately?**
		Joanna Louise Coleman
		National University of Singapore, Singapore
12.25 - 12.40	**AO14-107**	**Distributional Ecology of *Pteropus lylei*: Conservation Implications for Vulnerable and Disease Reservoir Species**
		Aingorn Chaiyes
		Kasetsart University, Thailand
12.40 - 13.45	Lunch & Poster	
Parallel Session: Old World Fruit Bat Ecology and Conservation (Continued)		
Chair: Tuanjit Srithongchuay, Xishuangbanna Tropical Botanical Garden		
Co-chair: Sheema Abdul Aziz, Rimba; Tammy Mildenstein, Cornell College		
13.45 - 14.00	**AO5-127**	**Body-size dependent foraging strategies in the Christmas Island flying-fox (*Pteropus natalis*): implications for seed and pollen dispersal within a threatened island ecosystem**
		Christopher M. Todd
		Western Sydney University, Australia
14.00 - 14.15	**AO3-126**	**The impact of the Endangered Mauritian flying fox *Pteropus niger* on commercial fruit farms and the efficacy of mitigation methods**
		Ryszard Z. Oleksy
		Ecosystem Restoration Alliance Indian Ocean, Mauritius

PROGRAM

Monday, 29 July 2019

Room: Tongkah 2

14.15 - 14.30	**AO13-100**	**Education and sensitization of Mauritians to conserve the Mauritius fruit bats, *Pteropus niger***
		Yogishah Bunsy
		Ecosystem Restoration Alliance Indian Ocean, Mauritius
14.30 - 14.45	**AO14-101**	**Using GPS Tracking Research for Applied Conservation in Livingstone's Fruit Bats**
		Isabella Mandl
		NGO Dahari, Austria
14.45 - 15.00	**AO14-111**	**From Genes to Ecosystem: Fruit bats and their diet in a lowland forest in the Philippines**
		Mariano Roy Martin Duya
		University of the Philippines Diliman, Philippines
15.00 - 15.15	**AO3-116**	**Conflicts Between *Pteropus dasymallus* and Tankan Orange Farmers in Northern Okinawa Island**
		Weerach Charerntantanakul
		Kyoto University, Japan/Thailand
15.15 - 15.30	**AO3-111**	**Monitoring two flying-fox hunted species: trends, population sizes and harvesting rates in New Caledonia, South Pacific**
		Malik Oedin
		Université de la Nouvelle Calédonie, New Caledonia
15.30 - 15.45	**AO5-177**	**Impacts of an Invasive Ant Species on Roosting Behaviour of an Island Endemic Flying-fox**
		Annabel Dorrestein
		Western Sydney University, Australia
15.45 - 16.05	Refreshment & Poster session	
Parallel Session: Conservation		
Chair: Jon Flanders, Bat Conservation International		
Co-chair: Cullen Geiselman, Bat Conservation International		
16.05 - 16.20	**AO3-134**	**Conservation of Forest Bats in Rwanda**
		Jon Flanders
		Bat Conservation International, USA
16.20 - 16.35	**AO3-137**	**Human knowledge and perceptions of bats - a pilot study in Singapore**
		Joanna Louise Coleman
		National University of Singapore, Singapore
16.35 - 16.50	**AO3-107**	**Can Humans and Bats Coexist? Farmers' knowledge and attitudes toward bats in Belize**
		Mallory Tate
		University of Tennessee, USA
16.50 - 17.05	**AO5-171**	**Bat Eco-Interactions Database**
		Cullen Geiselman
		Bat Conservation International, USA

PROGRAM

Monday, 29 July 2019

Room: Broome 1+2

Parallel Session: Taxonomy, Diversity and Monitoring		
Chair: Susan Tsang, American Museum of Natural History		
Co-chair: Faisal Anwar Anwarali Khan, Universiti Malaysia Sarawak		
10.40 - 10.55	**AO1-102**	**Bats of the World: A New Taxonomic and Geographic Database**
		Nancy B. Simmons
		American Museum of Natural History , USA
10.55 - 11.10	**AO1-105**	**Why are the Phenotypes of Flutter Detecting Bats So Similar: Does Innovation Constrain Diversity?**
		David Steve Jacobs
		University of Cape Town, South Africa
11.10 - 11.25	**AO1-108**	**Cryptic Story of an Endemic *Hipposideros* from Indian Subcontinent**
		Parvathy Venugopal
		University of Bristol, UK
11.25 - 11.40	**AO1-109**	**Not so Tangled: Nuclear Genes Support Phylogeny of the Old World Leaf-Nosed Bats**
		Alexander Yusefowich
		Moscow M.V. Lomonosov State University, Russia
11.40 - 11.55	**AO2-131**	**Elevational gradient and genetic diversity of bats at Gunung Mulu National Park, Sarawak, Malaysia**
		Burton Lim
		Royal Ontario Museum, Canada
11.55 - 12.10	**AO1-114**	**Radiation of the tube-nosed fruit bats (Nyctimeninae) in New Guinea**
		Kyle Armstrong
		South Australian Museum, Australia
12.10 - 12.25	**AO1-115**	**High Diversity of Bat Supports Hkakabo Razi Landscape for Natural World Heritage Status**
		Sai Sein Lin Oo
		University of Mandalay, Myanmar
12.25 -12.40	**AO1-116**	**Bats in Tropical Semi-Deciduous Forests of Malaysia**
		Juliana Senawi
		Universiti Kebangsaan Malaysia, Malaysia
12.40 - 13.45	Lunch & Poster	
Parallel Session: Taxonomy, Diversity and Monitoring (Continued)		
Chair: Charles M. Francis, Environment and Climate Change Canada		
Co-chair: Sai Sein Lin Oo, University of Mandalay		
13.45 - 14.00	**AO1-117**	**Biogeography of Southeast Asian bats and implications for conservation**
		Charles M. Francis
		Environment and Climate Change Canada, Canada
14.00 - 14.15	**AO1-118**	**Is the Balinese subspecies of *Pteropus vampyrus* still *P. v. pluton*?**
		Susan M. Tsang
		American Museum of Natural History, USA
14.15 - 14.30	**AO1-110**	**batTracker: New, Improved Software for Automatically Tracking and Counting Flying Bats from Thermal Footage**
		Amanda Bush
		Department of Environment, Land, Water and Planning, Australia

PROGRAM

Monday, 29 July 2019

Room: Broome 1+2

14.30 - 14.45	**AO1-113**	**Sex-specific Prediction Formula for Wrinkle-lipped Free-tailed Bats (*Chaerephon plicatus*) at Khao Chong Phran Non-hunting Area, Ratchaburi, Thailand**
		Nutthakarn Boonpha
		Kasetsart University, Thailand
14.45 - 15.00	**AO1-121**	**Scanning the underworld horizon: global diversity patterns, threats, and conservation priorities for cave-dwelling bats**
		Krizler Cejuela Tanalgo
		Xishuangbanna Tropical Botanical Garden, CAS, China
15.00 - 15.15	**AO1-111**	**Challenges in Accurately Determining Population Numbers and Trends for Critically Endangered Cave-dwelling Bats**
		Lindy Lumsden
		Department of Environment, Land, Water and Planning, Victoria, Australia
15.15 - 15.30	**AO1-112**	**Ecological Indicators for Long-term Acoustic Bat Surveys to Assess and Monitor Bat Responses to Climate and Land Cover Change**
		Xavier Puig Montserrat
		Museum of Natural Sciences of Granollers, Spain
15.30 - 15.45	**AO1-107**	**Long-term Monitoring on Population Size of Wrinkle-lipped Free-tailed Bat (*Chaerephon plicatus*) in Western Thailand**
		Prateep Duengkae
		Kasetsart University, Thailand
15.45 - 16.05	Refreshment & Poster session	
Parallel Session: Taxonomy, Diversity and Monitoring (Continued)		
Chair: Sigit Wiantoro, University of Adelaide		
Co-chair: Sebastien Puechmaille, University of Montpellier		
16.05 - 16.20	**AO1-119**	**On the Use and Misuse of Mitochondrial DNA in Taxonomy and Phylogeny**
		Sebastien J. Puechmaille
		University of Montpellier, France
16.20 - 16.35	**AO2-129**	**Whole Mitochondrial Genome Sequencing and DNA Barcoding of *Rousettus amplexicaudatus*– Implications on Taxonomy of Philippine Bats**
		Rogel Victor Domondon Mendoza
		Institute of Biology, College of Science, University of the Philippines-Diliman, Philippines
16.35 - 16.50	**AO1-122**	**Bats from mangrove of Vietnam with remarks on taxonomy and echolocation**
		Thong Vu Dinh
		Vietnam Academy of Science and Technology, Vietnam
16.50 - 17.05	**AO3-132**	**Diversity and Distribution of Colombian Caribbean Bats: a Spatial Approach**
		Victor Manuel Martinez-Arias
		Universidad Nacional de Colombia, Sede Medellín, Columbia
17.05 - 17.20	**AO5-160**	**Modelling Distributions and Habitat Relationships of Bats in Cambodia Using a Multi-method Occupancy Framework on a Country-wide Scale**
		Alan Thomas Hitch
		University of California at Davis, USA
17.20 - 17.35	**AO1-120**	**Systematics of Malaysian Molossid Bat with a New Distribution Record for Borneo Island**
		Faisal Ali Anwarali Khan
		Faculty of Resource Science and Technology Sarawak, Malaysia

PROGRAM

Tuesday, 30 July 2019

Room: Tongkah 1

Parallel Session: Win-win Solutions for Emerging Infectious Disease Surveillance and Bat Conservation		
Chair: Kevin Olival, EcoHealth Alliance		
Co-chair: Kendra Phelps, EcoHealth Alliance		
09.15 - 09.30	**AO6-124**	**Bat Research Networks and Viral Surveillance: Gaps and Opportunities in Western Asia**
		Kendra Phelps
		EcoHealth Alliance, USA
09.30 - 09.45	**AO6-130**	**Advancing Bat Research in Southern Africa through Interdisciplinary Collaboration**
		Wanda Markotter
		University of Pretoria, South Africa
09.45 - 10.00	**AO6-105**	**Acquisition of Antibiotic Resistant Bacteria by Australian Fruit Bats (*Pteropus poliocephalus*) in Urban and Captive Environments**
		Fiona McDougall
		Macquarie University, Australia
10.00 -10.15	**AO6-116**	**Pathogen detection in bat flies (Diptera: Nycteribiidae) and their potential utilization in host conservation**
		Tamara Szentivanyi
		University of Lausanne, Switzerland
10.15 - 10.30	Refreshment & Poster	
10.30 - 10.45	**AO6-122**	**Serological evidence of Filovirus in bats and bat-hunters in the Northeastern states of India**
		Pilot Dovih
		National Centre For Biological Sciences, India
10.45 - 11.00	**AO6-133**	**Linking Biodiversity Loss Mitigation and Infectious Disease Prevention**
		David Hayman
		Massey University, New Zealand
11.00 - 11.15	**AO6-131**	**A Target on Their Backs? Deriving Bat Conservation Strategies from Marburg Virus Surveillance Activities of Egyptian Rousette Bats**
		Jonathan Towner
		Centers for Disease Control and Prevention, USA
11.15 - 11.30	**AO6-114**	**Bats, disease, and dynamic densities: Investigating community structure as a driver of viral dynamics in flying-foxes**
		Tamika Lunn
		Griffith University, Australia
11.30 - 11.45	**AO6-113**	**Learning from bats: studying inflammation and its implications for health**
		Aaron Irving
		Duke-NUS Graduate Medical School, Singapore
11.45 - 12.00	**AO6-123**	**Life history variation in immune and metabolic gene expression in free-ranging little epauletted fruit bat**
		DeeAnn Reeder
		Bucknell University, USA
12.00 - 12.15	**AO6-104**	**Stressors Compromise the Bat-Virus Relationship Leading to Increased Virus Replication and the Potential for Spillover**
		Vikram Misra
		University of Saskatchewan, Canada

Tuesday, 30 July 2019

Room: Tongkah 1

12.15 - 12.30	**AO6-132**	**Coupling conservation with public health: Developing public health messaging and interventions that limit human exposure to bat-borne viruses and protect bats**
		Jonathan Epstein
		EcoHealth Alliance, USA
12.30 - 13.30	Lunch & Poster	
Parallel Session: Disease Ecology and Parasitology		
Chair: Juliane Schaer, Humboldt University Berlin		
Co-chair: Jaap van Schaik, University of Greifswald		
14.00 - 14.15	**AO6-107**	**Into the Wild: Integration of Human-Associated Parasites into *Pteropus* Microbiomes**
		Michelle Power
		Macquarie University, Australia
14.15 - 14.30	**AO6-117**	**Origins of bat protozoan parasites of the *Trypanosoma cruzi* clade**
		Philippe Christe
		University of Lausanne, Switzerland
14.30 - 14.45	**AO6-112**	**Detection of Influenza A Viruses (IAV) in Diverse Bat Species in Bangladesh**
		Ariful Islam
		EcoHealth Alliance, Bangladesh
14.45 - 15.00	**AO6-103**	**Molecular and Evolutionary Studies of Bat Viruses and Functional Gene Adaptation**
		Shuyi Zhang
		Shenyang Agricultural University, China
15.00 - 15.15	**AO6-108**	**Microbats of the South West Botanical Province of Western Australia: Pathogen Diversity and Host Genetic Connectivity**
		Diana Prada
		Murdoch University, Australia
15.15-15.30	**AO6-109**	**High Risk Excretion Periods of Diverse Coronaviruses in the Egyptian Rousette Bat in South Africa**
		Marike Geldenhuys
		University of Pretoria, South Africa
15.30 - 15.45	**AO6-110**	**Diversity and Excretion Dynamics of Henipa-, Rubula- and Related Viruses in *Rousettus aegyptiacus* from South Africa**
		Marinda Mortlock
		University of Pretoria, South Africa
15.45 - 16.00	**AO6-127**	**Molecular investigation of *Polychromophilus* infection in the bat-fly *Basilia nana* from *Myotis bechsteinii* bats across Europe**
		Juliane Schaer
		Humboldt University Berlin, Germany
16.00 - 16.20	Refreshment & Poster session	
16:20 - 19:00	**Workshop:** Bat1K- initiative to sequence to chromosome level assembly the genome of every species of living bat	

PROGRAM

Tuesday, 30 July 2019

Room: Tongkah 2

Parallel Session: Human Dimensions of Bat Conservation: Conflict, Drivers and Solutions		
Chair: Tigga Kingston, Texas Tech University		
Co-chair: Tanja Straka, Leibniz Institute for Zoo and Wildlife Research; Pia Lentini, University of Melbourne		
09.15 - 09.30	**AO11-105**	**Attitudes and emotions towards bats in northwestern Cambodia**
		David Ader
		University of Tennessee, USA
09.30 - 09.45	**AO11-106**	**Gauging attitudes of residents living close to flying-fox camps to inform conflict management**
		Pia Lentini
		The University of Melbourne, Australia
09.45 - 10.00	**AO11-107**	**Understanding Cultural Symbolism and Use of Bats in Southeast Asia for Conservation Interventions**
		Mary-Ruth Low
		Rimba, Malaysia
10.00 - 10.15	**AO11-108**	**Using social marketing approaches to improve attitudes towards the Mauritian fruit bat**
		Ewan A. Macdonald
		University of Oxford, UK
10.15 - 10.30	Refreshment & Poster	
Parallel Session: Flying Foxes Hunting and Conservation in SE Asia		
Chair: Merlijn van Weerd, Mabuwaya Foundation		
Co-chair: Tammy Mildenstein, Cornell College; Sheema Abdul Aziz, Rimba		
10.30 - 10.45	**AO10-109**	**Bat Hunting Overview: Which bats are hunted and how can we measure population-level impacts?**
		Tammy Mildenstein
		Cornell College, USA
10.45 - 11.00	**AO10-108**	**Drivers of Human Behaviors: The Theory of Planned Behavior and Flying Fox Hunting in Southeast Asia**
		Tigga Kingston
		Texas Tech University, USA
11.00 - 11.15	**AO10-101**	**An island wide effort to understand and address flying fox trade in Sulawesi, Indonesia**
		Sheherazade
		Tambora Muda Indonesia, Indonesia
11.15 - 11.30	**AO10-102**	**How to tell kids to not eat bats? A case study of outreach programs in North Sulawesi, Indonesia**
		Windi Liani Bukit
		Tasikoki Wildlife Rescue Center, Indonesia
11.30 - 11.45	**AO10-100**	**Attitudes and Behaviors of Indigenous People Toward Flying Fox Hunting in Agusan Marsh Wildlife Sanctuary**
		Sherryl Lipio Paz
		Caraga State University, Philippines
11.45 - 12.00	**AO10-103**	**Indigenous Children and Flying Foxes: their hunting attitude and behavior in Agusan Marsh Wildlife Sanctuary, Philippines**
		Petervir Altesing Paz
		Caraga State University, Philippines

Tuesday, 30 July 2019

Room: Tongkah 2

12.00 - 12.15	**AO10-104**	**Flying fox hunting and conservation in northeast Luzon, Philippines**
		Marites Balbas
		Mabuwaya Foundation, Philippines
12.15 - 12.30	**AO10-105**	**Understanding flying fox hunter motivations in Southeast Asia as a basis for conservation**
		Merlijn van Weerd
		Mabuwaya Foundation, Philippines
12.30 - 13.30	Lunch & Poster	
Parallel Session: Bioacoustics 1		
Chair: Joe Chun-Chia Huang, Southeast Asian Bat Conservation Research Unit		
Co-chair: Adria Lopez Baucells, Natural Sciences Museum of Granollers		
14.00 - 14.15	**AO4-100**	**Influence of Signal Direction on Sonar Interference**
		Amanda Adams
		Fort Hays State University, USA
14.15 - 14.30	**AO4-135**	**Variation in Echolocation Call Intensities and Detection Distances of Bat Assemblages Across an Environmental Gradient**
		David Barasa Wechuli
		University of Cape Town, South Africa
14.30 - 14.45	**AO4-103**	**Why Bats Do Not Apply a Jamming Avoidance Response?**
		Omer Mazar
		Tel Aviv University, Israel
14.45 - 15.00	**AO4-104**	**Segregating Signal from Noise Through Movement in Echolocating Bats**
		Mor Taub
		Tel Aviv University, Israel
15.00 - 15.15	**AO4-105**	**Different Functions of Two Types of Territorial Calls in the Great Himalayan leaf-nosed bats, *Hipposideros armiger***
		Chunmian Zhang
		Northeast Normal University, China
15.15-15.30	**AO4-106**	**Screaming out in Fright: Function and Description of Distress Calls in the Nectarivorous Bat *Glossophaga soricina***
		David Hörmann
		University of Ulm, Germany
15.30 - 15.45	**AO4-107**	**Will acoustic communities of insectivorous bats change after extreme rains?**
		Chia-Yun Lee
		Biodiversity Research Center, Taiwan
15.45 - 16.00	**AO4-108**	**The information and function of social calls in Asian particoloured bats**
		Tinglei Jiang
		Northeast Normal University, China
16.00 - 16.20	Refreshment & Posters session	
16:20 - 19:00	**Workshop:** Titley Scientific Acoustic Workshop	

PROGRAM

Tuesday, 30 July 2019

Room: Broome 1

Parallel Session: Diet and Foraging Ecology		
Chair: Neil Furey, Independent		
Co-chair: Nurul-Ain Elias, Universiti Sains Malaysia		
09.15 - 09.30	**AO5-100**	**Diet of the Wrinkle-Lipped Free-Tailed Bat in Central Thailand**
		Supawan Srilopan
		Prince of Songkla University, Thailand
09.30 - 09.45	**AO5-102**	**Foraging Range and Diurnal Roost Selection of the Tri-colored Bat**
		Emma Victoria Willcox
		University of Tennessee, USA
09.45 - 10.00	**AO5-116**	**Frugivorous Bats in Brazil's Atlantic Forest: Effects of Habitat Fragmentation on Diet**
		Phillip J. Oelbaum
		University of Waterloo, Canada
10.00 - 10.15	**AO5-104**	**Diet Analysis of Kitti's Hog-Nosed Bat by DNA Barcoding**
		Monsicha Wangthongchaicharoen
		Chulalongkorn University, Thailand
10.15 - 10.30	Refreshment & Poster	
10.30 - 10.45	**AO5-150**	**New Technological Approaches to Study Sensory Aspects of Foraging Behavior in Wild Bats**
		Stefan Greif
		Tel Aviv University, Germany
10.45 - 11.00	**AO5-146**	**Does foraging activity of insectivorous bat in organic rice fields is higher than conventional rice fields?**
		Ponsarut Boonchuay
		Prince of Songkla University, Thailand
11.00 - 11.15	**AO5-110**	**Aggregational response of bats during forest pest emergence**
		Ján Blažek
		Masaryk University, Czech Republic
11.15 - 11.30	**AO5-119**	**Finding Fruit: Olfactory Tracking Strategies of Foraging Bats**
		Alyson Brokaw
		Texas A&M University, USA
11.30 - 11.45	**AO5-111**	**Land use and insect pest consumption by bats in macadamia orchards, South Africa**
		Sina Monika Weier
		University of Venda, South Africa
11.45 - 12.00	**AO5-132**	**Vampire bat food sharing in captivity predicts post-release social networks in the wild**
		Simon Ripperger
		Ohio State University, Germany
12.00 - 12.15	**AO5-103**	**Light, Flight and the Night: Effect of Ambient Lighting and Moon Phase on Pteropodid Flight Activity**
		Baheerathan Murugavel
		Indian Institute of Science Education and Research (IISER), India

PROGRAM

Tuesday, 30 July 2019

Room: Broome 1

12.15 - 12.30	**AO5-124**	**Flying Solo: Juvenile Flower-visiting Bats Perform First Foraging Flights without their Mother**
		Andreas Rose
		University of Ulm, Germany
12.30 - 13.30	Lunch & Poster	
Parallel Session: Diet and Foraging Ecology (Continued)		
Chair: Emma V. Willcox, University of Tennessee		
Co-chair: Simon Ripperger, Ohio State University		
14.00 - 14.15	**AO5-136**	**From Dusk till Dawn: Foraging and Habitat Use by the African Large-eared Slit-faced Bat *Nycteris macrotis***
		Nina Averil Mazur
		University of Ulm, Germany
14.15 - 14.30	**AO5-180**	**Seasonal Diet Variation of Sympatric Insectivorous Bats Revealed by Stable Carbon Isotope**
		Nittaya Ruadreo
		Prince of Songkla University, Thailand
14.30 - 14.45	**AO5-159**	**Trophic groups in a Mediterranean bat community: are echolocation and foraging behavior really important?**
		Vanessa A. Mata
		CIBIO-InBIO, University of Porto, Portugal
14.45 - 15.00	**AO5-130**	**Until the Last Drop: Nectar Extraction Efficiency in Flower-visiting Bats at Real Flowers**
		Jan Philipp Bechler
		Ulm University, Germany
15.00 - 15.15	**AO5-117**	**Ontogeny of foraging via assisted learning by mothers in Egyptian fruit bat pups**
		Lee Harten
		Tel-Aviv University, Israel
15.15-15.30	**AO5-172**	**The Bird Species Diversity in the Diet and Its Foraging Strategy of the Great Evening Bat**
		Lixin Gong
		Northeast Normal University, China
15.30 - 15.45	**AO3-131**	**Response of hibernating bats to nontactile stimuli**
		Tomas Bartonicka
		Masaryk University, Czech Republic
15.45 - 16.00	**AO5-115**	**Vocal Adaptations of Insect-eating Bats in Response to Shifts in Temperature and Humidity**
		Paula M. Iturralde-Polit
		University of Costa Rica, Ecuador
16.00 - 16.20	Refreshment & Poster session	
16:20 - 19:00	**Workshop:** Bat House DIY	

PROGRAM

Tuesday, 30 July 2019

Room: Broome 2

Parallel Session: Phylogeny and Evolution 2

Chair: Bruce D. Patterson, Field Museum of Natural History

Co-chair: Shiang-Fan Chen, National Taipei University

09.15 - 09.30	**AO2-121**	**Diversification of South American Vespertilionidae Is Not Constrained by Evolutionary Priority Effects**
		Maria João Ramos Pereira
		Universidade Federal do Rio Grande do Sul, Brazil
09.30 - 09.45	**AO2-125**	**Mitochondrial Introgression Suggest Historical Replacement in Palaearctic Whiskered Bat Species**
		Frieder Mayer
		Leibniz Institute for Evolution and Biodiversity Research, Germany
09.45 - 10.00	**AO2-128**	**Using Multiple Fossil Calibration Scenarios Highlights the Impact of Poorly Supported Chiropteran Fossils on Divergence Estimates**
		Adam Stone
		Queensland University of Technology, Australia
10.00- 10.15	**AO2-130**	**Conservation genetics of the Formosan flying fox**
		Shiang-Fan Chen
		National Taipei University, Taiwan
10.15- 10.30	Refreshment & Poster	
10.30- 10.45	**AO2-102**	**Resolving phylogenetic relationships and species limits in Afrotropical bats**
		Bruce D. Patterson
		Field Museum of Natural History, USA
10.45- 11.00	**AO2-123**	**Multilocus phylogeny and species delimitation within the *philippinensis* group (Chiroptera: Rhinolophidae)**
		Lin Zhang
		Northeast Normal University, China
11.00- 11.15	**AO15-100**	**Neural codes for bats' natural navigation: representation of space, time, and conspecifics**
		Liora Las
		Weizmann Institute of Science, Israel
11.15- 11.30	**AO5-101**	**Hindlimb Steerage: Analysis of Running Gaits in the Common Vampire Bat**
		John W. Hermanson
		Cornell University, USA
11.30- 11.45	**AO2-113**	**Evolutionary History of *Myotis nattereri* sensu lato: How do the Phylogenies Reticulate?**
		Emrah Çoraman
		Museum für Naturkunde Berlin, Germany
11.45 - 12.00	**AO2-108**	**Effects of Dispersal Ability on Population Structure of Six Bat Species in Eastern Cape Forests, South Africa**
		Monika Moir
		Stellenbosch University, South Africa
12.30 - 13.30	Lunch & Poster	

PROGRAM

Tuesday, 30 July 2019

Room: Broome 2

Parallel Session: Behaviour and Community Ecology

Chair: Wieslaw Bogdanowicz, Polish Academy of Science

Co-chair: Iroro Tanshi, Texas Tech University

14.00 - 14.15	**AO5-157**	**Genetic analyses reveal alloparental care in the carnivorous bat *Megaderma lyra***
		Wieslaw Bogdanowicz
		Polish Academy of Sciences, Poland
14.15 - 14.30	**AO3-133**	**Habitat use of the Hawaiian hoary bat on Maui**
		Dave S. Johnston
		H. T. Harvey & Associates, USA
14.30 - 14.45	**AO5-122**	**Functional Diversity and Community Structure of Bats along an Elevational Gradient in the Himalayas**
		Rohit Chakravarty
		Leibniz Institute for Zoo and Wildlife Research, Germany
14.45 - 15.00	**AO4-102**	**Insectivorous bats in the Cerrado mosaic: fleeing drought and degradation**
		Adriana Patricia Arias-Aguilar
		Universidade Federal do Rio Grande do Sul, Brazil
15.00 - 15.15	**AO5-161**	**Competitors Versus Filters: Drivers of non-random Structure in Forest Interior Insectivorous Bat Assemblages along Elevational Gradients**
		Iroro Tanshi
		Texas Tech University, Nigeria
15.15 -15.30	**AO5-137**	**Morphology and Stable Isotope Analysis Demonstrate Different Structuring of Bat Communities in Rainforest and Savannah Habitats**
		Ara Monadjem
		University of Eswatini, Eswatini
15.30 - 15.45	**AO5-147**	**The secret lives of Tube nosed-fruit bats – insights into the behaviour and ecology of *Nyctimene robinsoni***
		Anita Freudmann
		Queensland University of Technology, Australia
15.45 - 16.00	**AO9-100**	**Rapid changes in bat demography and social structure following large-scale habitat disturbance: the case of hydroelectric dam flooding**
		Francisco Amorim
		University of Porto, Portugal
16.00 - 16.20	Refreshment & Poster session	

PROGRAM

Wednesday, 31 July 2019

Room: Tongkah 1

Parallel Session: White-nose Syndrome/Disease Ecology

Chair: Sebastien Puechmaille, University of Montpellier

Co-chair: Kate Langwig, Virginia Tech

09.15 - 09.30	**AO6-128**	**Population Genetic Structure and Movement of the White-nose Disease Fungus, *Pseudogymnoascus destructans*, within and between Continents**
		Sebastien Puechmaille
		University of Montpellier, France
09.30 - 09.45	**AO6-102**	**Determining Torpor and Emergence Behaviors of Four Cavernicolous Bat Species in Relation to *Pseudogymnoascus destructans* Susceptibility**
		Reilly Tempest Jackson
		University of Tennessee, Knoxville, USA
09.45 - 10.00	**AO6-118**	**Did you wash your caving suit? Cavers' role in the transport of White Nose Disease**
		Violeta L. Zhelyazkova
		Bulgarian Academy of Sciences, Bulgaria
10.00 - 10.15	**AO6-120**	**Global Host and Pathogen Dynamics of White-nose Syndrome**
		Joseph R. Hoyt
		Virginia Tech, USA
10.15 - 10.30	Refreshment & Poster	
10.30 - 10.45	**AO6-121**	**The effects of temperature on the white-nose syndrome bat population dynamics**
		Kate E. Langwig
		Virginia Tech, USA
10.45 - 11.00	**AO6-125**	**Maybe She's Born with It: Big Brown Bats Show Physiological Resistance to White-Nose Syndrome**
		Nicole Su-yin Dorville
		University of Winnipeg, Canada
11.00 - 11.15	**AO6-111**	**Effect of Fitness Traits and Weather Condition on the Infection of Coronavirus of Lyle's Flying Fox**
		Warong Suksavate
		Kasetsart University, Thailand
11.15 - 11.30	**AO6-119**	**Non-Lethal Longitudinal Viral Monitoring in European Bats**
		Lucy Burkitt-Gray
		University College Dublin, Ireland
11.30 - 11.45	**AO6-126**	***Staphylococcus aureus* Outbreak Following Introduction of Wild-Caught Bats into a *Rousettus aegyptiacus* Research Colony**
		Avishag Tuval
		Weizmann Institute of Science, Israel
11.45 - 12.00	**AO3-113**	**Bat Hunting and Risk of Disease Emergence at High-Risk Interfaces in Bangladesh**
		Shusmita Dutta Choudhury
		Institute of Epidemiology, Disease Control and Research, Bangladesh
12.00 - 12.15	**AO6-129**	**Investigating the Control and Clearance of Filoviruses and Paramyxoviruses by Egyptian Rousette Bats**
		Amy Schuh
		Centers for Disease Control and Prevention, USA

Wednesday, 31 July 2019

Room: Tongkah 1

12.30 - 13.30	Lunch & Poster	
Parallel Session: Microbiome and Ectoparasite		
Chair: Marco Tschapka, University of Ulm		
Co-chair: Luis Viquez-R, University of Ulm		
13.30 - 13.45	**AO5-131**	**A Gut Feeling: What Can We Learn from the *Leptonycteris yerbabuenae* Migration through its Gastrointestinal Microbiota?**
		Luis Viquez-R
		University of Ulm, Germany
13.45 - 14.00	**AO5-135**	**Don't Bug Me: Bat – Bat Fly Interactions and their Response to Habitat Alteration in Central Panama**
		Thomas Hiller
		University of Ulm, Germany
14.00 - 14.15	**AO5-106**	**Interactions Between Dietary Breadth and Microbiome Specialization in Neotropical Bats**
		Melissa R. Ingala
		American Museum of Natural History, USA
14.15 - 14.30	**AO5-169**	**Effects of Environment and Bat Ecology on the Microbiome of Ectoparasites**
		Kelly Speer
		American Museum of Natural History, USA
14.30 - 14.45	**AO15-103**	**The impacts of agricultural and urban expansion on the gut microbiota and conservation of desert bats**
		Evie Jean Morris
		University of Southampton, UK
14.45 - 15.00	**AO3-119**	***Glossophaga soricina* in Banana Monocultures: What they eat and how this shapes their Gut Microbiome**
		Marco Tschapka
		University of Ulm, Germany
15.00 - 15.15	**AO6-106**	**Coordinated change at the colony level in fruit bat fur microbiomes through time**
		Maya Weinberg
		Tel Aviv University, Israel
15.15 - 15.30	**AO5-145**	**Multivariate Analyses Elucidate Drivers of Bat Ectoparasite Specificity from Brazil**
		Alexis M. Brown
		American Museum of Natural History/Columbia University, USA
15.30 - 15.50	Refreshment & Poster	
15.50 - 17.45	**Wildlife Acoustics Workshop 2:** Hands-on training on Song Meter SM4BAT FS	

PROGRAM

Wednesday, 31 July 2019

Room: Tongkah 2

Parallel Session: Bioacoustics 2

Chair: Thong Vu Dinh, Vietnam Academy of Science and Technology

Co-chair: Hans-Ulrich Schnitzler, University of Tübingen

09.15 - 09.30	**AO4-120**	**Echolocation, morphs and harmonic relationships in hosrshoe bats of the *philippinensis* group**
		Roger Coles
		Queensland University of Technology, Australia
09.30 - 09.45	**AO4-121**	**Echolocation Behavior of *Natalus tumidirostris*: Continuous Sampling with Short High-Frequency Calls**
		Juan Felipe Sehuanes
		University of Tübingen, Germany
09.45 - 10.00	**AO4-114**	**Echolocation call variations of Taiwanese bats and call identification by ensembles of artificial neural networks**
		Han Cheng Chou
		National Chiayi University, Taiwan
10.00 - 10.15	**AO4-119**	**The Functional Extension of Echolocation – Eavesdropping or Communication in Horseshoe Bats?**
		Anna Bastian
		University of KwaZulu-Natal, South Africa
10.15 - 10.30	Refreshment & Poster	
10.30 - 10.45	**AO4-118**	**Optimising acoustic survey protocols for bat research in species-rich tropical forests**
		Adria Lopez Baucells
		Natural Sciences Museum of Granollers, Spain
10.45 - 11.00	**AO4-109**	**Acoustic Flow Perception in Bats and Applications in Navigation**
		Athia Haron
		University of Bristol, UK
11.00 - 11.15	**AO4-110**	**The benefits of insect-swarm hunting in echolocating bats, and its influence on the evolution of bat echolocation signals**
		Arjan Boonman
		Tel Aviv University, Israel
11.15 - 11.30	**AO4-113**	**The Energetics of Social Signaling During Roost Location in Spix's Disc-Winged Bats**
		Gloriana Chaverri
		Universidad de Costa Rica, Costa Rica
11.30 - 11.45	**AO4-112**	**Vocal Roles and Group Phenotypic Composition Facilitate Roost Finding**
		Maria Sagot
		State University of New York at Oswego, USA
11.45 - 12.00	**AO4-116**	**Evidence of Chiroptera Adapting their Specialised Acoustic Systems' Intensity and Detection Range in their Respective Habitats**
		Nikita Finger
		University of Cape Town, South Africa
12.00 - 12.15	**AO4-117**	**The Role of Social Calls for Species Discrimination in Three Sympatrically Living *Carollia* Species**
		Tania Bosia
		University of Veterinary Medicine, Hannover, Germany

PROGRAM

Wednesday, 31 July 2019

Room: Tongkah 2

12.15 - 12.30	**AO4-111**	**The Moth Assassin: Aerial Hunting in the Sword-nosed Bat (*Lonchorhina aurita*, Phyllostomidae)**
		Gloria Gessinger
		University of Ulm, Germany
12.30 - 13.30	Lunch & Poster	
Parallel Session: Bioacoustics 2 (Continued)		
Chair: Arjan Boonman, Tel Aviv University		
Co-chair: Kyle Armstrong, South Australian Museum		
13.30 - 13.45	**AO4-122**	**Biosonar Dynamics and Echoic Scenes in Wild Foraging *Myotis myotis***
		Laura Stidsholt
		Aarhus University, Denmark
13.45 - 14.00	**AO4-123**	**Contextual analysis of vocalizations in the Ryukyu flying fox *Pteropus dasymallus***
		Masato Hashizume
		Kyoto University, Japan
14.00 - 14.15	**AO4-124**	**Early-Age Auditory Development and Vocal Learning in Pre- and Postnatal Egyptian Fruit Bats**
		Grace Smarsh
		Tel Aviv University, Israel
14.15 - 14.30	**AO4-126**	**Doppler shift compensation and auditory fovea of the low frequency horseshoe bat, *Rhinolophus paradoxolophus***
		Annette Denzinger
		University of Tübingen, Germany
14.30 - 14.45	**AO4-127**	**The role of social interactions on vocal ontogeny in the babbling bat *Saccopteryx bilineata***
		Ahana Aurora Fernandez
		Freie Universität Berlin / Museum für Naturkunde, Berlin, Germany
14.45 - 15.00	**AO4-131**	**Acoustics and Occupancy of Endangered Tree-Dwelling Bats, *Murina ryukyuana* and *Myotis yanbarensis*, in Northern Okinawa Island**
		Jason Hideki Preble
		Kyoto University, Japan
15.00 - 15.15	**AO4-132**	**Social vocalizations of big-footed myotis (*Myotis macrodactylus*) during foraging**
		Guo Dong Ge
		Northeast Normal University, China
15.15 - 15.30	**AO4-133**	**Listening to Ghosts: Monitoring the Behaviour of Cryptic *Macroderma gigas* by Acoustic Proxy**
		Nicola Hanrahan
		Hawkesbury Institute for the Environment, Australia
15.30 - 15.50	Refreshment & Poster	
15.50 - 17.45	**Workshop:** Student and early career scientist mental health	

PROGRAM

Wednesday, 31 July 2019

Room: Broome 1+2

Parallel Session: Roosting Ecology		
Chair: Maria João Ramos Pereira, University of Rio Grande do Sul		
Co-chair: Benneth Obitte, Texas Tech University		
09.15 - 09.30	**AO5-125**	**Who has Access to the Best Roost?: Influence of Interindividual Differences in Behavior on Roost Competition**
		Christian Angelo Castillo Salazar
		University of Costa Rica, Costa Rica
09.30 - 09.45	**AO5-126**	**Seasonal Variation in Use of Torpor by a Leaf-roosting bat, *Kerivoula furva*, in Subtropical Taiwan**
		Jian-Nan Liu
		National Chiayi University, Taiwan
09.45 - 10.00	**AO5-149**	**Roost selection in concrete culverts by the large-footed Myotis, *Myotis macropus* in Brisbane, Australia**
		Vanessa Gorecki
		Queensland University of Technology, Australia
10.00 - 10.15	**AO5-134**	**Differences in Roost Resources for Tent-roosting Bats across a Lowland Rainforest Island System in Panama**
		Patrick Daniel Cvecko
		University of Ulm, Germany
10.15 - 10.30	Refreshment & Poster	
10.30 - 10.45	**AO5-138**	**Foraging and roosting site sharing in Egyptian fruit bats: the role of key individuals**
		Erik Bachorec
		Masaryk University, Czech Republic
10.45 - 11.00	**AO5-148**	**Factors Determining Roost Selection by Cave-dwelling Bats in a Karst Network Landscape in Meghalaya, India**
		Aishanya Sarma
		Wildlife Conservation Society, India
11.00 - 11.15	**AO5-133**	**Maternal and Colony Guidance of Juvenile Natterer's bats to a Suitable Hibernation Site**
		Jaap van Schaik
		University of Greifswald, Germany
11.15 - 11.30	**AO5-118**	**Field experiment reveals the interplay between three cognitive skills in locating day roosts by Bechstein's bats**
		Jesus Rafael Hernandez Montero
		University of Greifswald, Germany
11.30 - 11.45	**AO5-141**	**Linking Roosting Ecology and the Evolution of Bat Landing Mechanics**
		David Boerma
		Brown University, USA
11.45 - 12.00	**AO5-162**	**Landscape and Microclimatic Drivers of Roost Selection in *Rousettus aegyptiacus* Across Southern Nigeria**
		Benneth Obitte
		Texas Tech University, USA
12.00 - 12.15	**AO5-166**	**Neighbors Matter! Stability of Roosting Patterns in a Laboratory Colony of *Carollia perspicillata***
		Sabine Schmidt
		University of Veterinary Medicine Foundation, Germany

PROGRAM

Wednesday, 31 July 2019

Room: Broome 1+2

12.15 - 12.30	**AO5-167**	**Roosting Patterns of Kitti's Hog-nosed Bat**
		Thongchai Ngamprasertwong
		Chulalongkorn University, Thailand
12.30 - 13.30	Lunch & Poster	
Parallel Session: Movement, Activity and Reproductive Biology		
Chair: Christian Voigt, Leibniz Institute for Zoo and Wildlife Research		
Co-chair: Stuart Parsons, Queensland University of Technology		
13.30 - 13.45	**AO3-124**	**Skyrocketing Flights as a Previously Unrecognized Behaviour of Open-Space Foraging Bats**
		Christian Voigt
		Leibniz Institute for Zoo and Wildlife Research, Germany
13.45 - 14.00	**AO5-121**	**The Effect of Resource Availability on Individual Fruit Bat Movement Measured at High Temporal Resolution**
		Emmanuel Lourie
		Hebrew University of Jerusalem, Israel
14.00 - 14.15	**AO5-105**	**Long-term Banding of California Leaf-nosed Bats Along the Lower Colorado River to Determine Movements and Longevity**
		Patricia Elaine Brown
		UCLA, USA
14.15 - 14.30	**AO1-104**	**Stereo-Infrared Reconstruction of Flight Paths for Long Deployment Behavior Studies**
		Klaus Hochradel
		UMIT - Private University for Health Sciences, Austria
14.30 - 14.45	**AO5-170**	**Hydrogen isotopes reveal complex seasonal migratory structure in at-risk tree-roosting bats in North America**
		Caitlin Campbell
		University of Florida, USA
14.45 - 15.00	**AO5-155**	**The Costs of Flight- Getting to the Heart of the Matter**
		Shannon E. Currie
		Leibniz Institute for Zoo and Wildlife Research, Germany
15.00 - 15.15	**AO5-176**	**Understanding *Mystacina*: Ten years of research into the biology and behaviour of 50% of New Zealand's bat fauna**
		Stuart Parsons
		Queensland University of Technology, Australia
15.15 - 15.30	**AO5-142**	**Sex and the City: Reproductive Ecology in a Successful Urban Species, *Chalinolobus gouldii***
		Danielle Eastick
		La Trobe University, Australia
15.30 - 15.50	Refreshment & Poster	
15.50 - 16.05	**AO5-139**	**Trends at the Ends; Telomere Dynamics in Lifespan, Hibernation and Reproduction in *Rhinolophus ferrumequinum***
		Megan Power
		University College Dublin, Ireland

PROGRAM

Wednesday, 31 July 2019

Room: Broome 1+2

16.05 - 16.20	**AO3-108**	**A Novel Approach to the Investigation of Microclimatic Conditions for Bat Hibernation**
		Ralf Gyselings
		Research Institute for Nature and Forest, Belgium
16.20 - 16.35	**AO5-113**	**Temporal and spatial activity of bats in the ephemeral rivers of an arid Australian mountain range**
		Erin Louise Westerhuis
		Charles Darwin University, Australia
16.35 - 16.50	**AO5-164**	**How Far Do Bats Take It? A Review of Home Range Studies**
		Carol Chambers
		Northern Arizona University, USA
16.50 - 17.05	**AO5-107**	**Large PIT-Antenna System Detects Low Summer-Autumn Survival of the Australian Critically Endangered Southern Bent-wing Bat**
		Emmi van Harten
		La Trobe University, Australia

PROGRAM

Thursday, 1 August 2019

Room: Tongkah 1

Parallel Session: Ecosystem Services		
Chair: Rodrigo Medellin, Instituto de Ecología, UNAM		
Co-chair: Maria Cristina MacSwiney Gonzalez, Universidad Veraceuzana		
09.15 - 09.30	**AO3-141**	**A fresh view at ecosystem services provided by bats: opportunities and challenges**
		Rodrigo Medellin
		Universidad Nacional Autónoma de México, Mexico
09.30 - 09.45	**AO5-165**	**Bats as Bioindicators? Evidence of Strong Associations between Bats, Climate and Vegetation along an Environmental Gradient**
		Hugo Rebelo
		University of Porto, Portugal
09.45 - 10.00	**AO3-142**	**Restoring Agave for Migratory North American Nectivorous Bats, and Agave Use by Bats in the Paleotropics**
		Daniel A. Taylor
		Bat Conservation International, USA
10.00 -10.15	**AO5-156**	**Synanthropic Bats as Potential Suppressors of Multiple Agricultural Pests: A Case Study from Madagascar**
		Ricardo Rocha
		University of Cambridge, UK
10.15 -10.30	**AO5-144**	**Bats Pollinating Bromeliads: A Review**
		Maria Cristina MacSwiney Gonzalez
		Universidad Veraceuzana, Mexico
10.30 -10.45	**AO5-140**	**Nutrient contribution of cave bat colonies to surface ecosystems**
		Stanimira Deleva
		Universidad de Costa Rica, Costa Rica
10.45 -11.00	**AO5-179**	**Pest Consumption in a Vineyard System by *Rhinolophus hipposideros***
		Unai Baroja
		University of The Basque Country (UPV/EHU), The Basque Country
11.00 -11.15	Refreshment	

PROGRAM

Thursday, 1 August 2019

Room: Tongkah 2

Parallel Session: Bat Mortality and Conservation Solutions		
Chair: Winifred F. Frick, Bat Conservation International		
Co-chair: Joe Chun-Chia Huang, Southeast Asian Bat Conservation and Research Unit		
09.15 - 09.30	**AO3-127**	**Bats and Windfarms – Lessons from Europe and Western Palearctic. What about the rest of the World?**
		Daniela Hamidovic
		Croatian Biospelological Society, Croatia
09.30 - 09.45	**AO3-136**	**Conserving Caves in the Caribbean for Critically Endangered Bats**
		Winifred F. Frick
		Bat Conservation International, USA
09.45 - 10.00	**AO3-102**	**Bat Overpasses as a Solution to Increase Habitat Connectivity Depending the Context**
		Fabien Claireau
		Naturalia Environnement, France
10.00 - 10.15	**AO3-109**	**Identifying the Patterns and Potential causes of Bat Roadkill Incidence in Taiwan**
		Joe Chun-Chia Huang
		Southeast Asian Bat Conservation and Research Unit, Taiwan
10.15 - 10.30	**AO3-117**	**Are bats susceptible to vehicle collisions in Thailand? A case study in a biodiversity hotspot**
		Inês Silva
		King Mongkuts University of Technology Thonburi, Thailand
10.30 - 10.45	**AO3-120**	**A Connectivity Model for Bats in Fragmented Landscapes**
		Luc De Bruyn
		Research Institute for Nature and Forest, Belgium

PROGRAM

Thursday, 1 August 2019

Room: Broome 1+2

Parallel session: Adaptation and Climate/Environmental Change		
Chair: Julie Broken-Brow, University of Queensland / Titley Scientific		
Co-chair: Christoph Meyer, University of Salford		
09.15 - 09.30	**AO5-109**	**Dark Side of Climate Warming: Colorado Bats are Feeling the Heat**
		Rick Adams
		University of Northern Colorado, USA
09.30 - 09.45	**AO5-108**	**Phenotypic Responses of Bats to Climate and Land Use Change Over the Past Sixty Years in China**
		Xinke Yue
		Xishuangbanna Tropical Botanical Garden, CAS, China
09.45 - 10.00	**AO5-151**	**Food Limitation Slows Down Sperm Production But Not Torpor Use in Male Bats During Summer**
		Ewa Komar
		Polish Academy of Sciences, Poland
10.00 - 10.15	**AO3-114**	**The Road to Recovery: Temporal Effects of Matrix Regeneration on Amazonian Bats**
		Christoph Meyer
		University of Salford, UK
10.15 - 10.30	**AO5-168**	**The Effect of Fire on Insectivorous Microbats and Their Resources in Cape York Peninsula, Australia**
		Julie Broken-Brow
		University of Queensland / Titley Scientific, Australia
10.30 - 10.45	**AO3-105**	**Light on the Matter: The effects of artificial lighting on the activity of Namib Desert Bats**
		Angela Curtis
		Gobabeb Namib Research Institute, Namibia
10.45 - 11.00	**AO5-178**	**Landscape Context Matters for Effective Use and Attractiveness of Road Underpasses by Bat Communities**
		Alexis Laforge
		French National Institute for Agricultural Research, France
11.00 - 11.15	Refreshment	

18th **IBRC**

28 JULY - 1 AUGUST 2019

THE SLATE, PHUKET, THAILAND

ABSTRACTS

Keynote-1

Growing old yet staying young: do bats hold the secret of extended longevity?

Emma C. Teeling

School of Biology and Environmental Science, University College Dublin, Ireland

Of all mammals, bat possess the most unique and peculiar adaptations that render them as excellent models to investigate the mechanisms of extended longevity and potentially halted senescence. Indeed, they are the longest-lived mammals relative to their body size, with the oldest bat caught being >41 years old, living approx. 8 times longer than expected. Bats defy the 'rate-of-living' theories that propose a positive correlation between body size and longevity as they use twice the energy as other species of considerable size, but live far longer. The mechanisms that bats use to avoid the negative physiological effects of their heightened metabolism and deal with an increased production of deleterious Reactive Oxygen Species (ROS) is not known, however it is suggested that they either prevent or repair ROS damage. Bats also appear to have resistance to many viral diseases such as rabies, SARS and Ebola and have been shown to be reservoir species for a huge diversity of newly discovered viruses. This suggests that their innate immunity is different to other mammals, perhaps playing a role in their unexpected longevity. Here the potential genomic basis for their rare immunity and exceptional longevity is explored across multiple bat genomes and divergent 'ageing' related markers (e.g. microbiome, telomeres, mitochondria, cellular dynamics). A novel blood-based population-level transcriptomics approach is used to explore the molecular changes that occur in an ageing wild population of bats to uncover how bats 'age' so slowly compared with other mammals and to further validate *in silico* functional predictions. These findings provide a deeper understanding of the causal mechanisms of ageing, potentially uncovering the key molecular pathways that could be eventually modified to halt, alleviate and perhaps even reverse this process in humans.

Keynote-2

Bat viral ecology: past, present, and future

Kevin J. Olival

EcoHealth Alliance, New York, NY 10001, USA

The discovery and characterization of viruses from bats dates back to the 1950s. Although in the last 15 years, notably after the emergence of Severe Acute Respiratory Syndrome (SARS) coronavirus, there has been an explosion in bat virus research. Much of this past work, although still including hundreds of papers published each year, would constitute a “discovery phase” in bat virology - with new viruses being discovered and sequenced in large numbers without much context. However, we are currently in the midst of a more fascinating and hypothesis-driven era of bat virus research, one that is currently elucidating the dynamics and interactions of a previously unknown world hidden within bats. This relatively new, multidisciplinary field of *bat viral ecology* is advancing rapidly each year – linking virologists, veterinarians, molecular biologists, and public health scientists with bat ecologists, physiologists, systematists, and conservationists in new and exciting ways. In this talk, I will track the evolution of bat viral ecology from a personal perspective and highlight the successes and challenges I’ve observed over the last 17 years. One overarching theme that emerges is that bat ecological research/conservation *and* virus surveillance and public health research are synergistic, and should not be viewed as opposing. I end the talk by describing some of the exciting frontiers that lie ahead for the field, for example: characterizing the complete bat virome, integrating bat genomics and physiology to understand virus tolerance and host range, seasonal and co-infection dynamics, virus-host coevolution and co-phylogeography, and the role of anthropogenic ecological change in shaping transmission dynamics and potential for viral spillover.

All Eyes on Bats: Why Understanding People Benefits Bat Conservation

Tanja Straka

Leibniz Institute for Zoo and Wildlife Research, Alfred-Kowalke-Straße 17 Berlin, Germany

Major threats to bats range from habitat destruction and modification, to roost site disturbance, persecution, hunting and trade. While these issues are not all directly linked, they have one thing in common: they are consequences of human behaviours. These threats can be often compounded by common misconceptions about bats and a lack of information, even amongst decision makers. Therefore, it is critical for bat conservation to improve an understanding of human dimensions of bat-people interactions to ensure effective conservation and enables more influential communication strategies. While applying social sciences in conservation has gained increasing attention over the last few decades, it has received comparatively little attention in the field of bat conservation until recently. This keynote presentation will present some concepts and theories from the field of Human Dimensions of Wildlife alongside case studies to show the value of applying social science theories to bat conservation as well as addressing conservation challenges in the 21st century.

Keynote-4

Ecosystem services of insectivorous bats in Southeast Asia

Sara Bumrungsri

Department of Biology, Faculty of Science, Prince of Songkla University, Hat Yai, Songkhla, Thailand

There are more than 200 species of insect eating bats in Southeast Asia. With highest global deforestation rate and highest urbanization rate, this region experiences significantly habitat loss, which leads to bat mass extinction, up to 40% by 2100. In this particular region, in addition to pollination and seed dispersal services by fruigivorous bats, recent studies indicated that insect- eating bats play major role in insect regulation service especially in farmland and agroforest habitat. A colonial species such as *Chaerephon plicatus* is one among most well-studied species that contribute in pest suppression in paddy field. Several studies confirm that this bat feed on the most serious rice pest, planthopper, which migrate within the region. Recent authors also demonstrate that it also feed on mosquito. Other insect-eating bats are thought to be important pest suppressor in different landscape, and more studies are needed. These findings raise the conservation concern of bats in the region, and serious conservation measures should be undertaken both at the local and regional level.

Burst Echolocation: Another strategy of bats to detect fluttering insects in clutter

Hans-Ulrich Schnitzler[1], Vu Dinh Thong[2], Juan Sehuanes[1], Diana Schoeppler[1], Ying-Yi Ho[3], Joe Chun-Chia Huang[4] and Annette Denzinger[1]

[1]Animal Physiology, Institute for Neurobiology, University of Tuebingen, DEU
[2]Institute of Ecology and Biological Resources, Vietnam Academy of Science and Technology, Hanoi, VNM
[3]Department of Biological Sciences, National Sun Yat-sen University, Kaohsiung, TWN
[4]School of Environmental and Natural Resource Sciences, University Kebangsaan, MYS

Bats use the echolocation strategies aerial-hawking and trawling, active gleaning, passive gleaning, and flutter detection to find their prey in different acoustic habitats. Narrow space flutter detecting foragers produce long signals of constant frequency at high duty cycle and analyze amplitude and frequency modulations in echoes from fluttering insects to find their prey in cluttered environments. Here we show that the hipposiderid *Coelops frithii,* the phyllostomid *Micronycteris microtis*, the natalid *Natalus tumidirostris,* the thyropterid *Thyroptera tricolor,* and most likely vespertilionid bats of the genera *Kerivoula* and *Phoniscus* have evolved another so far undescribed echolocation strategy to assess flutter information. Bats using this burst echolocation strategy sample the wing movements of fluttering prey with groups or bursts of many ultra-short frequency-modulated signals of high frequency. Amplitude and frequency modulations in the resulting pulse-echo sequences allow the discrimination of fluttering insects from stationary background targets, and deliver information on the nature and angular orientation of the prey.

Bats of the World: A New Taxonomic and Geographic Database

Nancy Simmons and Andrea Cirranello

Division of Vertebrate Zoology, American Museum of Natural History, New York, USA

The last comprehensive list of chiropteran species published in Mammal Species of the World in 2005 recognized 1,116 bat species. Although this represented a significant increase over previous tallies, known bat species diversity has continued to climb since that time, with ~1,400 valid species now recognized. Similarly, our understanding of the geographic ranges of many species has continued to change with new revisions and inventories. Researchers in diverse fields ranging from evolutionary biology to ecology and conservation need access to up-to-date information on bat species diversity, taxonomy, and geographic ranges to inform research and management decisions. Although definitive published volumes are desirable for many reasons, the modern digital age provides an alternative: a citable online database. With ongoing input from the Global Bat Taxonomy Working Group of the IUCN Bat Specialist Group, we have accordingly launched a new database at www.batnames.org that provides basic information on every valid bat species currently recognized. Long entries are available for many species and include name, authority, citation, common name, synonyms, type locality, distribution, map, threat status, comments, and references. Short entries (including name, authority, citation and common name) are provided for taxa that we have not yet fully finished revising and updating. We hope to upgrade all of the short entries to long entries over the next year. Once all the original entries have been revised, the website will be updated biannually. This database has the advantage over other online sources in that it is fully vetted by experts in bat taxonomy.

AO1-104

Stereo-infrared Reconstruction of Flight Paths for Long Deployment Behavior Studies

Klaus Hochradel[1*], Felix Günther[2], Sören Greule[2], Stefanie Hartmann[2], Bruntje Luedtke[2], Hendrik Reers[2], Horst Schauer-Weisshahn[2] and Alexander Sutor[1]

[1]*UMIT - Private University for Health Sciences, Medical Informatics and Technology GmbH, AT*
[2]*FrInaT, Freiburg Institute for Applied Animal Ecology GmbH, GER*

Modern single board computers (SBC) facilitate the use of former complex engineering technology like stereo cameras for animal behavioral studies. Still, numerous studies neglect the possibility to utilize stereo-camera systems due to their complexity and involved costs. We present an easy to use and inexpensive stereo-infrared-camera system to reconstruct three-dimensional flight paths of bats. Our easily accessible system is based on the popular Raspberry Pi SBC and two infrared sensitive cameras with a CS mount for lenses and the sensor OV5647 by OmniVision. We had the opportunity to deploy and test the system during two research projects investigating the behavior of bats around small wind turbines (SWTs). During the first project ten existing sites were equipped with our system and each recorded a minimum of 4 h after sunset for four weeks. During this time, we altered the operation mode in four days cycles between up- and downtime and recorded altogether 499 flight paths. In the second still ongoing project with one stereo-camera system, 7400 three-dimensional partial trajectories were recorded within 27 nights a 4 hours. Flight paths enabled us to determine behavioral parameters like density of bats in defined volumes, proximity to structured or flight directions.

AO1-105

Why are the Phenotypes of Flutter Detecting Bats So Similar: Does Innovation Constrain Diversity?

David S. Jacobs

Department of Biological Sciences, University of Cape Town, Cape Town, ZAF

An important question in biology is why some taxa are speciose while others are not. For example, the bat family Rhinolophidae is a monogeneric family of about 78 species compared to the family Vespertilionidae which comprises several genera and more than 300 species. The emergence of an innovative trait that confers substantial survival and reproductive advantages may constrain phenotypic diversification through the evolution of adaptive complexes between the innovation and other traits. The evolution of flutter detection may have restricted rhinolophids to similar foraging modes resulting in phenotypic stasis with respect to the ancestral character state. We investigated the potential constraint of flutter detection on the diversity of phenotypes among 16 species of African rhinolophids within a phylogenetic framework. Although distantly related lineages converged with each other (DFA classification success < 13–67%) and the ancestral character state, suggesting stasis, some lineages also diverged phenotypically (classification success > 83%) notably in body size and resting frequency. However, there was no sexual size dimorphism in mass, forearm length and wingspan within species (R^2s < 0.26, F-ratios < 5.28, $Ps_{(1, 11)} > 0.05$) and there was marked interspecific similarity in both wing and echolocation variables (classification success < 53%). Correlations of wing and echolocation variables with mass (R^2s > 0.52, F-ratios > 14.16, $P_{(df\,1,\,11)} < 0.003$) suggest that variability within rhinolophids was largely the result of selection on body size with allometric responses in wing and echolocation parameters, a potential consequence of constraints imposed by their specialized echolocation.

AO1-107

Long-term Monitoring on Population Size of Wrinkle-lipped Free-tailed Bat (*Chaerephon plicatus)* in Western Thailand

Prateep Duengkae[1], Nutthakarn Boonpha[1], Warong Suksavate[2], Supaporn Wacharapluesadee[3], and Chumpon Kaewket[4]

[1]*Department of forest biology, Faculty of Forestry, Kasetsart University, Bangkok, 10900, THA*
[2]*Biodiversity and Conservation Research Unit, Walai Rukhavej Botanical Research Institute, Mahasarakham University, Mahasarakham, 44150, THA*
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Wrinkle-lipped free-tailed bat (*Chaerephon plicatus*) is a major contributor to ecosystem services as agent of pest suppression in rice fields and producing plant fertilizer. We used long-term monitoring data on the largest population of wrinkle-lipped free-tailed bat in Thailand based on an analysis of data collected for over 20 years (1997-2018) from a cave at Khao Chong Phran Non-hunting Area. The monthly monitoring scheme was using of image counting techniques to detect population size. From the results, the population size was stable from 1997 to 2018, approximately (mean ±SE) 2,641,060 ± 34,967.44 individuals. However, seasonal fluctuations between varied from 1,242,692 to 6,144,420 individuals. The population size of wrinkle-lipped free-tailed bat has the seasonal pattern associated with precipitation. The population size was at highest (~4,000,000-6,000,000 individual) during rainy season and decline (~1,200,000-2,000,00 individual) in dry season. According to the warmer and drier climate in western Thailand, the situation might worsen the trend of population. We recommend to maintain the critical ecosystem services of this dominant bat species by conservation efforts and sustainable utilization.

AO1-108

Cryptic Story of an Endemic *Hipposideros* from Indian Subcontinent

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Bats are promising candidates for studying morphometric and acoustic responses to geographical isolation. The present study tried to understand the cranial variation and acoustic differences in *Hipposideros lankadiva*, an endemic species to the Indian subcontinent. The specimens from India are referable to *H. l. indus* and are relatively small in size when compared to the specimens described from Sri Lanka which are referred to *H. l. lankadiva*. A new subspecies called *H. l. gyi* was described recently by Bates et al. (2015) from Myanmar with individuals comparable in morphometrics to the Sri Lankan and north-east Indian specimens. In order to unravel the cryptic status of these subspecies, we examined 116 specimen of *H. lankadiva* from various museums in India, Sri Lanka and the UK. Fourteen craniodental measurements were recorded by using an analog calliper accurate to 0.01mm. Principal Component Analysis (PCA) was performed in SPSS Statistics Ver.23. to combine information for multivariate analyses. The first two principal component axes, PC1 and PC2, accounted for 78.27% and 13.69% of the total variation, respectively. Large values for PC1 will be associated with larger skull sizes in general and that of PC2 will be with skull shape. A hierarchical clustering of skull data from *H. lankadiva* was derived from a cluster dendrogram which identified at least three major groupings. We assume these results support the recent findings by Bates et al. (2015). Acoustic analysis also revealed significant variations in peak frequency, across regions. Molecular analysis for this work is ongoing.

AO1-109

Not so Tangled: Nuclear Genes Support Phylogeny of the Old World Leaf-nosed Bats

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Being one of the largest mammalian genera, *Hipposideros* is insufficiently studied taxonomically. At the same time it proved out to be an unexpectedly rewarding group for studying, with a high congruence of the results obtained from different datasets. For the comparison with earlier mtDNA data, original sequences of the seven nuclear genes were obtained (ABHD11, ACOX2, RAG2, SORBS2, THY, ROGDI2 и COPS), and data were analyzed for individual genes and in multigene analysis by MRP method.

Intron THY appeared to be the most informative of all markers. It supports monophyly of larger Asian species, while placing *H. diadema* as most basal in this clade. Of the smaller species, monophyly of the «bicolor» species group was well supported. Exon RAG2 supports basal position of African *H. jonesi* respective to all analyzed *Hipposideros* spp. Smaller African species form sister clade to the «bicolor» complex, while *H. galeritus* occupies more basal position. *H. halophyllus* is the most basal within the «bicolor» group itself.

On the tree obtained by MRP method, all the lineages above species level get maximal support, except for *H. jonesi*; and its topology in general corresponds well to mtDNA data. Larger Asian species are monophyletic, thus justifying separation of the subgenus *Phyllorhina*, with *H. diadema* as most basal branch. Complexes «armiger» and «larvatus» form joint monophyletic cluster. Within the smaller species, *H. galeritus* occupies more basal position than the African *H. abae* and *H. ruber*, suggesting Australasian origin of the whole clade.

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AO1-110

‘batTracker’: New, Improved Software for Automatically Tracking and Counting Flying Bats from Thermal Footage

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Conservation and management of communally-roosting cave bats requires accurate and timely identification of changes in population numbers. Monitoring has previously been undertaken by recording bats exiting caves (a flyout) using thermal video with missile tracking software (‘T3’) to provide automated counts. However, this software is old and uses obsolete hardware. To address these issues, we have developed ‘batTracker’ in Matlab to enable the use of modern recording equipment and computer hardware, and multiple video formats. batTracker uses Matlab’s image processing toolbox to analyse thermal image video recordings. Like T3, this new program uses a two-stage process, firstly analysing individual video frames to determine the location of objects (bats), and then tracking the objects between frames to determine flight paths. Bats are counted when their tracked flight path either enters or leaves a user-defined polygon. The accuracy of object tracking algorithms is dependent on several factors, including the quality and frame rate of the images, placement of the camera in relation to the objects (bats) to be tracked, the size of the object (bat) in the image and the number of objects (bat exit rate). A number of parameters can be tuned to obtain the best results. Unlike T3, batTracker incorporates a number of features specifically designed to assist the user with the tuning process. Based on comparisons with manual counts of segments of the video, the automated program consistently provides counts within five percent. This system thus provides a more effective and efficient process for estimating bat flyout counts.

AO1-111

Challenges in Accurately Determining Population Numbers and Trends for Critically Endangered Cave-dwelling Bats

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Obtaining accurate population estimates of threatened species is critical for monitoring trends and evaluating the effectiveness of management actions. However, there are challenges in accurately estimating population numbers of cave-dwelling bats. We illustrate factors to consider, using the Critically Endangered Southern Bent-wing Bat *Miniopterus orianae bassanii* in south-eastern Australia as an example. This subspecies breeds in just three maternity caves, where the majority of individuals congregate over the breeding period, facilitating estimates of total population size. Approximately 17,000 adults use the main Victorian maternity cave. Counting roosting bats is precluded by the large size of the cave and the disturbance caused by entering during the day. Instead, dusk flyouts are videoed using a thermal camera. Multiple thermal cameras have been trialed, with the resolution influencing the proportion of bats detected. ‘T3’ missile tracking software was initially used to automate counting, however to improve efficiency and accuracy, a new program ‘batTracker’ was developed. Not all bats emerge during the flyout, so those remaining are photographed using infra-red camera and illuminators and incorporated into population estimates. Counts are undertaken over multiple nights as there is nightly variability. In addition, flyout counts are simultaneously undertaken at two non-breeding caves (within 20 km) as there is regular interchange between these and the maternity cave. Numbers can fluctuate markedly at the non-breeding caves (e.g. from 100 to 2000 over 5 days) which could result in misleading trends if not factored into the total population count. Incorporating factors that influence nightly counts has been key to obtaining accurate population estimates for this Critically Endangered bat.

AO1-112

Ecological Indicators for Long-term Acoustic Bat Surveys to Assess and Monitor Bat Responses to Climate and Land Cover Change

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Bat acoustic monitoring has boosted during the last decade due to a considerable increase in affordability and capacity of the recorders available in the market. The design of statistically robust monitoring protocols capable to track bat populations changes both across sites and time has received an increasing attention during the last years though, to date, no generally accepted protocols or indices have appeared. From 2016 to 2018 a network of full spectrum ultrasound recorders was established in Catalonia (NE Iberia) as part of the national bat monitoring program, encompassing 90 sampling sites and covering a wide variety of altitudes and ecosystems, thus providing excellent datasets to study the effect of both climate and habitat change on bat populations. A set of seven different community, climatic and habitat indices has been developed and tested, i.e. thermal, precipitation, openness, specialism, richness, Shannon and activity indices. The indices predict accurately the observed changes in bat communities along the various gradients covered (temperature, precipitation, habitat complexity, openness and altitude), thus constituting an excellent approach to determine trends in bat populations and the responses of particular species and communities to both the global and local drivers of change.

AO1-113

Sex-specific Prediction Formula for Wrinkle-lipped Free-tailed Bats *(Chaerephon plicatus)* at Khao Chong Phran Non-hunting Area, Ratchaburi Thailand

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Wrinkle-lipped free-tailed bats (*Chaerephon plicatus)* are insectivorous bats, of which at least eight million individuals are contained within 18 cave dwellings in Thailand. These bats play an important role as pest controllers in ecosystem services, especially at our study area, the Khao Chong Phran Non-hunting Area, where the largest cavern houses 2.6 million of *C. plicatus.* Field collections were conducted over 2016 from January through December. At least one-hundred individuals were trapped two times per month, first at the opening of the main carven in the evening when bats started to emerge for foraging and second inside the cave in the morning when they turned to roost. Forearm length (mm) and body mass (gram) of non-reproductive mature bats (males = 1, females = 0) were used to fit the binomial regression analysis. The result indicated prediction formula and probability of bat being male is positively associated with forearm length and body mass. This is the first formula for forecasting the sex of *C. plicatus.* Long-term monitoring of bats and climatic factors will useful for predicting future bat population trends and then will benefit authorities of the Department of National Parks, Wildlife and Plant Conservation, the Khao Chong Phran cave-dwelling managers and other cave managers for sustainable utilization and management.

AO1-114

Radiation of the tube-nosed fruit bats (Nyctimeninae) in New Guinea

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The island of New Guinea has seen the diversification of the tube-nosed fruit bats in the absence of other similar-sized genera that dominate forest systems west of Lydekker's Line. The Nyctimeninae are remarkable for their mottled and sometimes greenish colouration that provides camouflage amongst foliage, as well as their protruding snorkel-like nasal tubes. Previous taxonomic studies have likely underestimated the number of species that have spread across the elevational range of habitats on the island of New Guinea and surrounding islands. Field identifications made as part of biodiversity surveys, including environmental impact assessments (EIA), are problematic because of unresolved taxonomy and the likelihood of cryptic taxa that have unknown distributions. Genome-scale whole-archive DNA sequencing was combined with morphological analyses to gain new insights into the level of diversity of the group in New Guinea, and the distribution of taxa. Much new material has been collected in the last decade through EIA, which has expanded the taxonomic and geographic scope of the analyses. The patterns of diversification suggest an adaptive radiation that has also been influenced by the elevational distribution of habitats and the central cordillera.

AO1-115

High Diversity of Bat Supports Hkakabo Razi Landscape for Natural World Heritage Status

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In February-March, 2016, our team conducted bat survey in 11 locations of the Hkakabo Razi Landscape by using mist nets, four-bank harp traps and bat detector. This area in Kachin State, northern Myanmar includes Hkakabo Razi National Park (NP), the Hponkan Razi Wildlife Sanctuary (WS), and the proposed Southern Extension of Hkakabo Razi NP. The purposes were to make an inventory of poorly known bat fauna from Hkakaborazi landscape, to confirm historic bat records in Kachin State and also to gather further information on the study of bat diversity in Kachin State. These information will further support to nominate Hkakaborazi landscape as the natural World Heritage Site under Criteria IX and X. We recorded 34 bat species from the survey areas, one of which has already been described as a new species, *Murina hkakaboraziensis* by our team and it is likely to be an endemic to the Hkakabo Razi Landscape. Additionally, three bat species are new to Myanmar (*Megaerops niphanae*, *Phoniscus jagorii* and *Murina pluvialis*). The results of this survey show that there is much still to be discovered in the region and emphasise the high diversity of bats in Hkakabo Razi Landscape, a relatively small geographical area. The present study has added the numbers of bat species to the faunal checklist of Myanmar and these findings are congruent with those for birds and other mammal species.

AO1-116

Bats in Tropical Semi-Deciduous Forests of Malaysia

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Semi-deciduous rainforests include both evergreen and deciduous trees which make up to one-third of the taller trees, though not all are necessary leafless at the same time. This forest only occurs at the region of the Kra isthmus north of the Thailand-Malaysia Peninsular border, due to decreasing rainfall and increasing seasonality in climate northwards. Perlis is the smallest and northernmost State of Peninsular Malaysia, covering an area of only 81,063 ha. Despite this, Perlis covers the largest area of semi-deciduous forests and is unique to Malaysia because of its Thai-Burmese affinities. Unfortunately, most of this forested area has been lost due to high demands for various land-use, and what is left, lies in a belt along the western border where this study took place. Four-bank harp-traps were positioned across trails, natural openings in vegetation, and cave entrances. The traps were checked at 2100 hours, and left overnight and rechecked at 0700 hours. Mist-nets of varying lengths were deployed at ground level at forest edges, forest gaps, open areas, and over rivers and streams. Stacked nets and canopy-nets were also used. They were deployed before dusk and left open for the entire night and checked every 15 minutes. A total of 34 species from 7 families were recorded. Two of which are possibly new species from the genus *Rhinolophus* and *Myotis*. Our findings also include the second record of *Rhinolophus marshalli* for Malaysia. Aspects of morphological variations and extended knowledge of the distribution of some species are discussed.

AO1-117

Biogeography of Southeast Asian bats and implications for conservation

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Effective conservation planning depends upon understanding the distribution of species and the factors that may limit their ranges. Conservation of widespread species can be achieved through a network of protected areas spread across many different regions or countries. In contrast, species with restricted ranges require targeted conservation efforts within their range. Until recently, many species of bats were thought to be widespread in Southeast Asia. However, research over the past 10-15 years using genetic techniques, combined with updated morphological studies, has shown that many of these are actually species complexes with individual species having much more limited distributions. I reviewed currently available information on distributional limits of Southeast Asian bats, to look for common patterns across species groups, as well as to highlight gaps in current understanding. Many species of bats, particularly species dependent upon intact forests, appear to separate into distinct biographical areas, similar to those of other taxa such as birds. In particular, many species of bats reach their northern or southern limits in peninsular Thailand. In many cases, a species found in peninsular Malaysia and Thailand is replaced by a morphologically similar but genetically distinct species in the rest of Thailand and/or Indochina. The major exceptions appear to be species that are tolerant of disturbed areas, which seem to be widely distributed throughout the region. However, some of these taxa have only had limited genetic research, and further studies are required to test whether they are all, in fact, the same species.

AO1-118

Is the Balinese subspecies of *Pteropus vampyrus* still *P. v. pluton*?

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Pteropus vampyrus is a widespread species in Southeast Asia, with four of its five subspecies found in Indonesia. These subspecies were associated with a suite of morphological and geographical characteristics which allowed for easy identification. However, the recent increase in threats to the species posed by hunting and habitat loss has brought into doubt the continued persistence of *P. vampyrus pluton*, the subspecies native to Bali and Lombok. The subspecies is very distinct given that it is the largest of the melanistic forms of *P. vampyrus*, yet most recent Indonesian records of *P. vampyrus* in Bali with a forearm length >210 mm are non-melanistic, which would identify them as the Javanese subspecies *P. vampyrus vampyrus*. Using UCE and mitogenomic data, we determined that individuals sampled from Bali were not genomically distinct from other *P. vampyrus* subspecies. Many Balinese individuals were also sister to those from Java. The combined morphological and genomic data suggest that what was historically recognized as *P. v. pluton* is no longer found in Bali.

AO1-119

On the Use and Misuse of Mitochondrial DNA in Taxonomy and Phylogeny

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Mitochondrial DNA (mtDNA) is widely used in taxonomic studies and still predominates as a phylogenetic marker despite the many caveats known to affect this locus (e.g. selection, introgression, mode of inheritance, Numts). The subtle but important distinction between gene trees and species trees is still ignored in many studies today. As the mitochondrial genome is inherited as a single unit, whether individual regions, multiple regions or indeed the whole mitogenome is used, these do not represent independent information sources; they all give rise to a mitochondrial gene tree. Aside from amplifying multiple mtDNA regions, it is still common practice to combine this approach with one, or very few nuclear loci. Due to the higher mutation rate (and thus parsimony informative sites) of mtDNA, we demonstrate with empirical datasets from the rapidly diversifying clades of horseshoe bats (Rhinolophidae) and evening bats (Vespertilionidae) that the mtDNA signal overpowers the nuclear signal; when a single nuclear locus is combined with the mtDNA, the mtDNA topology is recovered and that this is still the case when six nuclear loci are used. Although all genes have the potential to disagree with the true species tree, these problems are more substantial for mtDNA than for nuclear loci. Besides phylogeny, these issues with mtDNA have important consequences for taxonomy when it comes to species recognition (e.g. barcoding) and species description. Whether phylogenetic or taxonomic questions are of interest, a good approach would be to amplify at least two variable nuclear markers (but more if possible), and to analyse and present these separately from mtDNA.

AO1-120

Systematics of Malaysian Molossid Bat with a New Distribution Record for Borneo Island

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Members of molossid bats are among those that minimally surveyed and studied in Malaysia due to their high-flying nature that rarely caught in mist-nets. Thus, very few information especially the systematics and distribution of this group in Malaysia. The Northern free-tailed bat, *Chaerephon johorensis*, has a limited distribution in the Sunda region and have been recorded only from mainland Malaysia and Sumatra. This species is listed as vulnerable with a declining population trend due to its narrow range distribution. The northern free-tailed bat has a scarce distribution with only a few known records from Peninsular Malaysia, and only one record from Sumatra. A recent survey in the rainforest of Sarawak and Sabah have recorded individuals of *C. johorensis*, confirming the presence of this elusive species in Borneo. Notes on its distribution from other parts of Malaysian Borneo together with the morphometric and genetic information within our sample collections is reported herein. Genetic data suggest that despite echolocation variation among members from different locality, all individual are similar to their conspecifics in Peninsular Malaysia. The new geographic record highlights the significance of constant survey and monitoring especially in areas with limited access, which emphasize the value of forested areas for species conservation.

AO1-121

Scanning the underworld horizon: global diversity patterns, threats, and conservation priorities for cave-dwelling bats

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Bats are “keystone species” in cave ecosystems due to their crucial role in delivering organic material and energy. Thus protecting cave-dwelling bats provides a mechanism to protect the whole cave ecosystem. Understanding their diversity patterns and conservation status requires a concrete baseline, which is central to establishing appropriate priorities for regional and global biological conservation targets. In this study, we attempt to address this gap to inform and develop strategic ideas to effectively protect bats and cave ecosystems at multiple scales and dimensions. Our analyses showed that over 40% (612 bat species) are at least partially dependent on caves. While 26% (*n*=159) of cave bat species were country endemic with the highest species richness recorded in Madagascar (*n*=23, 79% of country cave bat species record), Indonesia (*n*=21, 18%), Australia (*n*=18, 50%), the Philippines (*n*=12, 26%), and China (*n*=10, 10%). While, combining species richness and endemism patterns, the Indo-Malayan realm turned to be the epicentre for cave-dwelling bat diversity. The recent increase in exploration and elucidation of cryptic and complexes in the region has facilitated understanding of these patterns. However, 41% of the cave-dwelling bat species are chiefly imperilled by deforestation, 34% tourism and caving activities, 24% mining and quarrying, 23% shifting agriculture and 17% by hunting. In addition, 78 species cave-dwelling bats or 6% of global species are on the threatened status and 60 species remains data deficient. It is undeniable that caves are important ecosystems and are vulnerable to many forms of disturbance. Therefore, it is imperative that conservation priorities and policies should be properly aligned allocated to prevent future losses and to certainly maintain these ecosystems and associated services.

AO1-122

Bats from mangrove of Vietnam with remarks on taxonomy and echolocation

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Mangrove ecosystem is essentially important for human life and ecological environment. It occurs throughout the coastal areas of Vietnam. However, prior to 2014, bats from this ecosystem of the country were almost unstudied. Between 2015 and 2018, we conducted a series of bat surveys in selected mangrove areas in Vietnam. Results from the surveys comprise 16 species belonging to 5 families (Embanolluridae, Hipposideridae, Pteropodidae, Rhinolophidae, Vespertilionidae). Of which, several species were poorly documented from the country over the past decades (*Pteropus hypomelanus*, *P. lylei*, *P. vampyrus*, *Cynopterus brachyotis*). On the other hand, we obtained unusual forms of *Cynopterus* and *Taphozous*, which are different from all published descriptions. Remarkably, *Cynopterus horsfieldii* was distinguished from other species of the genus by its dental diagnoses with “ridge and cusp” on the surface of the first and second lower molar. Our results in morphology and genetics indicated that the “ridge and cusp” are not diagnoses of the species. Furthermore, identification of *Taphozous* from the Southeast Asian countries is still unclear due to lack of data in genetics and echolocation. Our recordings suggested a cryptic species of *Taphozous* and provided new findings in echolocation calls of emballonurid bat species. Key words: Echolocation, fruit bat, taxonomy, Tomb bat, Vietnam.

AO2-101

Collagen fiber orientation within the bones of long-lived big brown bats (*Eptesicus fuscus*) relative to mice

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Insectivorous bats offer a novel perspective in aging research compared to typical model taxa as they live at least 3 times longer than terrestrial mammals of an equivalent body size. No studies have quantified age-related changes in the orientation of the bone matrix across the lifespan of long-lived bats. This study uses quantitative polarized light microscopy (qPLM) to test two hypotheses. First, we expect that bats display a different pattern of bone tissue organization compared to mice. Second, we expect that bats and mice share similar strategies for age-related changes in bone organization. This study compared the matrix of the forelimb bones of big brown bats (*Eptesicus fuscus*) and C57BL/6 mice. Results showed bats retain a larger endocortical region (10-25%) of bone cross-section compared to mice (0.5-3.5%), even with age, suggesting that they are unique (Hyp. 1) and display a different aging strategy compared to mice (Hyp. 2). Within this endocortical region, bats displayed overlapping lamellae with more helical collagen fiber orientations with age. Within the cortex of both taxa, collagens were oriented more longitudinally compared to that of the endocortical region and few age-related changes were seen. Among bats, 56% of variation within cortices was explained by a proximodistal gradient in bones along forelimb, and only 6% of variation was explained by age. Results therefore suggest that bats differ from mice in the large size and helical organization of the endocortical region that is retained throughout their lifespan, and that bats uniquely display a proximodistal gradient in matrix structure.

AO2-102

Resolving phylogenetic relationships and species limits in Afrotropical bats

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We have recently surveyed phylogenetic relationships and species limits in several widely distributed and speciose bat genera in the Afrotropical Region. Our analyses are based on recent, dense sampling from East Africa and neighboring regions, using sequences of mitochondrial (Cytb) and nuclear intron (ACOX2-3, COPS7A-4, ROGDI-7, STAT5A, and occasionally also ACPT and ABHD11) loci. To date, we have analyzed *Rhinolophus* (Rhinolophidae), *Nycteris* (Nycteridae), *Otomops* (Molossidae), *Myotis* and *Scotophilus* (Vespertilionidae), and *Miniopterus* (Miniopteridae). In each case (save with *Otomops*), lineage delimitation analyses have uncovered cryptic lineages that appear to qualify as undescribed species. For *Rhinolophus,* as many as 12 new lineages are recovered in four of the six Afrotropical species groups, and these include cases of sympatry. On the other hand, expanded population and gene sampling challenges the validity of some recognized species (2-5 in the case of *Rhinolophus*). We are now characterizing clades using their morphology and vocalizations to assess congruence in genetic, morphological, and bioacoustic variation and to apply names to the recovered groups; integrative taxonomy is needed to resolve the taxonomic implications. We also plan to determine shared and particular aspects of the historical biogeography of these co-distributed genera. The utility of these genetic markers in resolving both phylogenetic relationships and species limits and their mounting numbers in GenBank offer promise that genera distributed throughout the Paleotropics and adjacent Palearctic can finally be analyzed comprehensively. Many tropical areas remain unsampled both in the Afrotropics and in the Indomalayan region, so additional species discovery and phylogenetic surprises are practically assured.

Transcriptome Assembly and Functional Annotation in Five Tropical Bat Species by Using High-Throughput RNA Sequencing

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Next generation sequencing is an innovative tool to perform and predict detection of novel transcripts. We assessed transcriptomes from liver tissue of five Neotropical bat species belonging to distinct families: *Artibeus jamaicensis* (Phyllostomidae), *Mormoops megalophylla* (Mormoopidae), *Nyctinomops laticaudatus* (Molossidae), *Peropteryx macrotis* (Emballonuridae), and *Myotis keaysi* (Vespertilionidae). Our main goal was to describe the transcriptome assembly by RNA-Seq. Our Hi-Seq 4000 multiplex sequencing provided 403 million paired-end reads with an average length of 101 bp. After confirmed sequences quality, we used the 99% of the paired end reads to perform a *de novo* assembly by using the Trinity protocol for each specimen (3 repeats by species). Resulted transcripts consisted of 685,849 for *A. jamaicensis*, 469,620 for *M. megalophylla*, 456,572 for *M. keaysi,* 617,036 for *N. laticaudatus* and 634,439 for *P. macrotis.* We performed an orthologue analysis between our species with other vertebrates, and found a 75% consistency among them. We detected 226,373 genes of 20,467 potential orthogroups, but only 78 genes were placed in the inferred groups, and almost 37% were shared among studied species. We concluded the presentation of *de novo* transcriptomes for five tropical species with good quality and large enough to provide data for future analysis (i. e. metabolic routes, enzymatic paths, etc.).

AO2-104

Population genetic structure of island flying fox *Pteropus hypomelanus* Temminck, 1853 in Thailand

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Study of population genetic structure can provide information for conservation planning, especially in threatened species. Most flying fox species (Pteropodidae) are distributed on islands and threatened mostly by habitat loss and hunting for bushmeat. Island flying fox *Pteropus hypomelanus* is one of threatened species with high extinction risk due to limited dispersal ability, small home ranges and high hunting pressure. In Thailand, island flying fox can be found on islands along the coast in the Gulf of Thailand and the Andaman Sea. However, information regarding roosting sites and genetic relationship among populations in Thailand is inadequate. Thus, this study aims to investigate population genetic relationship of island flying foxes in Thailand. DNA was extracted from tissue and fecal samples (n=24) obtained from Chan, Khram Yai and Talu Islands in the Gulf of Thailand, and Similan islands in the Andaman Sea. Mitochondrial control region was amplified and sequenced. A total of 16 haplotypes (478 bp) were obtained with 49 variable positions, 42 of which were parsimony informative and 7 were singletons. Nucleotide diversity (π) was 0.03213, whereas overall haplotype diversity (h) was 0.960. Interestingly, shared haplotypes were detected at all localities including Chan and Similan islands which were approximately 600 kilometers apart. Our results suggest substantial gene flow among populations and panmixia paradigm in Thai island flying foxes. These information would be helpful for conservation management and planning as well as disease surveillance program in island flying foxes.

AO2-105

Genomic signatures of evolutionary divergence among Hawaiian hoary bat populations

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We examine the genetic and population status of Hawaiian hoary bats (*Lasiurus cinereus semotus*), and their relationship to North American *L. cinereus*, through whole-genome analysis of single-nucleotide polymorphisms (SNP) mapped to a *de novo*-assembled reference genome. We also report levels of genomic diversity and divergence, population structure, and gene signatures of selective sweeps in populations on the islands of Hawaii, Maui, Oahu, and Kauai. Based on sequencing of 23 genomes, we find that Hawaiian hoary bats are distinct from continental hoary bats, and form a monophyletic group. SNP data suggest Hawaiian hoary bats are genetically distinct by island. The greatest difference in population structure is between Hawaii and Oahu, while Maui and Hawaii are most similar. The site frequency spectrum (SFS) analysis reveals a relative deficit of rare alleles in the Hawaii population, consistent with recent population expansion. The population on Oahu had more genomic regions that showed putative selective sweeps than the populations on Maui and Hawaii combined. Notable differences found in gene ontology that we identify may inform our understanding the evolution of echolocation in the Hawaiian hoary bat. Effective population size estimates were similar between islands (average ~139,000), and are approximately 83 percent smaller than estimated effective population size of the North American hoary bat. Because this endangered species is experiencing fatalities at wind energy generating facilities a clearer understanding of the population genetics of this bat in the Hawaiian Islands is of timely importance.

AO2-106

Phylogenetic Analyses Show Bat Communities in Baja California Harbour a High Diversity of Cryptic Ectoparasite Species

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Background. Characterising bat ectoparasite diversity is fundamental to studies of host-parasite interactions (e.g. influence in bat fitness, pathogens transference) and for understanding how ectoparasite community structure can be shaped by hosts' ecological constrains. However, ectoparasite fauna are poorly known for most species. This study aimed to characterise bat bugs, flies and ticks diversity from 20 species of bats captured along the Baja California peninsula, Mexico.

Methods. We used a phylogenetic approach to describe taxon identity of 221 ectoparasites. This was done by sequencing Cytochrome C Oxidase subunit I and 18S ribosomal gene fragments using Bayesian and Maximum Likelihood methods.

Results. Multiple novel lineages of bat bugs (*Cimicidae*), flies (*Nycteribiidae* and *Streblidae*) and soft ticks (*Argasidae*) were revealed, and two new records of Streblid flies. Within families, the new linages showed more than 10% sequence divergence, consistent with separation at the species level. Both bat flies families showed host specificity, also finding specimens from one lineage parasitizing *Myotis* species only. One Nycteribiid haplotype from *Antrozous pallidus* specimens was found throughout the peninsula, suggesting host migration. Different bug and tick communities were found in the North and the South, suggesting roosting sites and environmental factors may play a role in their range boundaries.

Conclusions. This is the first systematic study of bat ectoparasites in the peninsula, discovering highly genetically differentiated lineages and patterns of bat migration through ectoparasites haplotypes. This work is the initial step for understanding how ecological and evolutionary interactions shape parasite community structure along hosts and environmental gradients.

AO2-107

IS STRESS MANAGEMENT A KEY FACTOR IN THE LRS OF FEMALE GREATER HORSESHOE BATS?

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We studied stress impacts on LRS of bats in southwestern UK exposed to oceanic climate. Severe reproductive stresses were associated with short night length in June, and the extreme early growth needs of pups. We hypothesise that bats have a stress assessment system that allows them to take key decisions relating to four reproductive events. They were: when to first breed; pup sex; when to give birth annually, and when to omit a breeding year.

The reproductive performance of female bats born to different matrilines was followed over 11 years from 1987 through 5 generations to 2018. Matrilines were divided into two mega ranks (MR1 & MR2) based on combined LRS. Highly successful female bats from both MRs (named Stars) were also selected for certain analyses. Breeding starts at either age 2 years (early breeder or EB) or later at 3+ years (later breeder or LB); pup sex, and annual birth date (day from 1st June). Years with breeding omission may occur in any year after first parturition.

MR1 mothers show higher resistance to reproductive stresses. In good climate years they produce fully-grown Stars that have mostly female pups. Stunted MR1 pups can survive to breed, but have more male pups, shorter lifespans and may omit breeding. MR2 mothers show lower stress resistance. They are often LBs whose LRS is male-dominated with years of omitted breeding. Stunted MR2 females rarely survive to breed, or die after their first pup.

Our hypothesis is supported by these data.

AO2-108

Effects of Dispersal Ability on Population Structure of Six Bat Species in Eastern Cape Forests, South Africa

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The dispersal ability of an animal is an important determinant of genetic connectivity and population structure, especially for volant taxa such as bats. The effects of correlates of dispersal ability (body size, aspect ratio, wing loading and wingtip shape index) were tested on four estimators of molecular diversity (haplotype diversity, nucleotide diversity, k and F_{ST}) for six insectivorous bat species. A negative correlation between genetic structure (F_{ST}) and wing loading was hypothesized. Mitochondrial DNA sequences, cytochrome-*b* (1,140 bp) and D-loop (400 – 550 bp), were sequenced for *Laephotis botswanae* (N=23), *Miniopterus fraterculus* (N=56), *Myotis tricolor* (N=40), *Neoromicia nana* (N=43), *Pipistrellus hesperidus* (N=90) and *Rhinolophus swinnyi* (N=37) collected from forests of the Eastern Cape Province of South Africa. Contrary to expectations, a significant relationship was not found between genetic structure and wing loading (r = -0.81). However, wing loading was found to have a significant positive correlation with nucleotide diversity (r = 0.94, p = 0.03) and k (r = 0.91, p = 0.02); and wing tip shape index was negatively correlated with haplotype diversity (r = -0.89, p = 0.03). Thus, forest associated taxa, *Miniopterus fraterculus, Myotis tricolor* and *Pipistrellus hesperidus*, are better adapted for agility and speed (typically habitat generalist clutter-edge species) have greater genetic variation than clutter-adapted forest specialists such as *Rhinolophus swinnyi*. Our data suggests that reduced habitat connectivity, due to forest fragmentation, may be reducing genetic diversity in forest specialist species. This points to the need for effective forest management to maintain genetic connectivity in specialist species populations.

Evolution of skull diversity across the bat radiation

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The skull performs multiple functions (e.g., feeding, protecting the brain and supporting sensory organs), but few studies have tested the joint impact of these functions on skull morphological diversification. Bats are ideal to investigate this issue because they are extremely diverse in species richness, skull morphology, diet, and sensory modalities. We explore the potential impacts of sensory and dietary functions on the evolution of skull shape across bats. We used micro-Computed Tomography scanning to generate 3D geometric morphometric datasets of the cranium and mandible of 203 bat species, spanning all families, diets and sensory modalities. We used these data in phylogenetic comparative analyses to uncover macroevolutionary patterns and potential functions shaping skull diversity across bats. These included: (1) estimation of adaptive landscapes of skull shape evolution, (2) quantification of skull shape disparity during bat evolution, and (3) tests of associations between shifts in modularity of the skull and sensory transitions. We found that early divergences in cranial shape across major bat lineages are best explained by selective regimes based on echolocation, including transitions between echolocators and non-echolocators, and between oral and nasal emitters. Echolocation type also seems to have strongly influenced cranial morphological disparity, and may be associated with changes in skull modularity, allometry and lability. Recent shifts in cranial and mandible shape evolution were associated with dietary diversification primarily within Phyllostomidae, and may have been driven by increased cranial morphological integration. These results illuminate potential drivers and mechanisms of morphological and ecological diversification across bats.

AO2-111

Evolution of developmental sequence in bats and its peculiarity among mammals

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To understand how bats, the only group that has acquired powered flight and undergone drastic morphological changes, deviate developmentally from other mammals is one of the key avenues to unravel the evolutionary history of bats. Here we present a comprehensive comparative analysis on prenatal developmental sequence of bats and other closely related mammals. Fetal specimens of more than 20 chiropteran species and 50 non-chiropteran mammals were studied by microCT technique and macroscopic observation. We found that considerable heterochronic shifts occurred in the common ancestor of bats. The developmental duration of both the forelimb and hindlimb was much extended compared to other mammals. We also detected that the development of the hindlimb was particularly extended and even initiates its development much earlier than the forelimb. The outgrowth of the limb bud of the hindlimb and ossification of the foot digits occur much earlier than the forelimb, a pattern not seen in any other closely related mammals. It is known that the bat's newborn foot is generally highly precocial and its size is already comparable to that of adults. Given that the foot is required to be firm and stable enough at the time of birth to allow continued attachment to the mother and/or cave walls, we suggest that the accelerated development of the hind limb is linked to the unique life history of newborn bats. Since the forelimb requires extended postnatal time to be large enough to be fully functional, we postulate that prenatal bats invest in earlier development of the hindlimb.

AO2-112

Limiting the damage: longitudinal comparative transcriptomics reveals novel mechanisms underlying extended healthspan in bats

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Bats are the longest-lived mammals given their body size, showing little signs of ageing. However, the underlying molecular mechanisms of their extended healthspans are poorly understood. To address this question we carried out an eight-year longitudinal study of ageing in long-lived bats (*Myotis myotis*). We deep sequenced ~1.7 trillion base pairs of RNA from 150 blood samples collected from known aged bats to ascertain the age-related transcriptomic shifts and the possible miRNA-directed regulation that occurred. We also compared ageing transcriptomic profiles between bats and other mammals by analyzing 298 longitudinal RNA-Seq datasets. Bats did not show the same transcriptomic changes with age as commonly observed in humans and other mammals, but rather exhibited a unique, age-related gene expression pattern associated with DNA repair, cell cycle regulation, immunity and tumor suppression that may drive their extended healthspans. We show that bats have naturally evolved transcriptomic signatures that are known to extend lifespan in model organisms and identify novel genes not yet implicated in healthy ageing. We further show that bats' longevity profiles are partially regulated by miRNA, thus providing novel regulatory targets and pathways for future ageing intervention studies. These results further disentangle the ageing process by highlighting which ageing pathways contribute most to healthy ageing in mammals.

Evolutionary History of Myotis nattereri sensu lato: How do the Phylogenies Reticulate?

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There is an increasing evidence showing that interspecific gene flow played a major role in the evolutionary history of several species groups. Such admixture events lead to introgression of genes and reticulate the species phylogenetic trees. In this study we present the biogeography of a widely distributed Western Palaearctic bat species complex, namely *Myotis nattereri* sensu lato. This complex exhibits high genetic diversity and is composed of deeply diverged genetical lineages. We analysed mitochondrial and nuclear DNA markers to infer the phylogenetic relationship of the lineages and found that their mitochondrial and nuclear phylogenies were discordant. Some lineages are placed to different branches depending on the analysed markers, which we interpret are caused by past hybridization. We identified three such introgression events, which occurred when spatially separated lineages came into contact after range expansions. Our findings suggest that the *M. nattereri* complex has a reticulate evolutionary history with multiple cases of hybridizations between some of the identified lineages.

AO2-114

Penis size and sperm quality, are all bats grey in the dark?

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Penises play a key role in sperm transport and in stimulating female genitals. This should impact post-copulatory competition, and expose penis characteristics to sexual selective pressures. Studies of male genitalia have repeatedly reported negative static allometries, which mean that, within species, large males have disproportionally small genitals when compared with smaller individuals. Males of some sperm-storing bat species may stand as an exception to such a pattern by arousing from hibernation to copulate with torpid females. The selection for large penises might take place, if a long organ provides advantages during post-copulatory competition and/or if females have evolved mechanisms allowing the choice of sire, relying on characters other than pre-copulatory traits (e.g., penis size). In this study, we measured dimensions of the erected penis in 4 sperm-storing bat species. Furthermore, we collected sperm and evaluated the link between penis dimensions and sperm velocity. Our results revealed steep allometric slopes of the erected penis length in *Barbastella barbastellus* and an inverse allometry of penis head width in *Myotis nattereri*. Furthermore, penis head width correlates with sperm velocity in *Plecotus auritus*. For this last species, we propose that penis shape might act as a marker of male fertility. This work was founded by the Polish National Science Centre on the basis of decision number DEC-2013/10/E/NZ8/00725 and Swiss Science Foundation number P2BEP3_168709.

AO2-115

Aerial Righting in Response to Flight Perturbation in *Carollia perspicillata*

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Locomotion requires the ability to recover from unexpected perturbations. Natural environments impose frequent, diverse disruptions to steady locomotion, which has led to the evolution of mechanisms that enhance rapid, effective perturbation responses. Most knowledge about recovery from disruptions to motion comes studying terrestrial locomotion, and little is known about the flying case. We investigated perturbation recovery in *Carollia perspicillata* by administering well-defined gusts during forward flight, inducing two types of "aerial stumbles": to the body, which induced upward pitch, and to one wing, which induced roll about the head-to-tail axis. Bats recovered pre-disturbance body orientation and left-right motion symmetry in a single wingbeat. Their primary adjustment was to the degree of flexion/extension of wing joints. Bats recovered from body perturbations by symmetrically extending their wings cranially and dorsally during upstroke, and from wing perturbations by asymmetrically extending their wings throughout the recovery wingbeat. We used a dynamical model to test the hypothesis that wing extension asymmetry generates inertial torques large enough to produce the body reorientation we observed after wing perturbations. Results support the hypothesis, and show that following the adjustments of recovery, restoring symmetrical wing extension contributed to decelerating the recovery rotation via passive aerodynamic mechanisms. Response to perturbation varied among joints along the wingspan: shoulder rotations changed little, but motions at the elbow and especially the wrist were modified. This pattern is similar to the proximo-distal gradient in neuromechanical limb control observed in terrestrial locomotion, and could be a general feature of tetrapod motor control.

AO2-116

Biomechanics and not ecology describe variation in cross-sectional shape of the humerus in bats

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The wing in bats is an extreme postcranial adaptation for self-powered flight. Bats exhibit a wide ecological diversity associated with different foraging strategies and diets. Studying the morphological variability of forelimb bones can help us elucidate whether biomechanical or ecological aspects of the wing shaped the phenotypic diversification in bats. The humerus experiences one of the highest levels of biomechanical stresses during flight. For this reason, understanding the functional capabilities and limitations of the humerus could shed some light on the ecological differentiation across bat taxa. Cross-sectional geometry is a good indicator of the biomechanical properties of a bone (e.g. resistance to bending). To describe humeral cross-sectional shape differences among bats, we used 3D geometric morphometrics to quantify cross-sectional morphological diversity. We sampled 27 bat species, 15 families, and a wide range in size and foraging behaviors. We compared the cross-sectional shape of the humerus at three different locations (25, 50 and 75%) along the length of the bone. Differences in humeral cross-sectional shape across the bone were consistently associated with changes in size. Interspecific differences in cross-sectional shape were only detected closer to the epiphyses (25 and 75%). Cross-sectional humeral shape did not correlate with diet or foraging behavior. Our results indicate that morphological differences among bats in humeral cross-sectional shape could reflect to size-dependent biomechanical demands during flight. Moreover, despite the importance of locomotory adaptions for habitat use, ecological aspects of the wing (e.g. diet and foraging behavior) did not explain the morphological variability seen in our results

Diversification of the Indo-Australasian bent-winged bats

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The bent-winged bats *Miniopterus* spp. (Miniopteridae) are abundant and distributed widely across the Indo-Australasian region. The similarity of appearance within the family and the consequent lack of clear diagnostic morphological characters has exacerbated the difficulty of classifying a group over bats that has diversified over thousands of islands and a history of sea level changes. The piecemeal approach to their taxonomy over more than a century by multiple taxonomists using traditional taxonomic methods, who had only limited access to geographic and phylogenetic sampling, has led to a confusing array of names and peculiar distributions. Eleven species are recognised currently, but undiscovered cryptic species are likely. We have generated a comprehensive view of diversity and distributions of Indo-Australasian Miniopteridae using single nucleotide polymorphisms (SNPs) generated using a genome-scale DNA sequencing method ('DArTseq') from 650 individuals. We integrated traditional morphometric measurements (225 individuals) with landmark-based geometric morphometric analysis of 3D models from micro-CT x-ray scans (70 skulls) to identify diagnostic characters for each identified genetic lineage. Phylogenetic analysis (RAxML) and structure-like population assignments (sNMF) identified 20 distinct genetic clusters/lineages, each suggesting one putative species. This effectively doubles the number of species identified based on past morphological analyses. Examination of regional distributions reveals the historical expansion and diversification of several lineages representing three main size forms, the result of past land connections and separations, and possible over-water dispersals.

AO2-119

Evolution and Ontogeny of the Bat Calcar

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The appearance of novel anatomical structures in the evolutionary record has long puzzled biologists. Bats, with their extraordinary morphological innovations across approximately 1400 species, are an ideal clade for exploring the origin and evolutionary impacts of novel vertebrate forms. Here, we tell a story of evolutionary novelty from development through diversification by considering the neomorphic calcar, a skeletal element unique to bats. We integrated multiple methods, including CT scans and histological sectioning, to study calcar anatomy across embryos, neonates, juveniles, and adults distributed among several species, with a primary focus on *Carollia perspicillata* (Phyllostomidae), *Tadarida brasiliensis* (Molossidae), and *Eptesicus fuscus* (Vespertilionidae). We then interpreted this developmental data in the context of a broader data set of adult calcar morphologies from species across Chiroptera. Our anatomical data demonstrates that a mass of cells associated with the calcaneus ankle bone in bat embryos has, over evolutionary time, diversified into a variety of adult forms. Some aspects of calcar ontogeny have implications for calcar function, such as the development of calcified tissues and flexible joints. This anatomical data also suggests some hypotheses for the initiation of calcar development. Because the bat calcar is an anatomically diverse novelty found in a speciose clade, it serves as a model for understanding how novel anatomical structures might arise and prompt clade diversification.

AO2-121

Diversification of South American Vespertilionidae Is Not Constrained by Evolutionary Priority Effects

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Diversity-dependent diversification (DDD) claims that as groups experience cladogenesis, diversification slows down as a response to the gradual filling of niches. However, stochastic events such as immigration history may prevent the establishment of secondary colonizers due to preemption of niches, a phenomenon known as priority effects. To investigate the influence of historical contingency in South American vespertilionids, we evaluated diversification rates of incumbent clades of aerial insectivorous bats in South America (SA non-vesper) and North/Central American vespertilionids (NA vesper) versus vespertilionids in South America (SA vesper), where this clade is a secondary colonist. Within a phylogenetic framework, biogeographic origin and species occurrence, we assessed the distribution of speciation events across time, fitting of time-variable diversification models, and clade dependent and geographic state estimates of diversification rates in each of the clades. Most cladogenetic events are concatenated in the early evolution of all clades. Incumbent clades (SA non-vesper and NA vesper) show a decline in diversification towards the tips, while SA vesper shows a burst of lineage accumulation around 15–10 Mya, with steady increase until present-day. Time-dependent procedure presents best fit for models with exponential speciation and constant extinction for incumbent clades, whereas a constant rates model best described SA vesper, which also showed higher speciation rates. Our results are inconsistent with DDD and evolutionary priority effects constraining SA vesper diversification, probably resulting from shorter evolutionary history of the clade and not from competitive inferiority or phylogenetic niche conservatism. Vespertilionids are likely a case of hidden diversity in South America.

AO2-123

Multilocus phylogeny and species delimitation within the *philippinensis* group (Chiroptera: Rhinolophidae)

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Rhinolophids are a widespread and diverse family. Their high level of morphological convergence has made taxonomic identification and estimation of species diversity problematic. The *Rhinolophus philippinensis* group, which is characterized with huge ears and low echolocation frequency relative to body size, is a specific group among all the rhinolophid groups, but the phylogeny of this group is poorly understood. In this study, we performed integrated analyses of the morphology, acoustic, and genetic data, and constructed the first multilocus phylogeny for the *philippinensis* group using four mitochondrial genes, four autosomal introns and one Y-linked intron in 95 specimens representing nine taxa. Phylogenies were constructed based on concatenated phylogenetic methods and a multilocus coalescence approach. The estimated phylogenies revealed the polyphyly of the *philippinensis* group. Except for *R. philippinensis*, all the other species formed a monophyletic cluster, named herewith as "*R. macrotis*" species group. Phylogenies, genetic and phenotypic divergence, and species delimitation analyses supported the revised status of *R. paradoxolophus* as a subspecies of *R. rex*, *R.* cf. *macrotis* as a subspecies of *R. macrotis*, and *R. huananus* and *R.* cf. *siamensis* as junior synonyms of *R. siamensis*. Significant discordances were found between the mitochondrial and nuclear gene trees, suggesting incomplete lineage sorting or ancient introgression events within the *philippinensis* group. The *macrotis* group appeared to have undergone a rapid radiation approximately 2.57 Ma during the early Pleistocene period due to palaeoclimatic oscillations. Reconstruction of the ancestral ranges suggested a wide distribution of the common ancestor for the *philippinensis* and *macrotis* groups.

AO2-124

Diversification Rates Have No Effect on the Convergent Evolution of Foraging Strategies of *Myotis*

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Convergent evolution, the independent development of the same trait in different taxa, appears to be a common process in natural systems, but it is unclear if diversification rate shifts can promote or prevent the reappearance of phenotypes. Here we investigate if the convergent evolution of traits is linked to diversification shifts using phylogenomic, biogeographic and comparative approaches. We use as an example the species-rich chiropteran genus *Myotis*, the only bat genus with a worldwide distribution, to investigate processes that promote convergent adaptation. *Myotis* contains three main ecomorphs linked to foraging strategies that seem to be evolved repeatedly in several biogeographic regions. We first analyze genomic and morphological data sampled from 106 *Myotis* lineages (~70-80% of extant taxa) by estimating species relationships, divergence times, biogeographic history and quantifying morphological divergence in such lineages. Second, we document the ecological lability of *Myotis* by analyzing an extensive morphometric dataset and show phylogenetic informative traits related with the shape of the cranium, and use ancestral state reconstruction to identify shifts towards optimal foraging strategies. Finally, we explore whether shifts in the diversification rates are related to the colonization of new biogeographic regions or appearance of new ectomorphs in a region. While diversification rates in the genus as a whole are roughly constant, speciation rates seem to be area-dependent for temperate and tropical taxa and independent of ecomorph evolution. Taken together, our results document the phylogenetic and biogeographic basis of a striking example of adaptive convergence in one of the most successful groups of mammals.

AO2-125

Mitochondrial Introgression Suggest Historical Replacement in Palaearctic Whiskered Bat Species

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Palaearctic whiskered bats form a morphologically cryptic species complex. Especially two of these, *Myotis mystacinus* and *M. davidii*, are particularly interesting because they share the same mitochondrial lineage in some parts of their distributions. In this study, we analyse mitochondrial and nuclear DNA markers to infer the phylogenetic relationship of these cryptic species, covering their entire distribution ranges. We found that samples in Anatolia and the Balkans have discordant mitochondrial and nuclear population assignments. We interpret that these discordances are caused by past hybridization, which subsequently led to mitochondrial introgressions. Our findings suggest that *M. davidii* replaced *M. mystacinus* in Anatolia and the Balkans, when they expanded their distribution range to the west.

AO2-127

Comparative Transcriptome Sequencing Among Natural *Rhinolophus ferrumequinum* Populations with Different Acoustic Phenotypes

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Although the sensory drive hypothesis can explain the geographic variation in echolocation frequencies of some bat species, the molecular mechanism underlying this phenomenon are still unclear. The three lineages of greater horseshoe bat (*Rhinolophus ferrumequinum*) in China, northeast, central-east and southwest, have significant geographic variation in resting frequencies of echolocation calls. Here we reported transcriptome of cochleae collected from three genetic lineages of *R. ferrumequinum*, an appropriate organism to study geographic variation in echolocation signals, and tried to understand the mechanisms behind this phenomenon of bats by analyzing gene expression and sequence variation. A total of 8,190 differentially expressed genes (DEGs) were identified, and the regression analysis obtained a significant linear correlation between the number of DEGs and resting frequency difference of pairwise comparisons. We identified five modules which were significantly related to resting frequency or forearm length from all the DEGs. Genes in the largest module relating to resting frequency significantly enriched in the gene categories involved in the neural activity, synaptic function, and ion channel activity. Using 21,945 single nucleotide polymorphisms, we identified 18 outlier loci associated with hearing. Five of them expressed differently among populations. We also found five genes which were both under positive selection and related to hearing from 4,105 one-to-one orthologous gene pairs between three lineages of *R. ferrumequinum*, and three other Chiroptera species. The variability of gene expression and sequence divergence at the molecular level provide evidence to parse the genetic basis of geographic variation of echolocation signals of greater horseshoe bats.

Using Multiple Fossil Calibration Scenarios Highlights the Impact of Poorly Supported Chiropteran Fossils on Divergence Estimates

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Bats include 20% of all described mammals, however their origins remain uncertain. Shortcomings of the molecular clock and a contentious fossil record have compounded uncertainty regarding the clade's age. Vetting appropriate fossils to inform Bayesian priors is a difficult and often overlooked step when conducting Bayesian molecular dating analysis and can lead to divergence estimates which are invalidated by fossil data. At present bats are believed to have diverged between 54 and 75 Ma, with some of the highest-cited estimates placing the divergence close to the 66 Ma, 10Ma earlier than the oldest stem bat taxa in the fossil record. This study assesses the effect of fossil selection criteria on divergence estimates by reanalysing the timescale of bat evolution under variously calibration scenarios ranging from appropriately conservative to unjustifiably liberal. Bayesian molecular clock analyses were conducted using unique calibration scenarios to determine the impact of increasingly stringent selection criteria for fossils used to inform Bayesian priors. Our results suggest a divergence estimate of 52 - 56 Ma for the chiropteran crown and 48 - 52 Ma and 43 - 47 Ma for Yinpterochiroptera and Yangochiroptera respectively. Asymmetric treatment of confidence between very liberal minimum bound and overly conservative maximum bounds can explain large temporal discrepancies between most previous molecular dates and fossil record interpretations for the timing of bat origins.

AO2-129

Whole Mitochondrial Genome Sequencing and DNA Barcoding of *Rousettus amplexicaudatus*– Implications on Taxonomy of Philippine Bats

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Molecular phylogeny of organisms using whole mitochondrial genome is useful in resolving intra-familial phylogenies in comparison to the use of single genes, due to the presence of more variable sites and information from possible gene reordering. On the other hand, DNA barcoding using small fragments of the mitochondrial genome is still widely used to confirm the identity of morphologically identified species. In the Philippines, however, mitochondrial genome sequences of bats have been lacking in the genetic database, thereby causing gaps in molecular phylogenetic studies which could be useful in resolving the taxonomy of bats in the country. To address this, we assembled the whole mitochondrial genome of *Rousettus amplexicaudatus* obtained from Illumina NextSeq500 platform. We also amplified the Cytochrome oxidase I (COI) gene from *R. amplexicaudatus* samples obtained from different locations in the Philippines. Construction of a maximum likelihood tree (GTR+G model) using the assembled mitogenome of *R. amplexicaudatus* and mitogenome of bats obtained in the genetic database supports the modern division of bats into Yinpterochiroptera and Yangochiroptera. On the other hand, COI barcodes show that *R. amplexicaudatus* samples closely matches the *R. amplexicaudatus* sequences in the genetic database (89.30%-90.32% Identity). However, maximum likelihood tree (TPM2uf+G model) using COI sequences of the genus *Rousettus* suggests the division of *R. amplexicaudatus* obtained from the Philippines to rest of the *R. amplexicaudatus* in Southeast Asia (maximum corrected sequence divergence = 27.97%). Thereby suggesting possible divergence of *R. amplexicaudatus* in the Philippines to other populations in Southeast Asia.

AO2-130

Conservation genetics of the Formosan flying fox

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Genetic management of small or fragmented populations is crucial for biodiversity conservation, particularly for endangered and threatened species. With detailed genetic information, we could effectively monitor the loss of genetic diversity and, therefore, develop proper management decisions accordingly. The Formosan flying fox, *Pteropus dasymallus formosus*, a subspecies of the Ryukyu flying fox, once abundant on Lyudao, southeastern coast of Taiwan, is now almost into extinction due to severe hunting and habitat loss. Since most of the Ryukyu flying fox subspecies are morphologically almost indistinguishable, the phylogenetic status and evolutionary uniqueness of the Taiwanese subspecies including the newly recorded population on the Gueishan Island remains questionable. Here, we propose to study the conservation genetics of the Formosan flying foxes. We will take a genomic approach to reveal the phylogenetic relationship, levels of genetic diversity, and possibility of gene flows between *P. d. formosus* and its closely related subspecies on the Ryukyu islands. Our preliminary results have revealed a severe reduction of genetic diversity in *P. d. formosus*. In addition, the allele frequency spectrum of this population is strongly skewed toward an excess of intermediate frequencies, consistent with a drastic decline of population size. Future work will focus on studying the levels of population differentiation and gene flows between *P. d. formosus* and its sister subspecies inhabiting on the Ryukyu islands.

AO2-131

Elevational gradient and genetic diversity of bats at Gunung Mulu National Park, Sarawak, Malaysia

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Mulu is located in Gunung Mulu National Park, a UNESCO World Heritage Site, and is the second highest mountain in Sarawak. Despite this prominence, few studies have surveyed the species and genetic diversity along the altitudinal transect to the summit. The typical species pattern is a decrease in diversity with an increase in elevation, but some groups of animals such as rodents usually exhibit a mid-elevation rise. Genetic patterns have been less studied, but a phylogeographic break in elevation may indicate a barrier to gene flow and a potential mechanism for speciation. Objectives of a 1-month expedition to Mulu in May 2013 were to test the hypotheses that this Palaeotropical fauna has a typical species pattern and that there are no molecular differences with changes in elevation. Sites were surveyed up to 5 nights each at 5 different altitudes from 35 to 2,325 m. Species diversity and relative abundance was used to assess measures of biodiversity and DNA barcoding was used to assess genetic variation. There were 26 species of bats documented during the survey of Mulu, four of which were new records for the locality. Although the regression line was a poor fit, there was a decrease in species diversity with increasing elevation and no bats were caught on the summit. As similarly found in a montane Neotropical bat fauna in the Guianas, there were no genetic differences in elevation suggesting that there are no isolated montane populations in the species we surveyed.

AO3-102

Bat Overpasses As a Solution to Increase Habitat Connectivity Depending the Context

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Roads have a multitude of negative effects on wildlife, including their prominent role in habitat fragmentation. Habitat fragmentation particularly affects bats during their nightly movements between roosts and foraging areas. Bat overpasses are among the proposed improvements intended to reduce the fragmentation impact of roads, but they have rarely been tested. We studied four bat overpasses in France and developed two innovative methods: (i) Acoustic Flight Path Reconstruction (AFPR) for characterize bat crossings using acoustic recorders and (ii) Bat Tracking Toolbox (BTT) for characterize bat flight height using a thermal camera. Among the four bat overpasses, we performed a Before-After Control-Impact analysis for one site. The three others were already installed during our sampling. We obtained more than 1000 bat crossings of five taxa for all sites. Our results suggest that crossings are more numerous if an overpass is located on a pre-existing bat commuting route and can increase habitat connectivity if they are placed on a narrow commuting route (e.g. hedgerow). But when overpasses are located in a large commuting route (e.g. woodland), the proportion of bat crossings along the commuting route was the same with or without an overpass. In this case, overpasses do not fully restore habitat connectivity. Concerning bat flight height, overpasses seems to reduce the collision risk for bats after their installation. Our studies demonstrate that AFPR combining to the BTT are a useful approach to evaluate mitigation measures and emphasize the importance of field testing the effectiveness of mitigation measures with appropriate sampling design.

AO3-105

Light on the Matter: The Effects of Artificial Lighting on the Activity of Namib Desert Bats

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The large scale use of artificial lighting at night has occurred over the last 150 years and is increasing globally at an estimated rate of 6% per annum. Effects of artificial lighting at night have been both detrimental and beneficial, affecting many diurnal and nocturnal taxa. Reactions to artificial lighting are often species specific and vary with the wavelengths of light emitted. The aim of the project was to investigate the effects of different colours of artificial lighting (with different emission spectra) on bats in a minimally developed, rural area in the Namib-Naukluft Park in the Namib Desert in Namibia. White, yellow and ultraviolet spotlights, and a dark control, were erected along the dry Kuiseb River. Each spotlight was accompanied by a bat detector which recorded bat echolocation calls in the vicinity of the light. Recordings took place over 160 nights under both dark and light conditions. Eight bat species were identified. Open air and clutter edge foraging species increased in activity in the vicinity of the lights while activity of the only clutter foraging species decreased. The largest activity increases were seen at the white light followed by the yellow light with the ultraviolet light the lowest, contrary to expectation. Activity of the clutter foraging species declined most at the white light followed by the ultraviolet light and least at the yellow light.

AO3-107

Can Humans and Bats Coexist? Farmers' knowledge and attitudes toward bats in Belize

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Bats in Belize are facing rising pressures from rapid agricultural expansion and intensification. Initial communications with farmers of the Vaca Forest Reserve and our local NGO partners revealed various organizations train farmers to trap and poison bats to protect their livestock from bat-transmitted rabies. During summer 2018, we surveyed 44 farmers in and around the Vaca to quantify farmer knowledge and attitudes toward bats. Survey questions addressed farmer knowledge of bat behavior, ecosystem services, and disease risk; farmer emotions and attitudes toward bats; and farmer sociodemographics. Farmers' attitudes toward bats were moderately negative, with farmers thinking they are ugly (70%), worthless (40%), and dangerous (43%). These negative attitudes are likely due to economic damages associated with bats rather than human health concerns, as farmers with livestock ($M = 2.48$; $SD = 0.87$) had significantly lower attitudes towards bats than farmers without livestock ($M = 3.09$; $SD = 0.92$). More farmers with livestock wanted bats to be managed (85.7%) compared to farmers without livestock (59.1%), with almost all management suggestions calling for the removal or death of bats from their farms. Educational materials and conservation efforts should emphasize the services (pest control, pollination, seed dispersal) bats provide farmers and be tailored to whether or not a farmer owns livestock.

AO3-108

A Novel Approach to the Investigation of Microclimatic Conditions for Bat Hibernation

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Knowledge about the temperature and humidity at which bats hibernate is important for a proper conservation and management of bat hibernacula. However, data published in the literature are highly variable and not always consistent. Most published data are based on single measurements during bat surveys, not taking into account seasonal effects. However, seasonal change in conditions however can be of high importance. We used temperature and humidity loggers to investigate these variables in different types of hibernacula, ranging from small bunkers, old military fortresses to a large underground system, in Belgium and in Poland. We combined this data with different bat censuses undertaken throughout the hibernation season and developed a transfer function model to analyze the time series. Temperature in the hibernaculum is modeled as a function of the outside conditions time series and the system properties that influence the dynamics of its internal climate (insulation and air flow). To our knowledge, no such models have been used for bat hibernacula so far. We show that this approach, that takes into account the seasonality and the dynamics of the system, gives a better understanding of bat hibernation preferences. Furthermore, we present a number of case studies where the transfer function model has been used to design improvements to the hibernacula for a better conservation of hibernating bats. Finally, since the transfer function model depends on system properties and outside conditions, the model can be used to investigate the effect of climate change on bat hibernacula.

AO3-109

Identifying the Patterns and Potential causes of Bat Roadkill Incidence in Taiwan

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With the development of road system and the popularity of motor vehicle, roadkill has identified as a novel threat to bats in the anthropogenece. Studies on bat roadkill have been focused mostly in the Europe and the New World. The influence of roadkill to bat diversity in Asia, where the development of roadway infrastructure is conspicuous, is still poorly studied. We investigate the spatio-temporal patterns and potential causes of bat roadkill incidences in Taiwan and nearby islets from August 2011 to January 2019. Bat roadkill data were acquired from the Taiwan Roadkill Observation Network (https://roadkill.tw/en), an online platform designed for citizen scientists to collect wildlife roadkill information. A total of 1,156 bat roadkill incidences are exclusively reported from the main island. August and September, when first-year born individuals are capable to fly, were the months with the highest incidences number recorded in a year. Most of the bat roadkill incidences (94%, n = 1,083) are reported from low elevation (< 500m), despite the wide elevational range of the survey area (up to 3,146 m). About 58% (n = 667) of the total records are identified to 21 bat species of four families, nearly two thirds of the island count (33 species). We found species with high roadkill incidence numbers were those roost in artificial constructions and with lower elevation distribution upper limit. The potential roles of environmental factors, including habitats, elevation, climatic patterns, road density and light pollution, in affecting bat roadkill incidence intensity at the lowland will be further analyzed.

AO3-111

Monitoring two Flying-fox hunted species: trends, population sizes and harvesting rates in New Caledonia, South Pacific

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Assessing the trend of a population and its underlying factors is critical to propose efficient conservation actions. We investigated the dynamics of harvested flying-fox populations of *Pteropus ornatus* and *P. tonganus* in the Northern Province of the New Caledonian biodiversity hotspot (South Pacific). First, an ethno-ecological survey involving 219 experts allowed identifying 494 roosts of *Pteropus*. Current status was assessed for 379 of them, among which 125 were no longer found, *i.e.* a third loss in 40 years (1969-2009). Moreover, 91% of the expert panel reported a decline in the number of flying-foxes linked to hunting pressure (71%). Second, 35 roosts were monitored for specific composition, revealing that the endemic species, *P. ornatus*, was dominant (73% ±27, $N = 19{,}997$). Between 2010 and 2016, 30 of these roosts were counted annually during the pre-parturition period (September). Flying-fox roost size averaged 1,425 ±2,151 individuals ($N = 180$ counts) and showed high among-year variations (CV = 37-162%). A GAMM analysis revealed the occurrence of inter-annual variation at the population level ($edf = 3.52$, $P = 0.021$). We did not detect a significant decline over the 7-yr period, although three roosts showed temporary desertion and another went possibly extinct. Population size of the two species estimated in the study area was comprised between 338,000 and 859,000 individuals distributed among 399 roosts. Estimates of annual hunting bags in the same area suggest harvesting rate could reach 4.7% just for Kanak tribes. More detailed information on spatial ecology and demography are needed to design adapted and sustainable flying-foxes management strategy in New Caledonia.

AO3-113

Bat Hunting and Risk of Disease Emergence at High-Risk Interfaces in Bangladesh

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Background: Bat hunting is a major public health concern in relation to zoonotic disease transmission. There are limited studies on bat hunting, trading, and consumption patterns at the community level in Bangladesh. This qualitative study aims to understand hunting behaviors and consumption patterns and the wildlife value chain, to understand the risk of zoonotic disease transmission in Faridpur communities.

Methods: Participant observation and 37-targeted ethnographic interviews were conducted from October to December, 2015 and November to December 2018. Participants included wildlife hunters, collectors, transporters, vendors, and consumers.

Results: Bat hunting and trading was centered in 'Sharder' communities as a traditional practice and key protein source. Hunting provides additional sources of income in the community. Men were involved in hunting where as women were primarily involved in butchering. Hunters were mostly illiterate and unaware of disease risks associated with bats. Communities with religious prohibitions against hunting were reported to be involved in hunting and consumption of bats as well. Consumption of bats was not limited to food sources alone, participants were observed to use bat bones to remedy joint pain and asthma. Participants reported declining local bat populations due to over hunting and deforestation.

Conclusion: Hunting and interactions with bats may represent a previously unrecognized pathway for zoonotic viruses emergence in Bangladesh. Unprotected hunting practices and limited or no hygiene measures can yield greater risk of zoonotic disease spillover. However, successful mitigation and reduction in hunting strategies in communities need sustainable alternative livelihood opportunities and protein sources.

AO3-114

The Road to Recovery: Temporal Effects of Matrix Regeneration on Amazonian Bats

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As is increasingly being acknowledged, the prevailing treatment of the matrix in studies of habitat fragmentation as temporally invariant is not appropriate for most real-world situations, yet we lack a clear understanding of how species responses to fragmentation are mediated by changes in matrix composition over time. Across the tropics, vast deforested areas are undergoing forest regeneration due to land abandonment. Here, we used an Amazonian whole-ecosystem fragmentation experiment to investigate how changes in matrix structure and composition over time through secondary forest regeneration affect bat assemblages from both a taxonomic and a functional diversity perspective. We comprehensively surveyed bat assemblages in continuous forest, forest fragments and secondary forest matrix ~15 and again ~30 years after initial fragment isolation. The regeneration of the second growth matrix had overall positive effects on the occupancy and abundance of old-growth specialists across all habitats. Conversely, effects on habitat generalist species were negligible for forest fragments and negative for secondary forest. The addition over time of species that perform different ecological functions increased functional alpha-diversity and functional uniqueness, altered functional trait composition, and resulted in functional beta-diversity changes via trait gains that were most prominent in secondary forest. However, ~30 years of secondary forest regeneration were insufficient for the functional recovery of bat assemblages to levels observed in continuous forest. Our findings suggest that restoring degraded habitats while protecting primary forest will be key to safeguarding high taxonomic and functional diversity of bats and their vital contributions to ecosystem functioning in fragmented tropical landscapes.

Conflicts Between *Pteropus dasymallus* and *Tankan Orange* Farmers in Northern Okinawa Island

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The Ryukyu Flying Fox *Pteropus dasymallus*, a "Vulnerable" species according to the IUCN Red List, was listed as one of the main pests of *tankan* orange. This study aimed to investigate the damage to *tankan* orange caused by wildlife in Northern Okinawa Island, as well as potential threats to *P. dasymallus* related to conflicts with farmers. Three survey methods were used in this study: 1) acquiring official records of wildlife damages from six local administration offices in the region, 2) interview survey with 43 farmers to investigate the situations of the conflicts between wildlife and the farmers, and 3) time-lapse camera monitoring at 14 locations in January-February 2018. The official records and the interview survey showed similar results and indicated that the Jungle Crow *Corvus macrorhynchos* caused most damages (53-56%), followed by *P. dasymallus* (18-28%). Time-lapse camera monitoring suggested that *C. macrorhynchos* was responsible for most damages (92%), and *P. dasymallus* was responsible for the rest of the damages (8%). The interview survey also revealed that at least 2,000 *P. dasymallus* died in *tankan* orange orchards between years 2007 and 2017. In conclusions, *C. macrorhynchos* was the species causing the most damage to *tankan* orange orchards, followed by *P. dasymallus*, and the intensity of damages caused by *P. dasymallus* varied greatly between years. In addition, a huge number of *P. dasymallus* died in *tankan* orange orchards due to entanglement in nets, and current crop protection practices could potentially be a serious threat to the survival of the species.

AO3-117

Are bats susceptible to vehicle collisions in Thailand? A case study in a biodiversity hotspot

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Road effects on wildlife are major contributors to the global biodiversity crisis. In addition to direct mortalities caused by traffic, roads can reduce populations indirectly through habitat fragmentation and loss, leading to loss of genetic diversity or local extinction. Bats in particular pose an intriguing challenge to road mitigation as common prevention measures such as underpasses and fences are not effective solutions. Additionally, little is known about the impacts of roads on tropical and sub-tropical bats. To address this concern, we conducted standardized road surveys on a highway transect that bisects two national parks (a UNESCO world heritage site) and a UNESCO biosphere reserve, in Northeastern Thailand. We collected data on all the main vertebrate groups (mammals, birds, reptiles and amphibians) for comparison purposes. We used R and GIS software to conduct spatial analyses and visualize wildlife–vehicle collision hotspots. Over the course of 110 sampling days, and omitting domestic animals, we detected 1395 new mortalities. Of the 212 mammals, 81.6% were bats (12.4% of all vertebrate mortalities), representing 21 species and five families. The highest mortality peak was between June-August, with 72% of all bat mortalities. Other road ecology studies in the Paleotropics have reported very low numbers of bat mortalities (<1%), but it might be due to methodology bias (not specifically looking for small carcasses, e.g. bats). Road impacts on Southeast Asian bats are an important research priority, as over 21% of bat species in the region are listed as Near Threatened or higher.

AO3-119

Glossophaga soricina in Banana Monocultures: What they eat and how this shapes their Gut Microbiome

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Landscape modification for food production is one of the largest threats to biodiversity. Despite a current forest coverage of approximately a quarter of its area, Costa Rica has over time been widely modified by large monocultures. Over many years bananas were one of the country's main products, both in terms of land use and in exports. For the native nectar-feeding bats, banana flowers in plantations represent an attractive nectar source. Nonetheless, dietary changes imposed by anthropogenic landscapes might alter other aspects of the bats' biology, such as the gut microbiome, thereby negatively affecting the fitness of the animals. Our objective was to compare the diet of *Glossophaga soricina* (Phyllostomidae: Glossophaginae) individuals foraging in intensive banana plantations, to that of animals foraging in native forests and to assess the effects on the respective gut microbiome. We combined classical diet sampling techniques (fuchsine glycerin gelatine) with cutting-edge molecular approaches (Next Generation Sequencing) to describe this relationship. Additionally we used telemetry to corroborate the habitat use of *G. soricina* foraging within banana monocultures. Most bats captured inside the banana plantations showed no pollen from native food plants. The radio-tracked bats were active all night inside the plantations and were roosting in nearby abandoned houses. Thus, it is safe to assume they were feeding almost entirely on banana flower nectar. Gut microbiome was variable, showing differences between time of the year and sexes. Current work includes an evaluation of microbiome changes in response to agrochemical use.

AO3-120

A Connectivity Model for Bats in Fragmented Landscapes

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Human activities such as urbanization, industrialization or agricultural intensification induce landscape fragmentation. Bats depend on commuting routes to move between roost and hunting areas. Habitat fragmentation hampers movement between the sometimes widely dispersed target patches. To mitigate the effects on bat populations, conservationists attempt to improve the landscape through the creation and/or protection of habitat linkages. Modeling landscape connectivity is acknowledged as a helpful decision tool to identify and mitigate critical barriers or bottlenecks in the landscape. Here we develop a connectivity model for bats in a mosaic of small forest fragments in an agricultural/urbanised landscape based on electrical circuit theory. The study was carried out in Belgium, Europe. Models are constructed for ecotypes of insectivorous bat species with different habitat requirements (forest affinity, light sensitivity, …). The models are validated by (1) assessing the use of the predicted corridors and (2) relating population-activity levels in the forest fragments to accumulated costs to reach the fragments. Field data collection is based on acoustic surveys. The data analysis revealed that the recorded bat species indeed used the modeled corridors and that population-activity in the forest patches was correlation with the modeled connectivity values.

AO3-124

Skyrocketing Flights as a Previously Unrecognized Behaviour of Open-Space Foraging Bats

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The airspace within the lower troposphere (<1000 m above ground) is an important habitat for many airborne animals, including open-space foraging bats. Yet, we are missing a detailed understanding about how bats forage in the seemingly unstructured airspace. Recently, we showed that *Taphozous theobaldi*, an open-space foraging bat from central Thailand, performs landscape guided flights, using the topography of mountain ridges to launch into the skies (Roeleke et al. 2018). Here, we present additional data on the foraging behaviour of *T. theobaldi*, using data loggers that record temperature, barometric pressure, light intensity and acceleration. Based on data of 5 individuals over a total period of 26 observation days, we show that each night *T. theobaldi* foraged for 4.9 ± 3.1 h (mean ± one standard deviation). They spent 14% of the foraging time in altitudinal flights 200 m above cave elevation. Each night, *T. theobaldi* performed on average 4.0 ± 1.2 altitudinal flights during which they reached a peak height of 313 ± 56 m above cave elevation. In summary, this species performs regular ascents to higher altitudes in vicinity to hilltops and mountain ridges. We conclude that *T. theobaldi* is a regular, but not obligatory exploiter of high altitudes. We speculate that *T. theobaldi* may either follow hill-topping insect swarms to higher altitudes or that this species may hunt temporarily at higher air layers where insect prey accumulates because of favourable ambient temperature and general jet streams, or because of local turbulences or winds caused by landscape topography. Cited literature: Roeleke, M., Bumrungsri, S., & Voigt, C. C. (2018). Bats probe the aerosphere during landscape guided altitudinal flights. *Mammal Review*, *48*(1), 7-11.

AO3-126

The impact of the Endangered Mauritian flying fox *Pteropus niger* on commercial fruit farms and the efficacy of mitigation methods

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The endemic Mauritian flying fox *Pteropus niger* is perceived to be a major fruit pest. Lobbying of the Government of Mauritius by fruit growers to control the flying fox population resulted in national culls in 2015 and 2016, with a further cull conducted in 2018. A loss of over 40,000 individuals has been reported and the species is now categorized as Endangered on the IUCN Red List.

To assess the damage bat cause to the fruit farms, four orchards were monitored during the 2015/2016 and three orchards during the 2018/2019 fruiting season. Additionally, smell repellents, sound system and full exclusion netting was tested in 2018/2019 fruiting season.

The results indicated that bulbuls and monkeys as well as bats fed on commercial fruits. However, bats are able to cause major fruit losses. The sound system was successful in decreasing the damage caused by bats to both mango and lychee orchard. The full exclusion netting gave 100% protection against bats.

Commercial orchards in Mauritius must implement non-lethal fruit protection, such as full exclusion netting or the sound system to decrease the damage bats cause to the fruits. It is equally important to restore forest ecosystems in Mauritius to increase native food supply for the bats.

Bats and Windfarms – Lessons from Europe and Western Palearctic: What about the rest of the World?

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Climate change is one of the most important threats for humans and biodiversity, as recognized by the Convention of Biological Diversity, the International Panel on Climate Change, and the World Economic Forum. A switch from fossil fuels to renewable energy seems mandatory to reduce atmospheric CO_2. Accordingly, energy production by wind has expanded rapidly over recent decades and is booming in many countries worldwide. Bat collisions at wind turbines were first documented at the beginning of the 21st century, and since then an increasing number of species have been shown to be affected by wind turbine operation. In 2008, the Intersessional Working Group on Wind Turbines and Bat Populations of the UNEP/EUROBATS´ Advisory Committee released the first Guidelines on Bats and Windfarms. This document was updated in 2014. Here, we report the results from a questionnaire sent out to 63 countries across EUROBATS range. The feedback demonstrates that post-construction monitoring is not obligatory for most windfarms operating across the Western Palearctic. If monitoring is commissioned, however, EUROBATS Guidelines are often ignored. Additionally, the results of monitoring efforts are usually not made available to the public. Lastly, the efficacy of implemented mitigation methods is usually not validated and, in many cases, no mitigation schemes are applied at all. Considering that we lack overall guidelines beyond the geographical range of the EUROBATS, we plead that an international effort should be adopted to formulate guidelines worldwide and to ensure that windfarm developments follow them in order to safeguard bat populations across the world.

AO3-131

Response of hibernating bats to nontactile stimuli

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During the hibernation season, bats alternate between prolonged bouts of torpor with a reduced body temperature and short arousals with a return to euthermy. Two different kinds of arousals were found, i.e., normotermic (> 25 °C) and cold (< 25 °C). Hibernating bats are sensitive to nontactile stimuli and arouse or even fly following changes in climatic conditions, disturbance from other bats and a potential predator or human. Temperature data loggers registered body temperature of 40 individuals of *Myotis myotis* between January and March in two winters when regular human visits of hibernaculum were carried out. Visits to the mine resulted in cold arousals in 82% of bats within 2 hours. Hence, we believe that cold arousals reflect a physiological and behavioural adaptation aimed at avoiding the energetic constraints of disturbance that can lead to fat reserve exhaustion. It was assumed that the warming of the bat body only by a few degrees is less energy demanding and probably sufficient to activate the sensory system to assess the relevance of the external stimulus.This project was financially supported as a part of a specific university research project at Masaryk University (MUNI/A/1436/2018).

AO3-132

Diversity and Distribution of Colombian Caribbean Bats: a Spatial Approach

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Spatial analysis of biodiversity patterns can lead to the understanding of how taxa spatial distributions, are influenced by ecological, biogeographic, evolutive, or even human-related circumstances. This kind (spatial) of information is also valuable while systematic conservation exercises are carried out, and especially when the identification of distribution patterns is tied to questions regarding its own origins and historical contexts. In the present research, from georeferenced registers we studied species richness and phylogenetic diversity distribution of the Colombian Caribbean lowlands bats, using spatial statistics methods (IDW, Kriging) and the analyses of several structural arrangements related with ecoregions, biogeographical districts, and Berhmann's grids. Our results show relevant diversity hotspots around some important geographic units with a high variety of ecosystems as the Sierra Nevada, Montes de Maria, and Paramillo National Park. The founded patterns exhibit a strong geographic component, associated with the classical hypothesis of the biogeographical districts in Colombia. Furthermore, some climatic events occurred during the Pleistocene, seems to have been influenced the actual richness distribution alongside the studied territory. Finally, using our results, we suggest some relevant areas for conservation prioritization alongside a highly intervened region.

AO3-133

Habitat use of the Hawaiian hoary bat on Maui

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The foraging ecology of the Hawaiian hoary bat has been poorly characterized and lack of information is hampering efforts to develop effective recovery plans. We used acoustic surveys to describe how bats used the landscape, and although acoustic studies on this species have been conducted on several of the Hawaiian Islands, no long-term, widespread studies have previously been conducted on Maui. We used the Generalized Random Tesselation Stratified survey design to select acoustic sampling sites across nine habitat types covering a ~30,000 ha study area. Calls were recorded for three nights in each habitat and rotated five times (round) every other month for five sampled months for a total of 223 deployments. We analyzed the impact of three environmental variables: 1) habitat type; 2) elevation; and 3) temperature; as fixed effects on bat activity (number of call minutes), with the round number as a random effect. We applied generalized linear mixed effects models with the package glmmPQL to account for overdispersed count data and used a negative binomial distribution with a log link. Bat activity (minutes with bat calls) was highest in grasslands, gulches and low-intensity developed habitats and lowest in forested habitats, although feeding buzz data could not be explained as an independent variable. A combination of structural features and resource availability likely drive habitat use. Our data has substantial implications for management decisions and demonstrates the need for caution when applying acoustic data from habitats among different islands in Hawaii.

AO3-134

Conservation of Forest Bats in Rwanda

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Nyungwe National Park in southwestern Rwanda is one of the most biologically important montane rainforests in central Africa. The park protects 1,019 square kilometers of montane rainforest which is home to a diversity of wildlife species, including many species endemic to the Albertine Rift region of Africa. Fifty-one species of bats are known to occur in Rwanda, but additional, previously undocumented, species likely occur in Rwanda's forest habitats. In particular, Hill's horseshoe bat (*Rhinolophus hilli*) is a rare bat that is only known from the description of two specimens, both collected in the Uwinka region of Nyungwe National Park. *Rhinolophus hilli* was last seen in 1981 – nearly 40 years ago – and whether a population still existed in the forest of Nyungwe National Park was unknown. We conducted an intensive survey for bats in Nyungwe National Park in January 2019 to aid local biodiversity planning and habitat protection efforts. Nyungwe Park Rangers conducted reconnaissance surveys to identify the presence and location of cave and mine roosts within the national park which we surveyed for bats using acoustic detectors and visual surveys. Through our studies, we documented bats that were previously unrecorded in Rwanda and Nyungwe National Park. We also identified key bat roosts in both natural caves and mines. Further, in collaboration with the Nyungwe Park Rangers, we established a monitoring program to conduct acoustic sampling as part of routine park patrols to increase biodiversity records and local capacity for bat conservation in the region.

AO3-136

Conserving Caves in the Caribbean for Critically Endangered Bats

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Bat species that depend on subterranean habitats and aggregate in large numbers are particularly vulnerable to threats that destroy or degrade roosts. However, caves are also focal habitats that are tractable targets for conservation. If executed effectively, cave conservation efforts can provide meaningful protections to safeguard species from extinction. Here, we discuss recent efforts to identify and execute conservation measures to protect two caves identified as the last remaining roost sites for two critically endangered bat species in Jamaica – the Jamaican flower bat (*Phyllonycteris aphylla*) and Jamaican funnel-eared bat (*Natalus jamaicensis*). Jamaica is the most bio-endemic island in the Caribbean and an important contributor to biodiversity of the Caribbean Basin. Primarily due to the threat to its endemic species of bats, Jamaica is included in the International Union for the Conservation of Nature (IUCN) list of countries with the highest number of at-risk mammals. Twenty-one species of bat are found on Jamaica; 5 of these species are endemic to the island while another 8 species are restricted to the Caribbean. Almost half (10/21) of the species found on Jamaica are obligate cave dwellers. Human population growth driving agricultural, industrial and commercial expansion, has resulted in intense competition for land, leading to the loss or fragmentation of many natural habitats and a reduction and loss of biodiversity in Jamaica. Bat Conservation International and the National Environment and Planning Agency (NEPA) are collaboratively developing and executing cave conservation strategies to protect the remaining roosts of critically endangered bats in Jamaica.

AO3-137

Human knowledge and perceptions of bats – a pilot study in Singapore

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Bats are ecologically important and provide vital ecosystem services. They also have a high rate of endangerment, owing to the same, largely anthropogenic threats that are generally implicated in the biodiversity crisis. But bats face an added challenge – the fact that they are widely maligned. The problem is that decisions about where to allocate limited conservation resources are influenced by public attitudes. Indeed, most flagship species are charismatic. Raising support for the conservation of bats hinges on understanding what people know and feel about them and (because that likely varies among populations) addressing misconceptions in culturally-appropriate ways.

In this context, we argue that a global investigation of human knowledge and perceptions of bats (and the underlying drivers) is timely and useful. We carried out a pilot study in Singapore, using a sequential exploratory mixed methods study design (focus group discussions and door-to-door, semi-structured interviews). We tested predictors of positive perceptions using binary logistic regression.

Most respondents answered more than half of knowledge questions correctly and exhibited neutral to weak affective attitudes but positive social attitudes. Meaning, they felt that although bats are a natural part of the environment, they are neither attractive nor charismatic, and that although bats deserve protection, government funds should not be allocated to that. Those who owned pets and had positive prior encounters with bats were more likely to have positive cognitive attitudes toward them. This study, repeated in many locales worldwide, could provide useful data that will make bat-conservation outreach more targeted and culturally relevant.

A Fresh View at Ecosystem Services Provided by Bats: Opportunities and Challenges

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Much has been learned in recent years about ecosystem services provided by bats. Incorporating the variation in scope, scale, and spatiotemporal variables, has helped us understand how these crucial processes work and how valuable they are. And yet, we are still only learning about them. We will overview what we have learned about the services provided by Mexican free-tailed bats and how should we design future studies to improve our understanding of them. At the same time, other emerging examples are coming up and diversifying the way human well-being is benefited by bats, for example with nectar bats providing pollination services to highly useful plants like agaves. The concept of spatial, transborder subsidies must be considered to then promote joint, coordinated conservation efforts across borders. Identifying crucial bat colonies as per their overall contribution to population viability, pest population suppression, value for ecotourism, and risks towards the bat population and the roost itself are all very important elements to incorporate into an ecosystem service valuing exercise. The process is further complicated by the fact that so far our efforts have only focused on ecosystem services provided by insectivorous bats, but no effort has been conducted to date to value services provided by fruit-eating or pollinivorous species. The need to do this is illustrated with the recent highlights brought about by bat-friendly tequila and mezcal, a multibillion dollar industry that depends on the work of several bat species as pollinators of agave. The table is set to conduct a large-scale, worldwide valuation of these ecosystem services.

AO3-142

Restoring Agave for Migratory North American Nectivorous Bats, and Agave Use by Bats in the Paleotropics

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The lesser long-nosed bat (*Leptonycteris yerbabuenae*) and the federally-endangered Mexican long-nosed bat (*L. nivalis*) depend on the fruit, nectar, and pollen of cacti and agave along migration corridors and near roosts. The primary threats to these species are roost disturbance, a decline in agave due to overharvest for mezcal production, agricultural and urban development, and fire and its effects on habitat connectivity. To address these threats, Bat Conservation International (BCI) has embarked on an ambitious initiative to plant thousands of agaves near major *Leptonycteris* roosts and along their migratory corridors from Central Mexico to the Southwestern U.S. BCI is working with agave and *Leptonycteris* experts, non-government organizations, communities, and industry partners in the U.S. and Mexico to increase capacity for agave propagation, prioritize restoration sites, support sustainable agave harvest practices, and raise awareness about the connection between bats and agave. BCI recently facilitated the propagation of several thousand agaves in the Southwestern U.S. by conservation organizations that focus on restoring native pollinator plants. Bat Conservation International has already planted more than 1,500 agaves with its partners on National Park lands and mine reclamation sites within the foraging radius of long-nosed bat roosts in Arizona. BCI is also supporting conservationists and universities in Sonora and Nuevo Leon Mexico with educational outreach on bats and agave for commercial agave growers, the creation of agave demonstration gardens, and the planting of agave hedgerows in agave plantations. Agave (sisal) may also be important to several endangered nectar feeding bats in Africa, Asia, and Polynesia.

Influence of Signal Direction on Sonar Performance

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How bats mitigate mutual interference is a longstanding question that has both ecological and technological implications as biosonar systems continue to outperform man-made sonar systems in noisy, cluttered environments. Echolocating free-tailed bats display a mutual suppression response, slowing their pulse emission rates when flying in groups to gain a net improvement in sonar performance (Adams et al. 2017). However, flight paths, directional effects, plus contextual and attentional processes influence the levels of mutual interference causing some noises to be more deleterious than others. To tease apart the impact of these factors, we used playback experiments in flying free-tailed bats (*Tadarida brasiliensis*) to test whether the relative directionality of an interfering signal versus its returning echoes had a greater impact on a bat's sonar performance. We analyzed pulse emission rates and temporal patterns of bats navigating in both open and cluttered spaces while we varied the directionality of an artificial stimulus relative to the bat's flight trajectory. Both emission rates and navigational performance decreased significantly more when playback was directed in the same heading as the flying bat, indicating that competing echo wave-fronts are more disruptive to a flying bat than the much louder source signal that produced them. This observation is important because it potentially reveals the impact of attentional processes on sonar performance. This study provides new information on how echolocating bats experience interference and their behavioral strategies for overcoming jamming from conspecifics.

AO4-102

Insectivorous bats in the Cerrado mosaic: fleeing drought and degradation

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Eighty percent of the original area of the Cerrado tropical savanna, a world's biodiversity hotspot, has already been transformed for human uses. The maintenance of its biodiversity depends on the acquisition of scientific knowledge for defining effective conservation strategies. Ecological information on the *ca*. 118 species of bats occurring in this biome is scarce, especially for the insectivorous bat fauna. Here we investigate species composition and activity of insectivorous bats and their relationship with the degree of preservation, composition and configuration landscape of a Cerrado area under noteworthy anthropogenic pressure. We predict guild specific associations with particular phytophysiognomies and no major temporal differences on guild structuring. We acoustically sampled 31 points covering different phytophysiognomies and levels of land-use modification during the dry season for two consecutive years. In 282 hours of recording we registered 20 species from five bat families and eight sonotypes. Preserved habitat extensiveness and continuity revealed to be crucial for the maintenance of the Cerrado bat diversity and to fulfil bats´ foraging habitat requirements. Independently of the guild, activity of bats was particularly associated to veredas and forest habitats and negatively affected by the degradation of native phytophysiognomies. Temporal variation in bat activity indicates that species' habitat associations are highly susceptible to extreme local land-use changes. Also, with increasing drought conditions, water-associated environments become more important for Cerrado bats. We emphasize the urgency of protecting larger pristine patches of different natural phytophysiognomies in the Cerrado, ever more threatened by intensive agricultural schemes and uncontrolled fires.

Why Bats Do Not Apply a Jamming Avoidance Response?

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Echolocating bats emit sound-signals and process the reflecting echoes to sense their surroundings and hunt prey. Because of this reliance on sound, loud sound signals may mask faint echoes and reduce the ability to detect prey. Therefore, whenever bats hunt in a group, as many species do, conspecifics, emitting similar signals, may hinder the ability of each other to catch prey. This is known as the jamming problem, and there is an on-going debate how bats deal with it. Some studies have suggested that bats shift their signal-frequencies to cope with jamming, a response known as the jamming avoidance response. To quantify and unravel the effects of conspecific-masking on hunting, we developed a computer model, simulating numerous bats foraging in a confined area. Our integrated simulation consists of a comprehensive sensorimotor model of hunting bats and flying moths. It thus allows us to assess masking quantitatively for the first time. Our results demonstrate that there is no need for bats to perform a jamming avoidance response in order to overcome jamming. Sensory masking indeed reduces foraging success rate but only at levels of 10%-30%. Importantly, trying to avoid masking interference by shifting the signals' frequencies does not improve hunting performance. The main reason for this is that individuals already emit distinct signals because of their different behavioral phases (e.g., search vs. approach). Our study uses a mathematical approach to explain the results of several recent studies indicating bats do not apply a jamming avoidance response.

AO4-104

Segregating Signal from Noise Through Movement in Echolocating Bats

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Segregating signal from noise is one of the most fundamental problems shared by all biological and human-engineered sensory systems. In echolocating bats that search for small objects such as tiny insects in the presence of large obstacles (e.g., vegetation), this task can pose serious challenges as the echoes reflected from the background might be several times louder than the desired signal. Bats' ability to adjust their sensing, specifically their echolocation signal and sequence design has been deeply studied. In this study we hypothesized that in addition to adjusting their sensing, bats would also use movement in order to segregate desired echoes from background noise. Bats were presented with an acoustically echoic background (mimicking natural vegetation echoes) masking their target. They now had to deal with a problem of segregating the weaker signal (the target's echo) from the louder background noise - the echoes returning from the hedge-like masker. To quantify bats' response we monitored their flight and echolocation behavior. Bats responded to the acoustically echoic background by adjusting their angle of flight. Specifically, the bats in our experiment used movement and not sensory adaptation in order to overcome a sensory deficit. They approached the target from a lower angle of attack, which results in weaker echoes from the background as was also confirmed by measuring the echoes of the setup from the bat's point of view. When studying bats, it is thus important to remember the limitation of echolocation and take other degrees of active sensing into consideration.

AO4-105

Different Functions of Two Types of Territorial Calls in the Great Himalayan leaf-nosed bats, *Hipposideros armiger*

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Several features of phonology in human speech are shared with other species. One mark of human speech is that linguistic context affects the classification and production of phonemes. Here, we affirm earlier findings that Great Himalayan leaf-nosed bats emit two types of calls in different behavioral contexts: bent upward frequency modulation (bUFM) calls and stepped upward frequency modulation (sUFM) calls. We observed different responses of *Hipposideros armiger* to playback of bUFM calls and sUFM calls. Playback of bUFM territorial calls deterred the visits of bats to the side of a flight room with bUFM calls compared to playback of echolocation calls or silence. For the playback of sUFM calls, this was not the case; bats were located further away from the sUFM calls side of the flight room compared to their location after playback of echolocation calls, but not compared to silence. Our data suggest that bUFM territorial calls have the function of territorial defense, while sUFM territorial calls may not have such functions. Therefore, our results provide the first experimental evidence that the two types of calls have different functions depending on syllable parameters, syllable structure and behavioral context. The changes in the acoustic parameters of the two types of calls correspond to phonological changes in human speech, suggesting that context-dependent acoustic cues are important for the linguistic functions of human phonology.

AO4-106

Screaming out in Fright: Function and Description of Distress Calls in the Nectarivorous Bat *Glossophaga soricina*

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Distress calls are known from a variety of animals and are defined as vocalizations emitted during extreme physical stress. They can be strongly attractive both to conspecifics and heterospecifics. Even though distress calls have been studied for a long time, their precise advantage for emitters or meaning for receivers is still unclear. From January to April 2018, we investigated distress calls of Pallas' long-tongued bats (*Glossophaga soricina*, Phyllostomidae: Glossophaginae) in the Santa Rosa National Park, Costa Rica. Based on the analysis of 2508 distress call syllables from 15 individuals, we described the distress call repertoire of *G. soricina*, consisting of six different syllable types (downsweep, upsweep, downsweep modulated, upsweep modulated, modulated, point like syllables). The acoustic structure of the distress calls was comparable to that of other species. *Glossophaga soricina* distress calls encoded an individual signature, but no sexspecific signature. Further, we performed playback experiments to test the response behavior of different group sizes to different distress call stimuli. Bats kept in a group responded to distress calls, whereas single bats did not. Bats responded significantly to normal and distorted conspecific distress calls but not to heterospecific distress calls. We found no sexspecific difference in the response to different playback stimuli. In conclusion, our results indicate that distress calls of bats encode important social information that can be used by receivers and that the response behavior of receivers depends on whether they are alone or in a group.

AO4-107

Will acoustic communities of insectivorous bats change after extreme rains?

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Climate change affects individual fitness, population dynamics, and species abundance and distributions globally. The magnitude, frequency and duration of extreme rains and their impacts on biodiversity are predicted to increase under climate change. Extreme rains may limit bats' activities and flight performance because wet fur and wings could cause a loss of body temperature and wing aerodynamics. However, impacts of extreme rains on insectivorous bat communities are still unclear. In this study, we would like to answer two questions: (1) do activity levels of bats decline during extreme rains and how much time do they need to recover, and (2) do acoustic communities of bats change after extreme rains? We set up 10 ultra-soundscape long-term monitoring sites and collected more than 8-month recordings to capture rare and unexpected extreme rain events. Then, we used a machine-learning approach to reduce noise signals and categorize bat acoustic communities based on the energy distribution along frequency in the signals of bat echolocations. Results showed that (1) activity levels of bats declined when daily precipitation was >80mm, (2) bats needed 1-5 days to recover back to the original activity level after the rain stopped, and (3) acoustic communities of bats changed at some study sites after the extreme rain. Our study fulfilled the knowledge gap in the impacts of extreme rains on activities and acoustic community composition of insectivorous bats. The findings could be used to predict species richness changes or population dynamics under extreme events in the future.

AO4-108

The information and function of social calls in Asian particoloured bats

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Bats emit echolocation calls to navigate and locate, and they also produce complex social calls to communicate with conspecifics. However, little is known about the information and function of social calls in bats. The female Asian particoloured bat (*Vespertilio sinensis*) produces aggressive displays and calls when confronted by an intruder conspecific competing for roost position. Here, we investigated the relationship between body size, body quality, fighting ability, aggressive intent of the callers and their aggressive calls. At the syllable level, there were significant positive relationships between the duration of various syllables and forearm length, bite force and winning percentage. At the call level, heavier bats that produced calls with shorter mean inter-syllable silences had higher winning percentage and healthier bats produced calls with lower maximum frequency. There was a significant positive relationship between vocal complexity and immune response rather than winning percentage. These results suggested that aggressive calls in *V. sinensis* may be honest signals of body size and quality during the antagonistic interactions. Additionally, our results showed that the number of noisy/tonal syllables of the disturbed bats met the three criteria used to define aggressive intent: context criterion, predictive criterion and response criterion. Thus, we suggested that the number of noisy/tonal syllables within aggressive calls of *V. sinensis* functions to signal aggressive intent. These results suggested aggressive calls of *V. sinensis* may function to reduce physical contacts and settle conflicts at an early stage to reduce energetic costs as much as possible.

Acoustic Flow Perception in Bats and Applications in Navigation

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Echolocating bats are exposed to and process highly complex acoustic echo signals and use the information for efficient orientation and obstacle avoidance. In natural environments, many echoes from different directions but similar distances will overlap, thereby making 3D triangulation of all contributing objects a challenging/impossible task. The acoustic parameters of echoes (amplitude, frequency and time delay) from complex natural environments change dynamically when in flight, and some of these stochastic changes might provide bats with information in the absence of a comprehensive 3D acoustic image. The continuous flow of sound parameters, changing with the relative velocity of the bat and its environment, can be perceived as 'acoustic flow'. This project aims to understand how bats, specifically low duty-cycle broadband echolocators, perceive acoustic flow for navigation. This is studied both via field experiments manipulating the bats' acoustic environment and computational simulation of the bats' acoustic signal behaviour in that dynamic environment. The experiment manipulates the frequency of the echoes, by introducing controlled motion in the surrounding, creating a Doppler Shift effect on the frequencies. We hypothesise that the bats are balancing these changes in frequencies by controlling its speed in flight. The objective is to observe flight speed and patterns according to the Doppler Shift introduced. The results of both the field experiments and computational simulations will drive further analysis into how we can utilize this method for autonomous vehicle navigation.

AO4-110

The benefits of insect-swarm hunting in echolocating bats, and its influence on the evolution of bat echolocation signals

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Predation on swarms of prey, especially using visual information, has drawn much interest in studies of collective movement. Surprisingly, in the field of biosonar this aspect of prey detection, which is probably very common, has received little to no attention. Here, we combine computer simulations and actual echo measurements to accurately estimate the echo intensity of insect swarms of different size and density. We show that swarm echo intensity increases with 3dB for every doubling of insect number, irrespective of swarm density. Thus swarms will be much easier to detect than single insects. Many of the insects bats eat are so small that they are only detectable by echolocation at very short distances. By focusing on detection of swarms of insects, a bat may increase its operating range and diversify its diet. Interestingly, interference between the sound waves reflected from a swarm of insects can sometimes result in echoes that are much much weaker than echoes from single insects. We show that bats can reduce this problem by increasing the bandwidth of their echolocation calls. Specifically, a bandwidth of 3-8 kHz would guarantee receiving loud echoes from any angle relative to the swarm. Indeed, many bat species, and specifically bats hunting in open spaces, where swarms are abundant, use echolocation signals with a bandwidth of several kHz. Our results might also explain how the first echolocating bats that probably had limited echolocation abilities, could detect insects through swarm hunting.

AO4-111

The Moth Assassin: Aerial Hunting in the Sword-nosed Bat (*Lonchorhina aurita*, Phyllostomidae)

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Animalivorous phyllostomid bats feed on a broad variety of prey ranging from arthropods to small vertebrates. They forage in dense tropical forests and most of them are passive gleaners who rely on prey-generated cues for prey detection, classification and localization. Based on a molecular diet analysis the insectivorous phyllostomine *Lonchorhina aurita* is a moth specialist. Moths are difficult to catch in a passive gleaning mode because they do not vocalize and are mostly motionless when sitting on vegetation. Therefore, we hypothesized that *L. aurita* catches moths in flight, using an aerial hawking hunting style. In experiments we observed the hunting behaviour of *L. aurita* in a flight cage, offering free-flying and tethered moths. Flying bats spontaneously started to search for aerial prey and emitted calls composed of a quasi constant frequency (QCF) component at about 45 kHz, followed by a short frequency-modulated (FM) downward sweep. Occasionally they used also pure QCF-calls without the terminal FM-component. When approaching offered prey bats produced pure FM calls (without QCF-components) with reduced pulse intervals (< 5 ms) and call duration (< 2 ms). Attacks always ended with a rapid succession of very short calls (feeding buzz). Prey was mostly consumed while the bat was still in flight. This echolocation and foraging behaviour is highly similar to that of bats from other aerial hawking bat families (e.g., Emballonuridae, Vespertilionidae) and indicates that *L. aurita* is an edge space aerial hunter, indicating an evolutionary niche different from all other phyllostomid bats.

AO4-112

Vocal Roles and Group Phenotypic Composition Facilitate Roost Finding

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In group living, individuals can exhibit distinct social roles. Social role specialization is highly beneficial because it can reduce the social conflict and energetic expenditures, as well as increase cooperation. For instance, the Spix's disc-winged bat (*Thyroptera tricolor*), a highly mobile animal that uses ephemeral roosts, is known to have distinct social roles in acoustic signaling, to coordinate roost finding. *T. tricolor* groups are composed by one or few vocal individuals, while the rest of the group members produce none or few calls during roost finding. Such complex collective vocal behaviors often arise from simple interaction rules, such as groups pooling information to make accurate decisions. In this case, having a mix of informed and uninformed individuals (i.e. vocal vs non-vocal bats) can promote better decision-making. However, if the number of vocal bats is large, it might create confusion among group members and thus, decrease coordination in roost finding. In this study, we manipulated the number of roosts with vocal bats inside a flight cage to determine how the number of vocal individuals within groups affects coordination and roost finding efficiency. We found that having multiple vocal individuals within a group increases the time spent finding roosts and creates confusion by splitting group members. This demonstrates that groups composed by a mix or vocal and non-vocal bats are more efficient in roost finding. Our results allow us to understand the importance of group phenotypic composition on individual fitness, as well as evolutionary mechanisms determining group formation.

AO4-113

The Energetics of Social Signaling During Roost Location in Spix's Disc-winged Bats

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Long-term social aggregations are maintained by multiple mechanisms including the use of acoustic signals, which may nonetheless entail significant energetic costs. To date, however, no studies have gauged whether there are significant energetic costs to social call production in bats, which heavily rely on acoustic communication for a diversity of social tasks. We measure energetic expenditure during acoustic signaling in Spix's disc-winged bats (*Thyroptera tricolor*), a species that commonly uses social calls to locate the ephemeral furled leaves that they use for roosting. To facilitate this task, *T. tricolor* uses 'inquiry' and 'response' calls; the former are used to maintain contact with group members during flight, whereas the latter are used to signal roost location. This exchange of acoustic signals results in group members rapidly locating and entering the occupied tubular leaf. To determine the cost of sound production in roosting bats, we measured oxygen consumption using intermittent-flow respirometry methods, with and without social signaling. The social signaling trial involved the emission of inquiry calls during a 10-min period during which we recorded the number of response calls produced. The non-social signaling trials used the same method except no inquiry calls were broadcast. Our results suggest that the emission of acoustic signals, including response and echolocation calls, increase oxygen consumption, and that even a few response calls may demand a significant energetic investment; this may explain the presence of different vocal roles in this species.

AO4-114

Echolocation call variations of Taiwanese bats and call identification by ensembles of artificial neural networks

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To date, more than 30 species of insectivorous bat have been identified in Taiwan, including many that are endemic. We collected and analyzed over one thousand echolocation calls from 32 species between 2005 and 2018. The results showed that 3 species, *Rhinolophus formosae*, *R. monoceros* and *Hipposideros armiger terasensis*, emit constant frequency (CF) type echolocation calls, whereas the other 29 species use frequency modulated (FM) type echolocation calls. Among the 16 species studied, *Kerivoula titania* emits the highest frequency call with the maximum frequency approximately 255 kHz, and *Tadarida insignis* broadcasts the lowest frequency call at just 8 kHz. Echolocation calls of *Miniopterus fuliginosus* were shown to have regional variation. Acoustic surveys are a well-established tool in surveillance and monitoring programs for bats. Since the early 1990s, machine learning techniques such as artificial neural networks (ANNs) have been used to identify acoustic signals and have regularly been shown to be more accurate than other analytical methods. Calls of 28 Taiwanese insectivorous species were used to train and test ensembles of artificial neural networks (eANNs). The mean accuracy rate of species level identification, which included 4 species complex groups, was 91.61% (range 50 - 100%), providing accurate identification of most Taiwanese species and an estimate of classification error for each species.

AO4-116

Evidence of Chiroptera Adapting their Specialised Acoustic Systems' Intensity and Detection Range in their Respective Habitats

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Bats use high frequency echolocation pulses that have limited range but refined resolution for detection of small objects such as insects. Historically, research has focused on the methods by which bats vary the frequency of their calls to achieve optimal propagation distances. However, the intensity of these signal emissions is also under control of the bat and must play a major role in signal propagation and therefore in detection of prey. Newly developed multiple microphone arrays allow the position of a bat to be localized in relation to each microphone in the array. Using microphone arrays and three-dimensional (3D) landscaping methods we reconstructed the bats' acoustic flight path in relation to clutter. Our focal chiropteran species was the high duty cycle emitting; *Rhinolophus capensis,* which has previously been shown to vary its call frequency in relation to habitat structure. Our results indicate that both call frequency and intensity are essential for *R. capensis* to achieve appropriate call propagation distances for the detection of different sized prey in their respective habitat (fynbos vs. desert). In flight room experiments, *R. capensis* collected from both regions emitted calls of higher intensity when flown in an uncluttered (empty) vs. cluttered (82 % vegetated) flight room. Additionally, when flown in the uncluttered room, bats from the desert habitat produced significantly lower frequency, higher intensity calls than bats from the fynbos habitat giving them greater detection ranges. These initial findings highlight the importance of environmental pressures responsible for shaping the echolocation call parameters of bat species.

The Role of Social Calls for Species Discrimination in Three Sympatrically Living *Carollia* Species

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Nocturnal, fast moving animals such as bats may rely on vocalizations to communicate at a distance. Differences in social calls providing species information may ensure the long-term coexistence of closely related species living in sympatry. Showing a high similarity in morphology, and overlap in niche use, sympatric species of the genus *Carollia* represent an ideal model to investigate the role of social calls for species separation. We hypothesize that social calls across species differ more in reproduction-related contexts than in other situations. Here, we focus on vocalizations from dyadic interactions in which a bat lands on a conspecific. Social interactions and concomitant vocalizations of three independently kept groups consisting of five *C. perspicillata*, six *C. sowelli* and 14 *C. castanea* were recorded in a flight cage at Hitoy Cerere Biological Reserve, Costa Rica, for several weeks. Video recordings of individually banded bats were made with three cameras in infrared light, and synchronized with the output of an ultrasound recorder. A visual discrimination of the situation-specific sonagrams revealed that, based on time-frequency contours, the three species used shared, as well as unique, call elements. The number of different contours varied from one (*C. sowelli*) to three (*C. perspicillata*), and nine (*C. castanea*), respectively. In a first statistical analysis, the shared call element "down-sweep" differed in peak frequency between *C. perspicillata* and *C. sowelli* suggesting species specific differences. A multi-parametric analysis will show to what extent social call differences separate sympatric *Carollia* species.

AO4-118

Optimising Acoustic Survey Protocols for Bat Research in Species-rich Tropical Forests

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Owing to recent technological advances, bioacoustics has become a burgeoning field in ecological research worldwide. Autonomous acoustic recorders are becoming widely used and automatic classifiers have emerged to aid researchers in the daunting task of analysing massive acoustic datasets. However, the lack of reference calls still hampers their application. Choosing the proper sampling protocol is a challenging question due to time-cost commitment constrains. Capitalizing on a unique acoustic dataset of more than 650,000 bat call sequences collected over a 3-year period in the Amazon we (a) assessed how pre-identified bat recordings could be used to train automatic classifiers, b) evaluated the combination of automatic classification with visual post-validation, and c) optimised sampling protocols under different recording schemes. We confirmed the reliability of using free-flying bats calls to train a custom-built automatic classifier. Adopting a desired accuracy probability threshold of 95% for the classifier, the percentage of recordings required for manual post-validation could be reduced by up to 75%. Also, if lowering cost- effort became a necessity, we recommend, in terms of priority, reducing the replicas, the sampling hours per night, the years of surveys and finally the seasons. The minimum time-window to record a decent amount of bat species includes the first four hours after sunset, although it greatly depends on the homogeneity of the landscape. Combining automatic classification with manual ID help to overcome the risks associated with the sole reliance on automatic classification and optimized sampling protocols improve the economic viability of several projects when funding is limited.

AO4-119

The Functional Extension of Echolocation – Eavesdropping or Communication in Horseshoe Bats?

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The question if echolocation is a communication signal has been subject of research for the past decades and revealed some convincing cases. However, there is a crucial difference between a true communication signal and an acoustic cue used by eavesdroppers. In the latter, perceivers extract information leaked from cues given unintentionally by senders whereas communication includes an active role of the sender to intentionally emit a signal. This difference has consequences for the evolution of signal design, especially since the communicative function has been proposed to be a driver of signal divergence in horseshoe bats. To understand if echolocation is used in communication, both the sender and perceiver should be studied. In a series of experiments, we manipulated the social environment for the sender to see if the echolocation calls vary systematically with the situation. We specifically analyzed the occurrence of modifications on the FM component since they increase the individual signature of an echolocation pulse. Using a different experimental approach, we tested which type of information receivers perceive. Our results show that bats perceive species, gender and individual signatures from echolocation calls of other bats. Furthermore, we found an increase in the perceivers' ability to use minute acoustic cues in the pulses of other bats if they overlap in acoustic space. The senders on the other hand, did not vary their echolocation in response to different social environments. We therefore cautiously conclude, that echolocation may be an acoustic cue leaking information to eavesdropping bats, rather than a communication signal.

AO4-120

Echolocation, Morphs and Harmonic Relationships in Horseshoe Bats of the Philippinensis Group

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There are three versions of the genus *Rhinolophus* in Australia. Two size morphs (large & intermediate) of *R. philippinensis* have been recognized, as distinct from each other, and from *R. megaphyllus* (Churchill 2009 *Australian Bats* 2nd edition, Allen & Unwin). All versions of this genus are very close genetically (mtDNA), so separating the morphs remains unclear. However this group of CF-FM bats can be separated clearly by their echolocation call characteristics. A parallel situation exists for three size morphs of *R. philippinensis* in Sulawesi, Indonesia (Kingston & Rossiter 2004 *Nature* 429:654-657). In Australia, there is a restricted range of sympatry for the two morphs on Cape York Peninsula. There is allopatry because the range of the large morph extends further south. Both morphs remain sympatric with *R. megaphyllus* since it's range extends much further down the east coast. Field recordings have been made to study the geographical variation in call frequencies; *R. philippinensis* CF 27-35 kHz (large) and CF 40-42 kHz (intermediate); *R. megaphyllus* CF 74-67 kHz (north-south cline). Field experiments using a light gas mixture (heliox) with all three forms, to demonstrate the first harmonic, show unequivocally that the large morph of *R. philippinensis,* despite using very low CF frequencies, also expresses the second harmonic during pulse emission. Both the large *R. philippinensis* morph and *R. megaphyllus* are capable of DSC as tested in the field. An important finding here is that the first harmonic frequencies used by the Australian *R. philippinensis* morphs and *R. megaphyllus* are not related. This finding contradicts the conclusions drawn for the three size morphs of *R. philippinensis* found in Indonesia (op. cit.), where it is claimed that 'harmonic hopping' between morphs is based on the same fundamental. Re-examination of these published data indicate that the first harmonic frequencies used by the Indonesian morphs are not in fact related, as previously assumed.

AO4-121

Echolocation Behavior of *Natalus tumidirostris*: Continuous Sampling with Short High-Frequency Calls

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We describe for the first time the echolocating behavior of the trinidian funnel-eared bat, *Natalus tumidirostris*. By recording individuals in natural and semi-natural conditions at the Macaregua cave in Santander (Colombia), we documented the different echolocating behaviors of these bats with multi-channnel audio recordings, as well as single channel recordings synchronized with video.

Contrasting with other narrow-space foraging bats, *N. tumidirostris* do not produce clearly distinguishable call groups, but rather sample the environment in an almost continuous fashion, with call-batches of up to 21 seconds in duration. Pulse intervals during search phase correspond to 28.79±3.31ms and are continuously reduced down to 10ms during prey catch. These bats produce rather faint and short (2.36±0.23ms) frequency modulated calls with the main energy in the 2nd harmonic, ranging between 165-95 kHz and with a peak frequency on average at 121±7 kHz. During catch events however, the first harmonic can be additionally emphasized .

This continuous sampling echolocating behavior and the high flight maneuverability due to low wing loading and low aspect ratio indicates that *N. tumidirostris* most likely hunt within dense vegetation. We also hypothesize their echolocation strategy could well serve to detect flutter information from prey echoes in cluttered environments.

AO4-122

Biosonar Dynamics and Echoic Scenes in Wild Foraging *Myotis myotis*

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How bats adapt their sonar signals to different tasks has been shown in detail in a long series of thorough laboratory studies. However, we know little about the active adjustment of sonar outputs to guide sensory inputs in the wild. By recording the outgoing vocalizations, returning echoes as well as movement in three dimensions from on-board sound and movement tags, the auditory flow experienced by bats can be visualized and quantified. Here, we use these tags on wild *Myotis myotis* as they capture insects on the wing by echolocation and glean beetles off the ground by passive listening. This study allows us to infer how changes in outgoing emissions affect the returning echo information when bats are hunting for prey. We show that these bats decrease their output power by up to 1000 times prior to capturing prey on the ground to avoid masking of prey-generated cues. This consequently leads to a narrowing of their echoic scene to the minimum required for execution of prey pursuit, landing and attack; this sacrifice presumably maximizes foraging efficiency. In contrast, when foraging in open space, we show how the combination of increasing call repetition rate and decreasing output power filters out the reverberation and secures clear, unmasked prey echoes. This study highlights the changes in sensory volume ensonified during these two modes of foraging, and the flexibility of the sonar signal design adapted to different operational modes.

AO4-123

Contextual analysis of vocalizations in the Ryukyu flying fox *Pteropus dasymallus*

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Insular bats of the genus *Pteropus* are the subject of great conservation concern. Yet, too often, information about ecology, distribution or demographic trends remains scarce. Very little is known, for instance, about the status of local populations of the Ryukyu flying fox *Pteropus dasymallus* (VU, IUCN), a solitary island fruit bat inhabiting the Ryukyu archipelago in Japan and neighboring Taiwanese islands, for which no reliable population estimate exists. Here, we studied vocal communication in captive *P. dasymallus individuals* to assess the possibility of using acoustic signals in the frame of PAM (passive acoustic monitoring) to support ecological studies and monitoring programs. We carried out both audio and video recordings from winter 2017 to autumn 2018 at two zoos, NeoPark Okinawa and Okinawa Zoo & Museum. Following call segmentation, we extracted 12 Mel frequency cepstral coefficients as well as several other acoustic features for each syllables. From an ethological perspective, at least eleven call types with distinct associated behaviors were observed in captivity. Discriminant analysis using a SVM (Support Vector Machine) revealed that many calls were acoustically distinct from one another with over 80% balanced accuracy. SVM allowed to distinguish with high accuracy (over 80%) the sex of the emitter of "General Aggression calls", which accompany everyday interactions in these bats. We will also present here preliminary results on recordings from the wild and conclude on the early use of our classifiers within a PAM system to monitor wild flying fox populations.

AO4-124

Early-age Auditory Development and Vocal Learning in Pre- and Postnatal Egyptian Fruit Bats

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In-utero hearing abilities has attracted marketed vocal learning tools for expectant mothers, but the details of early age vocal learning in humans and mammals alike are still being uncovered. Vocal learning, the ability to receive and produce, understand, or correctly use novel sounds, is a critical part of vocal development in bats. The Egyptian fruit bat (*Rousettus aegyptiacus*) is a social, group-living species producing broadband echolocation and various social calls. Pups greater than six months of age learn the frequency of their calls from exposure to adult vocalizations. In this study we assessed vocal learning abilities at earlier ages- in utero and within the first 4 weeks post birth. We first addressed the auditory development of pups by using Doppler methods to assess fetal response to sounds in utero, and by conducting behavioral trials with pups postnatally to create behavioral audiograms from Day 0. We addressed vocal learning prenatally by exposing pregnant females to manipulated calls throughout pregnancy. Post birth we tested pup response to the manipulated conspecific calls. Additionally, we tested whether pups can discriminate conspecific calls from heterospecific calls, predator stimuli, and noise through acoustic playbacks. Pups can hear by age Day 0, but are sensitive to all sounds initially, including calls and noise. Pups exposed to manipulated calls during pregnancy did not show clear preferences within the first week. Thus bats may not learn prenatally, amd postnatally have a broadly sensitive window that can be investigated for a combination of auditory development and learning processes.

AO4-126

Doppler shift compensation and auditory fovea of the low frequency horseshoe bat, *Rhinolophus paradoxolophus*

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The horseshoe bat, *Rhinolophus paradoxolophus,* belongs to the *philippinensis* group, whose members differ from other standard rhinolophids in the morphology of sender and receiver antennae, and by lower species-specific call frequencies than expected from body size. We compared *R. paradoxolophus* with standard rhinolophids and show, that they compensate Doppler shifts with the same precision, possess a similar auditory fovea and a sonar beam with a similar directionality as standard rhinolophids. In flight, echo frequency was maintained constant at the reference frequency ($f_{ref)}$ independently of the flight speed, which indicates, that Doppler shift compensation had the same precision as in standard rhinolophids. Resting frequency and f_{ref} where tightly coupled at a mean offset of about 70 Hz. The behavioural audiogram of *R. paradoxolophus* revealed a similar threshold curve as in standard rhinolophids with a sharp minimum around the reference frequency (f_{ref}), typical for an auditory fovea, and a distinct maximum below f_{ref}. The directionality of the sonar beam was close to that measured in *Rhinolophus ferrumequinum* indicated by a -6 dB half beam width between 27° and 30°. Our results suggest that the echolocation system of *R. paradoxolophus* and probably also of all other bats of the *philippinensis* group are functionally similar to those of standard rhinolophids despite the changes in sender and receiver antennae.

AO4-127

The role of social interactions on vocal ontogeny in the babbling bat *Saccopteryx bilineata*

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Human speech acquisition includes different key factors, which are influenced by the infants ‘social environment. During speech acquisition, canonical babbling is the crucial step from innate vocalizations to the foundation of spoken language and studies showed that caregiver-infant interactions (verbal as well as non-verbal) have a significant influence on babbling features. To understand how language evolved, the study of vocal development can reveal insight into potential underlying mechanisms and factors of the language system. Therefore, comparative studies of vocal ontogeny in non-human species are a promising tool in the field of biolinguistic. A promising species to investigate vocal ontogeny is the bat, *Saccopteryx bilineata.* This species is a vocal production learner and owns a complex vocal repertoire which is acquired by pups during a conspicuous vocal practice phase (8-10 weeks) in form of babbling bouts, reminiscent of the canonical babbling in human infants. Babbling is accompanied by behavioural interactions between mother and pup. With our study, we want to elucidate whether the social environment, in particular, mother-pup interactions, influences the vocal ontogeny. Analyses showed that the behavioural displays of mothers have a significant influence on babbling bout duration as well as on the length of the babbling phase (N=19 mother-pup pairs, N=141 babbling bouts). Interactive behavioural sequences increase in number and in sequential complexity with pup age. In contrast, the number of pups and male tutors do not seem to have aasignificant influence. In conclusion, in *S. bilineata* mothers have the greatest impact on the pup’s vocal ontogeny.

AO4-131

Acoustics and Occupancy of Endangered Tree-Dwelling Bats, *Murina ryukyuana* and *Myotis yanbarensis*, in Northern Okinawa Island

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The Ryukyu tube-nosed bat *Murina ryukyuana* and Yanbaru whiskered bat *Myotis yanbarensis* were discovered in 1996 on Okinawa Island, Japan. Despite Endangered and Critically Endangered status, respectively, these species have yet to receive substantial research attention. We used autonomous acoustic recorders to determine the distribution and habitat preferences of these rare bats in northern Okinawa Island using both randomized and targetted recorder placements between Fall 2018 and Summer 2019. Random sites were selected using a roughly two km^2 grid, and occupancy was calculated based on detection rates over three consecutive nights. Despite low capture rates, *Murina ryukyuana* was found to be relatively widely distributed within forested areas using acoustic detection. *Myotis yanbarensis* appears to be more restricted, with strong preference for particular streams. These results were in agreement to results obtained through VHF tracking of roosts. *Murina ryukyuana* was found to have soft echolocation characteristic of a clutter specialist, but emitted more detectible social calls during all seasons monitored. Our results highlight important habitat for Okinawa's endangered microbats and provide further evidence for the utility of social calls for bat monitoring, especially for otherwise difficult to detect species.

AO4-132

Social Vocalizations of Big-footed Myotis (*Myotis macrodactylus*) during Foraging

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Acoustic signals play a crucial role in transmitting information and maintaining social stability in gregarious animals, especially in echolocating bats, which rely primarily on biological sonar for navigating in the dark. In the context of foraging without relying on tactile, visual or olfactory cues, acoustic signals convey information not only on food but also on ownership and defense of resources. However, studies on such information remain fragmentary. In the present study, we aim to document the social vocal repertoire of *Myotis macrodactylus* at natural foraging sites. Multiple acoustic analyses and spectrographic classification revealed a rich foraging vocal repertoire comprising 6 simple syllables and 2 composites. Discriminant function analyses associated with a subset-validation procedure provided an optimal method to spectrographically classify all recorded sounds into different syllable types. Multidimensional scaling of median values of multiple parameters further confirmed notable differences among these syllables in a 3-D space. In addition, Euclidean distance analysis showed that there were some spectral similarities between specific social vocal syllables and feeding buzzes, which implied a potential jamming role. Altogether, the data indicate that bats at foraging sites under natural conditions used variant social vocalizations with different functions in addition to echolocation calls, providing supporting evidence for further work on the function and vocal mechanisms of acoustic communication in mammals.

AO4-133

Listening to Ghosts: Monitoring the Behaviour of Cryptic *Macroderma gigas* by Acoustic Proxy

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The ghost bat *Macroderma gigas* is a carnivorous species endemic to Northern Australia and is threatened with extinction, with disturbance of maternity colonies identified as a high priority threat. This extreme sensitivity to disturbance means that little is known about its ecology and behavior. Here, we capitalize on recent advances in sound recording technology to develop new methods for monitoring and studying *M. gigas* in the wild.

We recorded eight terabytes of sound in full-spectrum from five cave roosts across Australia's Northern Territory over a two-year period. Using a subset of data from our primary site (Pine Creek), we characterized *M. gigas'* vocal repertoire using clustering and discriminant function analysis. This catalogue was used to develop an automatic classifier and categorize the recordings from all sites. To determine vocalisation function, we collated an inventory of behaviours (ethogram) based on observations of a captive colony. Finally, we assessed seasonal changes in the relative use of vocalisation types across the five sites as a proxy for behavior.

We found that *M. gigas* has a broad repertoire of at least six distinct non-echolocation vocalization types. Two of these vocalizations, 'squabble' and 'chirp-trill', are strongly associated with particular behaviors and vary predictably with season. Taken together with previous experimental work, these data indicate a complex acoustic communication system. These results show that our approach can be used successfully as a non-invasive proxy for investigating and monitoring behavior in this sensitive species and highlight the utility of eavesdropping on the social vocalizations of cryptic species.

Variation in Echolocation Call Intensities and Detection Distances of Bat Assemblages Across an Environmental Gradient

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Intensity is an ecologically crucial parameter, as it determines the extent of the bats' perceptual space and, specifically, prey detection distance. Intensity of signals is subject to atmospheric attenuation as it propagates through the physical environment in a habitat and this limits the effective range of bats prey detection and ultimately affects bat's foraging efficiency. The study aimed to investigate climate change effects, via changes in temperature and humidity on call intensities and detection ranges of bat assemblages in six biomes across South Africa. We used the state-of-the-art multiple microphone array system to record echolocation calls to measure intensities in 3D flight paths. Temperature, relative humidity, air pressure, were recorded using a portable weather station during echolocation calls recording session. Light traps were used to catch insects at the same time while recording bat calls in each biome. Insect's body length was measured using a graticule fitted to stereomicroscope to determine the size range and assign target strength. With measured intensities (as source levels) at different temperature and humidity, and range of insect sizes, the detection distances for the prey was calculated. Preliminary results shows a significant difference in bats prey detection distances of (R= 0.784, P= 0.0001) and (R= 0.4802, P= 0.0001) in fynbos and desert biomes, respectively. Thus, detection distances vary across different habitats in accordance with different prevailing environmental conditions.

Diet of the Wrinkle-lipped Free-tailed Bat in Central Thailand

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Dietary studies of insectivorous bats are essential for understanding their feeding behavior, food preference and their role in the ecosystem. The wrinkle-lipped free-tailed bat (*Chaerephon plicatus* Buchannan, 1800) is known as biological pest suppression agent for white-backed planthoppers, and may also regulate brown planthopper populations where this pest in common. Hence, it is highly important to investigate the diet of *C. plicatus* in areas where brown planthoppers are abundance. In addition, it is interesting to investigate if diet compositions vary with different proportions of rice fields. To accomplish this objective, we analyzed the diet of *C. plicatus* from two caves of central Thailand. Bat fecal pellets were collected monthly from October in 2015 to September in 2016. A total of 720 fecal pellets were analyzed, and the results revealed that *C. plicatus* feeds on at least 8 insect orders, including Coleoptera, Homoptera, Hemiptera, Diptera, Lepidoptera, Odonata, Hymenoptera and Orthoptera. Specifically, homopterans comprised the greatest diet volume in the rice field growing season. Moreover, most homopterans were identified as brown planthoppers. Diets from two study colonies were not significantly different, even though the proportion of surrounding active rice fields was different. Our results, suggest that tens of millions of brown planthoppers are consumed by this bat species each night. The similar diets of the two study colonies may be due to their high altitude foraging and preference for migratory insects. Thus, the wrinkle-lipped free-tailed bat is an important biological suppression agent of brown planthoppers in surrounding rice fields and in a larger landscape.

Foraging Range and Diurnal Roost Selection of the Tri-colored Bat

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Tri-colored bats populations are declining across the temperate portions of their range, primarily due to the impacts of white-nose syndrome. The U.S. Fish and Wildlife Service has been petitioned to protect the species under the Endangered Species Act. However, our limited understanding of tri-colored bat roosting and foraging ecology precludes our ability to effectively identify critical habitat for listing. The objectives of this research were to 1) characterize the summer diurnal roosts of tri-colored bats and examine roost selection at two spatial scales (i.e., stand and landscape), and 2) establish the size of tri-colored bat foraging ranges and explore foraging range selection at two spatial scales (i.e., overall and core). Over two years, we radio-tagged 7 male tri-colored bats in middle Tennessee, U.S., and tracked them daily to their diurnal roosts and on nightly foraging bouts. Bats primarily roosted in clumps of dead oak and hickory leaves. Stand level features were less important to roost selection than landscape level features. At the landscape scale, tri-colored bats selected roosts in large tracts of mature forest in close proximity to more open foraging areas. We biangulated an average of 102 (range 49-177) foraging locations for each bat. The mean 95% minimum convex polygon foraging range was 2,350 (range 234-9,655) ha. Selection of core foraging range (50% PVC) within the overall foraging range was significantly non-random (Wilk's $\lambda = 0.056$, $P = 0.016$) with bats selecting to forage over open water and wetlands significantly more than other available land covers.

AO5-103

Light, Flight and the Night: Effect of Ambient Lighting and Moon Phase on Pteropodid Flight Activity

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Pteropodidae is the only phytophagous bat family in the paleotropics and it predominantly relies on visual cues during long-range flight and foraging. Pteropodids are known to be exposed to varying light levels during the day from bright (>1000 lux) to dark (<0.1 lux), but the collective effect of ambient lighting and moon phases on their flight activity is understudied. To address this, we chose three species with different daylight exposures and observed their flight activity across five lunar cycles at their roosts in southern India. We found significant differences in the emergence initiation (F =49.61, p<0.001) and flight termination (F =18.01, p<0.001) timings among the three species. The dark roosting *Rousettus leschenaultii* initiated and terminated flights in the relatively darker twilight zones compared to the bright roosting *Pteropus giganteus* and foliage roosting *Cynopterus sphinx*. Moon phase had no effect on the overnight emergence and return flight patterns of *P. giganteus* and *C. sphinx* at the roosts, but *R. leschenaultii* clearly shifted their peak emergence across moon phases. Overall, these results indicate that ambient lighting during the twilight zones and across moon phases influences flight activity in pteropodids, but the effect is not uniform among the species. The dark roosting *R. leschenaultii* initiated and terminated flights in relatively lower light levels and showed altered activity patterns across moon phases, while no such trend was observed in bright roosting *P. giganteus* and foliage roosting *C. sphinx* at their corresponding roost sites.

AO5-104

Diet Analysis of Kitti's Hog-nosed Bat by DNA Barcoding

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Insectivorous bats are the most diverse mammals in Thailand. Due to their high abundance, they play an important role in ecosystem as insect controller. Kitti's hog-nosed bat *Craseonycteris thonglongyai*, the smallest insectivorous bat endemic to western Thailand and eastern Myanmar, feeds on insects within the surrounding area of their roost during their short foraging flights, just after sunset and once again in early morning. In this study, diet composition of Kitti's hog-nosed bats at Kanchanaburi province, Thailand was investigated using DNA barcode to identify the insect groups from their faeces. The cytochrome c oxidase subunit I (COI) gene was amplified by the polymerase chain reaction (PCR) using insect-specific primers ZBJ-ArtF1c and ZBJ-ArtR2c). Results from cloning and next-generation sequencing revealed that Kitti's hog-nosed bats prey mainly on insects in order Lepidoptera which composed of many families such as Noctuidae, Hyblaeidae, Geometridae, Depressariidae and Oecophoridae. Other insects like crickets (Orthoptera: Gryllidae) and stink bugs (Hemiptera: Pentatomidae) were also found in bat diets. Some insect pests e.g. *Hyblaea puera*, a native moth considered as one of the major teak pests, could be identified from this study. This highlights the role of this bat species as not only an insect controller but also a pest controller in ecosystem.

AO5-105

Long-term Banding of California Leaf-nosed Bats Along the Lower Colorado River to Determine Movements and Longevity

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California leaf-nosed bats (*Macrotus californicus*) are residents of the Sonoran Desert in California and Arizona and are active all year. These populations are interesting as representing the northern margin of the semitropical distribution of a non-hibernating phyllostomid genus. In 1958, a long-term banding study was initiated to examine demography and movements of these bats in the temperate zone along the Lower Colorado River (LCR). The bats were captured principally in the winter in warm mines along the LCR in ten mountain ranges. During banding or recapture, the degree of tooth wear (1-4) was recorded to develop an indicator of approximate age of un-banded bats in the population. In 60 years, over 15,000 bats have been banded, and over 5,000 individuals have been recaptured between one and nine times for a total of over 8,500 recapture events. Roost fidelity is high, and over 75 % of the bats were recaptured in the mine where they were initially banded. The remaining recaptures document movements primarily between adjacent mountain ranges both seasonally and between years. The greatest distance traveled between banding and recapture was 188 km (117 miles). The longest interval between initial banding and recapture was over 16 years, which is a notable age for a bat of tropical ancestry that is not capable of seasonal torpor.

AO5-106

Interactions Between Dietary Breadth and Microbiome Specialization in Neotropical Bats

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Bats are remarkable in their dietary diversity; in the Neotropics in particular, bats have radiated to fill nearly every possible terrestrial feeding niche. Some species are generalists, eating a variety of both plant and animal food resources, while other species appear to narrowly specialize on just a few food items. When a bat specializes on a nutritionally incomplete food resource such as fruit, a key question arises: how do they compensate for the lack of essential nutrients (e.g., fatty acids, proteins, and vitamins) in the diet? A standing hypothesis suggests fruit bats engage in facultative insectivory to meet their nutritional requirements, but a new hypothesis suggests that gut microbiota (the community of symbiotic bacteria inhabiting the digestive tract) may be functionally specialized to provision their hosts with missing nutrients, such that the host may not need to engage in insectivory. Using an ecologically diverse assemblage of 28 Neotropical bat species, we tested these hypotheses using 16S rRNA microbiome profiling, predictive functional reconstruction, and diet metabarcoding. We compared the dietary composition and microbiome function of strictly frugivorous bats to those of omnivores and strict insectivores ($n_{total} = 89$). We found that fruit-eating bats had microbiomes enriched for functions related to peptide biosynthesis, fatty acid metabolism and vitamin metabolism compared with insectivorous bats. Diet analyses also revealed limited insectivory in bat species previously considered to be strictly frugivorous, suggesting an interplay between dietary flexibility and microbiome functional specialization may have facilitated dietary specialization in Neotropical bats.

AO5-107

Large PIT-Antenna System Detects Low Summer-Autumn Survival of the Australian Critically Endangered Southern Bent-Wing Bat

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Passive integrated transponder (PIT) technology has facilitated wildlife monitoring without the need for physical re-trapping. While this has been effective where animals pass within centimeters of tag readers, in many situations, such as for cave-dwelling bats, the short detection-ranges of PIT systems have hampered their use. To address this problem, we optimized a 15 m long, looped PIT-antenna that detected bats flying within a maternity cave of the critically endangered southern bent-wing bat *Miniopterus orianae bassanii* in southern Australia. This subspecies has suffered serious population decline; however, the cause is not fully understood. We PIT-tagged 2966 bats and used capture-mark-resight to estimate survival rates by sex, age and season over a three-year period. In contrast to many other bat species, all cohorts exhibited lowest survival over summer and autumn, with particularly low survival in adult females in summer (when lactating), and juveniles in autumn (after weaning). Adult females had 8.4% higher mean body mass in late-summer compared to during peak lactation in mid-summer. The reverse was found for juveniles, with body mass markedly decreasing by 19.3% after weaning. Taken together, our results suggest that challenging conditions during the breeding season are impacting species viability – potentially due to resource limitation as a result of wetland drainage. Our population projections predict continued population decline, even if high female fertility and pre-volant juvenile survival are assumed, necessitating urgent conservation action to reduce extinction risk. Additionally, the success of our method demonstrates untapped potential for using large PIT-antennas to study cave-dwelling bats world-wide.

AO5-108

Phenotypic Responses of Bats to Climate and Land Use Change Over the Past Sixty Years in China

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Understanding of how different species respond to recent environmental changes is still insufficient, especially those linking ecological traits to adaptation. We examined both historical (1960s) specimens and individuals captured in 2017 from the same latitudinal range for one insectivorous bat species *Hipposideros armiger* and one phytophagous bats *Rousettus leschenaultia*, a total of 444 individuals, to explore their phenotypic responses to environmental change over 65 years in China. All two bat species showed non-significant decreases in their forearm length over this span of time, which is inconsistent with the prediction of Bergmann's rule, suggesting that increased heat dissipation may not be a common selective pressure under climate change for most bat species. With respect to land use change, bats with different diets showed consistent changes in diet-related morphological traits and in isotopic composition, suggesting altered foraging patterns. *Hipposideros armiger* showed a significant increase in forearm length and in three dimensions of diet-related cranial traits, profile length, length of tooth row and external width across lower molars, and significant changes in the carbon and nitrogen stable-isotope composition. Higher ratios of modified and open land use types based on land cover data between historical and modern periods suggests that *H. armiger* had to travel farther and may utilize different food resources. Ratios of modified and open land use type were relatively stable for *R. leschenaultia* and it also did not show significant changes in forearm length, but showed significant increases in dimensions of all diet-related cranial traits. This study provides evidence for significant and consistent phenotypic variations in different bat species in response to recent environmental changes and dietary-related structure changes may be somewhat general responses of bats to current environmental changes.

Dark Side of Climate Warming: Colorado Bats are Feeling the Heat

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The ecosystem effects of climate disruption are underway in the Southern Rocky Mountains. Reduced snowpack and less frequent summer precipitation decreases stream discharge rates and water availability for bats during the reproductive season. Over the last 20 years, overall reductions in capture rates of bats were evident, with *Myotis thysanodes*, a species of greatest conservation need in Colorado, being most affected. In drought years reproduction was compromised by nearly 50% in some myotis species and reduced stream discharge rates correlated significantly with decreased capture of lactating, rather than pregnant, females. Our data indicates that water availability, not specifically increased regional summer temperatures, is the most important climate change factor affecting bat populations. Surprisingly, we also found that sex-ratios have trended towards males over the last 20 years apparently due to increasing years with summer droughts. Specifically, in years when mean June, July, and August temperatures and precipitation hovered near 28.7C/7.5 cm, approximately 1:1 sex ratios occurred. However, in years when either cooler/wetter or hotter/drier conditions occurred, male-biased juveniles were predominately captured, especially in hotter/drier years. To explore the possible impacts of future climate conditions on various aspects of bat population dynamics, we built predictive logistic regression models and projected them through the year 2090 using four carbon emission scenarios. All scenarios showed declining population numbers and reductions in proportions of females in future years with declines occurred at different rates depending on scenario severity. We discuss ways to possibly mitigate some of the immediate impacts of climate warming in Colorado.

AO5-110

Aggregational response of bats during forest pest emergence

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Among arthropods, moths (Lepidoptera) are major agricultural and forest pests in many parts of the world and even in Europe they represent majority of lepidopterans. Many of them are of great economic importance as pests of crops, horticultural plants or stored products and woollens. Our focus is on two complexes of sibling moths, forest lepidopteran pests *Operophtera brumata* and *Erannis defoliaria* during their spring emergence of caterpillars. These species are known for their high foliage consumption. We hypotheses that bats will switch to more abundant emerging prey. We sampled caterpillars during spring and adult stages in autumn to determine level of infestation. We establish two infested sites and one control and monitored flight activity of bats between sunset and sunrise from 15th of April to 25th of May 2017, when the pest numbers peaked. Foraging activity of bats,i.e., two gleaning bats (*Myotis nattereri* and *Myotis bechsteinii*) and two species that use both gleaning and aerial hawking (*Plecotus auritus* and *Plecotus austriacus*) was assessed by bat detectors. On both infested sites we found significant increase in flight activity of all studied bat species during caterpillar emergence, we did not detect any significant increase of activity on control site. Based on our results we conclude that bats aggregated at sites with high numbers of pests and thus may contribute to pest control.This project was financially supported as a part of a specific university research project at Masaryk University (MUNI/A/1436/2018).

AO5-111

Land use and insect pest pest consumption by bats in macadamia orchards, South Africa

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Accelerating land use change is associated with the loss of species and their ecosystem services. South Africa is the world's largest producer of macadamias and the industry continues to grow. Insectivorous bat species are important for pest control, but bat populations are declining. Therefore, proactive management of bat communities in agricultural landscapes and incentivizing farmers to adopt a more integrated pest management approach is essential. We analyzed both the bat activity of the two main foraging guilds (open-air/clutter edge) in different land use types and with respect to arthropod abundances during one annual cycle in Limpopo, South Africa. Additionally, we used a molecular approach to analyze bat pellets with fluorescent-labelled and species-specific primers, targeting four of the main insect pests. All the species or families of bats sampled, foraged on at least one of the four insect pests, with sequences confirmed from 54 out of 103 samples (55.6%). Overall clutter edge guild activity decreased with macadamia and orchard (all other fruit) cover and increased with bush cover and distance to farmhouses (potential roost). Open-air guild activity increased with fallow cover. The activity of both guilds increased with abundance of true bugs, including the main macadamia pests, and bush cover. In conclusion, natural and semi-natural vegetation promote bat activity and bats are important for pest control. In times of accelerating land use change, remnants of natural and semi-vegetation need to be maintained or restored.

AO5-113

Temporal and spatial activity of bats in the ephemeral rivers of an arid Australian mountain range

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Insectivorous bats are the most diverse order of mammals remaining in the arid mountain ranges of central Australia, however little is known about spatial and temporal activity patterns. Ten of the twelve species known to occur are dependent on tree hollows for roosting and breeding and *Eucalyptus camaldulensis* woodlands on ephemeral rivers are one of the only plant communities in the region with abundant hollows. These woodlands are being degraded on a regional scale by increasing wildfire frequency and intensity, fuelled by an invasive grass- *Cenchrus ciliaris*. Large hollow-bearing trees are particularly at risk of complete destruction in fires. As a result there is potential for impacts on bat populations, particularly hollow-using species, to go undetected due to lack of information about their ecology in the region. The main aim of this research was to establish if riverine woodlands in central Australia were a site of increased bat activity and if any seasonal patterns in habitat use were evident. To address this aim, we investigated seasonal bat activity across twelve *E. camaldulensis* woodlands and twelve neighbouring vegetation communities with repeated acoustic monitoring over two years. We verified that bats were indeed significantly more active in these woodlands than in other habitat, regardless of season. In this paper we report on structural features in riparian woodland which are predictors of bat activity. This information can be used to focus monitoring and management and has significant implications for preserving bat habitat in fire-prone arid environments.

Vocal Adaptations of Insect-eating Bats in Response to Shifts in Temperature and Humidity

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Insectivorous bats play important roles in the ecosystem because they prey on insects, which often are agricultural pests. In order to effectively capture their prey, bats rely on their echolocation calls, however, the range over which these calls operate is a direct function of temperature and relative humidity, which determine sound attenuation. Hence, climate change may alter the distance over which bats can detect echoes to find food. An interesting possibility is that the vocal plasticity of bats will allow them to respond to shifts in temperature and relative humidity even at short temporal scales and adjust calls accordingly. We hypothesized that bats may decrease call frequency, increase call level, increase call duration, or any combination thereof to keep constant prey detection ranges. We recorded vespertilionid bats in pre-montane forests of Costa Rica with a four-microphone array inside a flight tent at four different combinations of temperature and relative humidity. We reconstructed flight trajectories to determine the position of the bats when they emit the call, and from each call, we analyzed duration, frequency, and level, to assess the range of 'view' of each individual under the experimental temperature and humidity conditions. We found that each individual kept the detection ranges relatively constant, independently of weather conditions. Our research is the first assessment that considers how changes in temperature and humidity affect call production under controlled conditions. It increases our understanding of the ability of insectivorous bats to adapt to climate change, and the potential effects on bat assemblages.

AO5-116

Frugivorous Bats in Brazil's Atlantic Forest: Effects of Habitat Fragmentation on Diet

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The effects of landscape structure on species persistence has long been an area of research but there are still many questions on how the biology of species that persist in a fragmented landscape may have changed. Using stable isotope analysis, we examined differences in the diets of three species of frugivorous bats from different habitat fragments in Brazil's Atlantic Forest. We hypothesized that individuals captured in habitat patches would have a different foraging strategy than those captured in contiguous habitats and species which are more mobile will be less impacted by small scale landscape changes. We predicted that (1) wide ranging species (*Artibeus lituratus*) which can move through open areas should be less affected by landscape and patch composition and (2) narrow ranging species (*Carollia perspicillata* and *Sturnira lilium*) will have higher variation in niche breadth and isotopic ratio ranges dependant on their environment (i.e. size, composition and degree of isolation of habitat patches). Using Akaike's Information Criterion (AIC) to rank hypotheses explaining this variation, we found that fragment composition, largely involving vegetation density, rather than landscape scale variables, had the most significant effect on the diet of fruit bats. This implies that bats are resident to these fragments and do alter their feeding behaviour to suit their environment.

AO5-117

Ontogeny of Foraging Via Assisted Learning by Mothers in Egyptian Fruit Bat Pups

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The transfer of information between parents and offspring is particularly important in mammals with relatively long periods of offspring dependency, such as fruit-bats. Offspring might learn several important skills during this period, especially how to and what to forage. Previous findings in non-bat species have revealed that juveniles learn a significant amount of what they know about foraging through social learning. Numerous bat species have been observed carrying non-volant young in flight, while both foraging and roost switching. This behavior is likely costly for mothers, and it is the benefits for the offspring that are still not fully clear. In this study, the developmental process from non-volant to independently foraging pups was monitored using high resolution GPS and telemetry tracking. Successful tracking of over 35 mom-pup pairs provides the first evidence of assisted learning of foraging by Egyptian-fruit-bat mothers. This process includes five distinct stages: (1) Pups are attached to their mothers 24/7 (2) Gradual-detachment: Mothers carry pups for shorter bouts, drop-off pups on a tree, forage alone, then pick-up pups on their way back to the cave (3) Pups are left alone in the cave (4) Pups fly independently to known sites, where their mothers previously dropped them off (5) Pups expand foraging to new sites unique to them. Our data shows that mother bats actively mediate learning of independent foraging by repeatedly placing pups on trees, which they then visit on their first foraging bouts.

Field experiment reveals the interplay between three cognitive skills in locating day roosts by Bechstein's bats

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Finding suitable roosts is a critical task for survival, especially for those bat species that change roost regularly. The identification of roost locations has been primarily investigated from a sensory ecology approach. However, the cognitive abilities of bats have not been studied under natural conditions in a roost selection context. We used a pairwise discrimination experiment with automatic RFID monitoring to assess how free-ranging Bechstein's bats (*Myotis bechsteinii*) locate suitable (familiar and unfamiliar) roosts through associative learning, spatial memory and social information use. Experimental pairs consisted of a suitable and an unsuitable bat box, which had distinctive echo-acoustic cues. Bats learned to associate box habitability with their echo-acoustic cue. As bats gathered experience, they discovered more box pairs by visiting first the suitable box ($p < 0.0001$) and performed more visits to suitable than to unsuitable boxes ($p < 0.001$). For testing the relocation of previously occupied boxes, we switched box positions within the experimental pair and compared the proportion of bats entering to the suitable box before and after switching box positions. Bats relied more on spatial memory than on associative learning for relocating suitable boxes ($p < 0.001$ before *vs* after). The use of social information, provided by the presence of conspecifics at roosts, improved the (re)location of suitable roost compared to when bats performed these task individually. Our experimental field study unveils how bats make a hierarchical use of multiple cues according to their perceptual and functional relevance for locating roosts.

AO5-119

Finding Fruit: Olfactory Tracking Strategies of Foraging Bats

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Tracking odors and finding their source is a complex task faced by nearly all animals. Research across many different taxa have identified common behavioral strategies used by animals to locate olfactory stimuli, such as serial and bilateral odor sampling. Olfactory cues are important for fruit and nectar eating bats, but the behaviors used by bats to exploit odor plumes is still unclear. We used an olfactory behavioral assay to quantify the olfactory search patterns of crawling Northern yellow-shouldered bats (*Sturnira parvidens*), a Neotropical fruit-eating species. Wild individuals were first trained to seek out a fruit reward and then placed in a test chamber where they were presented with a choice between control and odor-infused solutions of decreasing concentrations to evaluate how olfactory discrimination and tracking behavior change with strength of odor. A photoionization detector (PID) was used to quantify the olfactory environment experienced by the bats during tracking. Video analyses were used to quantify the time-course, search trajectories, and movement patterns of the bats localizing odors. Bat olfactory search trajectories were analyzed using generalized linear mixed models and compared to the measured olfactory environment. This is the first study to evaluate how fruit-eating bats locate the source of an attractive odor, and provides a baseline for addressing how bat odor tracking compares to other animals. Understanding the behavioral strategies used by bats to locate resources is important for predicting how environmental conditions influence foraging and decision-making by bats at the landscape scale.

The Effect of Resource Availability on Individual Fruit Bat Movement Measured at High Temporal Resolution

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The Egyptian fruit bat (*Rousettus aegyptiacus*) is a generalist forager with a wide distribution ranging from the tropics to the Mediterranean. In Israel, the species is known to perform exceptionally directed and long flights towards specific fruit-bearing trees, passing over seemingly adequate fruit trees on its way. Yet, the underlying mechanisms that result in such extremely selective foraging patterns remain unknown, mainly because it demands a detailed account of the movements of multiple individuals a well as the resources they use. Here, the movements of 47 bats were tracked throughout the year, at a 4-second frequency, using the ATLAS tracking system in the Hula Valley, Israel. In addition, >70% of the trees used or available to bats in the study area were recorded. To elucidate the mechanisms underlying movement choices, we first quantify individual movement patterns using network theory, which summarizes all individual movements between trees into metrics that describe the structure of individual space-use. We tested the response of two network metrics to fruit abundance, diversity and spread during phenological peak and transition seasons: (1) modularity, a measure of landscape fragmentation that is based on individual movement structure and (2) degree distribution, which indicates the level of centralization around a fraction of trees, also known as "hubs". We show how the combination of high-resolution tracking and network analysis can identify key resources and the landscape features that determine movement patterns. These insights have broader implications for the management of human-altered environments, whether for species conservation or human-disturbance control.

AO5-122

Functional Diversity and Community Structure of Bats along an Elevational Gradient in the Himalayas

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Climate change is one of the greatest threats faced by the natural world. Recent studies show that animals respond to climate change in several ways such as shifts in phenology, changes in breeding cycles, and range expansions to higher latitudes or elevations. Range shifts are increasingly common but little is known about the effects that range-shifting species have on the established native communities that have shaped over hundreds and thousands of years of interactions. Elevational gradients provide particularly suitable framework for understanding both how contemporary communities are structured and how they may change in the future. Bats-a taxonomically and functionally diverse group of vagile mammals that are sensitive to environmental perturbations-present interesting opportunities to study community ecology in montane environments. In the first part of this ongoing study, we sampled 65 bats from 17 species from 1400 m above sea level (asl) to 3500 m asl at Kedarnath Wildlife Sanctuary in the Indian Himalayas between March and June 2018. Specifically, we used passive acoustic monitoring to investigate nocturnal activity patterns of co-occurring bats. Additionally, we mistnetted bats to collect data on functional traits related to wing morphology and echolocation characters. Here we present preliminary results on functional diversity, activity patterns and community structure of bats across elevations. In the long run, this study is intended to improve our understanding of the impacts of climate change on Himalayan fauna and will provide a framework for assessing the future impacts on vulnerable montane species all over the world.

AO5-124

Flying Solo: Juvenile Flower-visiting Bats Perform First Foraging Flights without their Mother

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During transition from parental care to independent life, the development of adequate foraging skills is a major challenge for juvenile bats. Profiting from their parents' knowledge through social learning strategies might facilitate this task. However, while adult bats of several bat species readily use social information to learn about foraging, there is little information about foraging-related social learning processes during juvenile development. Following the mother during first foraging flights would represent a valuable option for a juvenile to socially learn about foraging (e.g. where to find food), but experimental approaches on communal foraging of mother-pup pairs are scarce. We investigated foraging behavior of juvenile flower-visiting bats (*Glossophaga soricina*, Phyllostomidae: Glossophaginae) in the dry forest of Santa Rosa National Park, Costa Rica. We tested whether recently volant, but still nursed pups perform first foraging flights alone, indicating rather individual learning strategies, or whether pups follow their mothers, which would enable pups to learn socially. For that, we performed a field experiment using artificial flowers with RFID (Radio Frequency Identification) reading systems and tested for communal and independent visits of RFID-tagged mothers and their pups (n = 16 pairs). Unexpectedly, artificial flowers near the day-roost were almost entirely visited by pups, while mothers seemed to forage further away. Our results demonstrate that juveniles perform first foraging flights apart from their mothers and might apply individual learning strategies while exploring the environment in spatial proximity to their day-roost.

AO5-125

Who has Access to the Best Roost?: Influence of Interindividual Differences in Behavior on Roost Competition

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Interindividual differences in behavior, or personality traits, can be considered a driving force in the evolution of populations, since individual variation in behavior is related to the survival and reproductive success of individuals. When there is competition for a resource or interactions between individuals, bolder animals typically present the most offensive and aggressive behaviors, and this level of aggressiveness may be influenced by the health condition and energy reserves of the individual. The relatively asocial woolly bat, *Kerivoula hardwickii*, uses developing tubular leavesas roost sites, which are suitable for only a short period of time; thus,when these leaves are scarce animals may compete for their access. Here, we investigate the influence of interindividual differences in the level of aggression and body condition during competition for roosts of different qualities in the bat *K. hardwickii*. We find that bats are able to evict other individuals from the roost they occupy through aggressive behaviors and direct physical interactions.We also find that aggression and body condition influence theability of individuals to evict others from a roost. We also record acoustic signaling of aggressive intent during agonistic encounters. Our study shows that interindividual differences in behavior may be defining an individual's access to the quality of the resource and the ability to defend that resource.

AO5-126

Seasonal Variation in Use of Torpor by a Leaf-roosting Bat, *Kerivoula furva*, in Subtropical Taiwan

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Daily torpor and hibernation are widely used by temperate bats. Less is known, however, about the pattern of torpor use of bats in warm areas. In subtropical Taiwan, the dark woolly bat (*Kerivoula furva*) forms small groups and uses furled banana leaves as day roosts all year long. In summer *K. furva* changed day roosts every day but in winter bats were occasionally found to use the same roost for more than one day. This study aimed to investigate whether *K. furva* is capable of entering daily torpor and/or hibernation. From June 26 to August 23, 2017 (summer), and from December 1, 2017, to February 9, 2018 (winter), we attached thermal-sensitive transmitters on ten adult females and two adult males of *K. furva* to investigate the pattern of torpor use in central Taiwan. The results showed that in summer a few individuals entered daily torpor with short torpor bouts during daytimes; the use of torpor occurred more frequently after rains. In winter, all individuals tracked frequently used daily torpor and hibernation. The arousals from torpor occurred mainly within 2 hours after sunset; the torpor bouts decreased with increasing ambient temperature. In a given day whether the bats aroused or remained in the state of torpor in the evening was influenced by the ambient temperature. This study confirmed that *K. furva* in subtropical Taiwan is capable of using short torpor in summer and multiple-day hibernation in winter.

Body-size dependent foraging strategies in the Christmas Island Flying-fox (*Pteropus natalis*): Implications for Seed and Pollen Dispersal within a Threatened Island Ecosystem.

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Knowledge of the scale of flying-fox movements and the underlying behaviors that influence their pollen and seed dispersal are important in determining the ecological services that flying-foxes perform on islands. This information is also useful for understanding the potential long-term consequences for forest dynamics resulting from flying-fox population declines or extinction and can aid in the development of evidence-based ecological management strategies. In this study, we examine the social interactions at foraging sites, floral resource use, and nightly movements of Critically Endangered Christmas Island flying-foxes (*Pteropus natalis*) using GPS telemetry ($n = 24$). Larger *P. natalis* exhibited a higher (75%, $P < 0.004$) foraging intensity at repeatedly used foraging sites, visited a lower (38%, $P < 0.016$) diversity of floral resources, traveled shorter (71%, $P < 0.023$) distances across nocturnal foraging sites, and had smaller (91%, $P < 0.016$) overall foraging ranges, on average, than smaller conspecifics. These findings suggest that the dispersal services of *P. natalis* vary among the age demographics within the population, with larger individuals more likely to provide localized dispersal services and smaller individuals acting as the primary vectors of long-distance dispersal of pollen and seeds. The diverse foraging behaviour, associated with body size, provides a vital mechanism for maintaining the genetic diversity of plants across Christmas Island, and highlights the need for more holistic research approaches that incorporate population demographics when assessing a species ecological services.

AO5-130

Until the Last Drop: Nectar Extraction Efficiency in Flower-visiting Bats at Real Flowers

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Neotropical flower-visiting bats (Phyllostomidae: Glossophaginae) face high energetic needs caused by a combination of an unfavorable body-surface-to-volume ratio, hovering flight. In addition with floral nectar being available only in small and spatially dispersed portions this should select for an efficient exploitation of their floral resources. A crucial step that determines the profitability of a flower visit lies in the efficiency of nectar uptake, which might be influenced by various factors such as nectar volume, nectar secretion rate or the shape of the flower. In the Caribbean lowland rainforests of Costa Rica flower-visiting bats encounter a variety of flowers of different profitability throughout the year. In order to meet their high energetic requirements, these bats should optimize their foraging behavior according to nectar availability. In flight cage experiments conducted at La Selva Biological Station, Costa Rica, we presented different levels of honey-water in flowers of bell-shaped *Merinthopodium neuranthum* (Solanaceae) and cup-shaped *Werauhia gladioliflora* (Bromeliaceae) to two flower-visiting bats, the food generalist *Glossophaga* sp. and the specialist *Hylonycteris underwoodi*, and measured the nectar extraction efficiency (NEE; $g \times s^{-1}$) using a computer-based light barrier system combined with an analytical balance. These results provide a first insight into the NEE at real flowers and can serve as valuable base for further studies assessing quantitatively the foraging conditions for flower-visiting bats throughout the night.

AO5-131

A Gut Feeling: What Can We Learn from the *Leptonycteris yerbabuenae* Migration through its Gastrointestinal Microbiota?

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The nectarivorous bat *Leptonycteris yerbabuenae* (Phyllostomidae) presents a partial migration where half of the female population migrates to SW Arizona and northern Mexico while the rest stays behind in Central Mexico. Since the species has only recently been taken off the red list of endangered species in both Mexico and the US, it is important to keep track of the population dynamics in order to secure its future. The partial migration creates a conservation problem, since we still do not know whether membership to either the migrant or non-migrant mode is set for life or whether the bats may switch from one mode to the other. Our objective in this project was to determine if the gastrointestinal microbiota could be used as a proxy to determine the stability of both migrational modes across a two-year cycle. We collected fecal samples from 745 bats from 3 different locations along the migratory route. We extracted total DNA from the pellets and sequenced the 16s V4 region from bacterial DNA. We then followed the bioinformatic pipeline using QIIME2 and the results were analysed using the Phyloseq package in R. The results show that a common core microbiome for all migrant and non-migrant bats persists throughout seasons and migratory stopovers. We also identified some site-, and season-specific signatures for the stopovers. Further diet analysis will yield key information for identifying more consistent patterns of the gastric microbiota of this long-distance migrating species.

Vampire Bat Food Sharing in Captivity Predicts Post-release Social Networks in the Wild

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Social interactions are extremely difficult to study in free-ranging bats. Therefore, most work on bat social behavior involves observations in captivity or simple measures of association (e.g. sharing the same roost box). However, recent advances in technology enable continuous documentation of social proximity among up to 60 wild bats simultaneously, giving us the first high-resolution dynamic social networks in bats (i.e. a complete social network every minute or day rather than every year). We developed miniaturized proximity sensors, as a part of the next-generation tracking system BATS, to study associations among wild vampire bats (*Desmodus rotundus*). We tagged and released a group of 23 females and their young. These bats were previously studied for 22 months in captivity to estimate their grooming and food sharing networks. Then we released them back into their original wild roost. As a control group, we tagged 27 wild-caught vampire bats from the same roost tree. We tracked all encounters among all 50 bats for 8 days. We found that formerly captive bats that were separated from their wild groupmates for almost 2 years reunited with genetic relatives in the control group upon their release. They also preferentially roosted near their nonkin grooming and food-sharing partners. Finally, we found evidence for social foraging. Our results show that automatically sensed proximity networks reflect social interactions and relationships in wild bats. Female vampire bat social bonds persist across contexts and are robust to dramatic changes in the social environment.

AO5-133

Maternal and Colony Guidance of Juvenile Natterer's bats to a Suitable Hibernation Site

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Juvenile bats born in maternity colonies in the temperate zone must locate a suitable hibernation site, often dozens of kilometers away from their birthplaces, to survive the winter. During autumn, many species aggregate at hibernation sites in a behavior known as swarming. Females from one maternity colony make use of multiple hibernation sites, and may also guide their offspring to these sites. Using molecular parentage analysis, we investigate the first visitation and overall use of a swarming/hibernation site in Germany by 681 RFID-tagged mothers and offspring from 5 Natterer's bat (*Myotis nattereri*) maternity colonies over a 10-year period. At least one member of the mother-offspring pair visited the site in 117 pairs. During the swarming phase, 15 male and 2 female offspring were recorded in close succession to their mother on their first visit to the site. For a further 39 offspring, of which 29 female, another colony member, but not the mother, was recorded at the swarming site on the same night. Additionally, of the 37 male offspring that were ever recorded at the site, 33 had mothers that also use the site for hibernation, compared to only 20 of the 42 female offspring. Taken together, we posit that juvenile males are guided to swarming/hibernation sites by their mothers, whereas juvenile females may follow other colony members to suitable hibernation sites.

AO5-134

Differences in Roost Resources for Tent-roosting Bats across a Lowland Rainforest Island System in Panama

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Fragmentation of natural habitat has caused major losses of species diversity worldwide. The responses of forest-dwelling animals to fragmentation may vary widely, especially within bird and bat communities. Particularly the diverse group of Neotropical leaf-nosed bats (Phyllostomidae) provides important ecosystem services such as pollination, seed dispersal and herbivorous insect predation. Adequate roosting sites are essential for these animals, influencing occurrence of species and population sizes. This may even limit species known to be quite flexible in their roost site choice, including bats which modify leaves into tents. Roost resource availability and plant species preferences of this group of bats are still largely understudied. The objective of this study was to understand how tent-roosting bats respond to availability of roost resources in a fragmented landscape. We investigated factors driving roost site and plant species preferences of tent-roosting bats and quantified availability of roost plants along 72 transects from six continuous forest and six island sites in the Panama Canal area. These data on roost preferences and availability were then linked to species occurrences from a recent bat survey. Suitable leaves for tent construction are not ubiquitously available in the forest understory, as they strongly depend on light levels and succession state. Plant species choice was favored towards larger leaved plants. Despite the focal bats occurring on the islands, the number of tents declined drastically, showing negative effects of isolation and fragmentation on the roost options of tent-roosting bats.

Don’t Bug Me: Bat–Bat Fly Interactions and their Response to Habitat Alteration in Central Panama

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Phyllostomid bats are the most diverse bat family in the Neotropics, both in species number as in feeding guilds. Recent studies revealed feeding guild dependent reactions to habitat alterations, resulting in increased abundances for some species while others go locally extinct. Strongly associated with bats are parasites, of which the most conspicuous are bat flies (Diptera: Streblidae, Nycteribiidae), obligate blood sucking insects. As they are highly host specific, we expected that changes in the host community, in response to habitat alteration, should result in changes in their associated parasite community. We captured bats between 2013 and 2015 in a standardized setup of study sites surrounded by three different matrix types in Central Panama. Focusing on the six most commonly captured bat species, we recorded information on prevalence (3456 bats), and intensity (1283 bats) of bat flies. Mean prevalence over all host species was 41.4%, ranging from 6.8% (*Dermanura watsoni*) to 69.3% (*Carollia perspicillata*), while intensity varied between 1.1 (*D. watsoni*) to 2.9 (*C. perspicillata*). Prevalence and intensity were both significantly influenced by roost type used by the host bats, capture rate, as well as host sex and age. We further detected habitat variables and matrix type influencing significantly the prevalence and intensity of parasitation, where responses were host species dependent. Our study emphasizes the complexity of this host-parasite system and points out the poorly studied life history of bat flies, especially regarding their potential as vector.

AO5-136

From Dusk till Dawn: Foraging and Habitat Use by the African Large-eared Slit-faced Bat *Nycteris macrotis*

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Radio-tracking provides excellent opportunities to gain insight into behaviour and ecology of animals. African bats are still largely understudied, despite living often in areas undergoing rapid land use changes. The large-eared slit-faced bat *Nycteris macrotis* is commonly found throughout Africa and is assumed to be an opportunistic species able to adapt to a wide range of different habitats. It is regarded to be a clutter edge forager using mainly a gleaning strategy. We radiotracked 16 adult male individuals using triangulation during two dry seasons from January to April in 2017 and 2018 near Techiman in the Brong-Ahafo region of Ghana. This agriculturally dominated region lies within the transitional zone between woodland and savanna. Agricultural areas include cashew plantations, yam and cassava fields, surrounded mainly by grassland. Bats were tracked from 6 pm to 6 am over 3 to 6 nights. We found *N. macrotis* to show quite regular activity patterns of approximately three foraging flights per night. Bats returned to their day roost after foraging excursions without using any additional night roosts. Home ranges were calculated using Localised Convex Hulls, and showed a large overlap between individuals. Our study gives a better insight into the activity patterns and habitat use of the widespread bat *N. macrotis* in an agricultural landscape. This is of importance in a conservation context but also for assessing potential interactions with humans, e.g., also regarding the potential spillover of zoonoses, which are more likely to happen in disturbed habitats.

AO5-137

Morphology and Stable Isotope Analysis Demonstrate Different Structuring of Bat Communities in Rainforest and Savannah Habitats

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Bats play important ecological roles in tropical systems, yet how these communities are structured is still poorly understood. Our study explores the structure of African bat communities using morphological characters to define the morphospace occupied by these bats and stable isotope analysis to define their dietary niche breadth. We compared two communities, rainforest in Liberia and savanna in South Africa, and asked whether the greater richness in the rainforest was due to more species "packing" into the same morphospace and trophic space than bats from the savanna, or some other arrangement. In the rainforest, bats occupied a larger area in morphospace and species packing was higher than in the savanna. There were also differences in morphospace occupied by different foraging groups. Stable isotope analysis revealed that the range of δ13C values was almost double in rainforest than in savanna indicating a greater range of utilization of basal C3 and C4 resources in the former site. The ranges in δ15N, however, were similar between the two habitats suggesting a similar number of trophic levels. Niche breadth was greater for the bat community in rainforest than in savanna, with all four foraging groups having larger niche breadths in the former than the latter. The higher inter-species morphospace and niche breadth in forest bats suggests that species packing is not necessarily competitive. By employing morphometrics and stable isotope analysis, we have shown that the rainforest bat community packs more species in morphospace and utilizes a larger niche breadth than the one in savanna.

AO5-138

Foraging and Roosting Site Sharing in Egyptian Fruit Bats: The Role of Key Individuals

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Many bat species have social structure and behavioral habits that may facilitate social learning. They often rely on temporally and spatially oscillating food sources and roosting sites. Such constraints should encourage sociality and cultural transmission of information which would eventually increase their success. Previous studies have already questioned the role of kin in foraging and roosting site sharing across number of species with various results. Here, we stressed this question in the Egyptian fruit bats (*Rousettus aegyptiacus*). The study took place in Dakhla oasis in Egypt, where fruit bats were sampled and radio-tracked. Roosts were localized in abandoned buildings of the Al Qasr old town, with everyday human activity around. Diet of fruit bats in this area consisted mostly of agricultural plants. As a result, this species is considered as pest, so eradication of roosts is quite common. Therefore, fruit bats would benefit from information about foraging sites with ripe fruits and safe roosting sites. Using social network approach, we found no direct link between relatedness and foraging or roosting site sharing. Our results show, however, that animals with many relatives are central in foraging and roosting network making them potentially important in information flow. Additionally, we found that fruit bats occupied few main roosts, but they have also visited alternative ones, suggesting that they had knowledge about alternative places to hide in case of human disturbance.

AO5-139

Trends at the Ends; Telomere Dynamics in Lifespan, Hibernation and Reproduction in *Rhinolophus ferrumequinum*

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The concept of trade-offs is central to our understanding of life histories. Differences seen within and among species in life history is generally framed as differences in resource investment into growth, reproduction and self-maintenance leading to differences in size, reproductive rate and lifespan. Another factor in a changing world is to understand why individuals vary in their responses to different environmental factors and why individuals differ mitigating these costs. However to quantify this in the wild, effective biomarkers that reflect the physiological consequences of individual-level experiences are required with telomeres being a proposed biomarker. Recent work has shed light on telomeres in relation to lifespan in bats yet little is known about telomere dynamics within bat species over different parts of their life cycle (i.e. reproduction, lactation and hibernation). Here, we measured telomere length in a long-term ringed population of *Rhinolophus ferrumequinum*, a colony studied extensively for ~60 years. To date, relative telomere length (RTL) from 1450 samples representing 489 individuals have been measured, which were caught over several sampling points from January 2016 to August 2018. The effect of early-life environment between years was explored and if RTL is indicative of survival to the next year. Telomere dynamics were examined in light of reproductive status (i.e. breeders versus non-breeders) and if RTL changes occurred in individuals recaptured over the reproductive and hibernation season. These findings provide the basis for further study into the mechanisms underlying variation in telomere dynamics and potential life-history trade-offs in a unique long-lived mammal.

AO5-140

Nutrient Contribution of Cave Bat Colonies to Surface Ecosystems

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Bat guano is rich in nutrients such as Nitrogen and Phosphorus-elements that are essential for plant growth. In caves bat guano is a main source of energy for the subterranean ecosystems, but in caves with underground rivers the water could transfer guano deposits into the surface systems. With such large aggregations of bats in caves, the nutrient contribution could be significant, especially to nutrient-deprived tropical soils; however, this connection has not yet been studied in detail. We investigated the contribution of cave-roosting bats to nutrient input into aquatic ecosystems in five caves with underground streams in Costa Rica. We measured the concentrations of total Nitrogen, total Phosphorus, phosphates, nitrates, nitrites and ammonia in water before and after the contact with the guano source. To further test if the nutrients from bat guano are assimilated by plants, we compared its $\delta 15N$ isotopic signature with mosses (Bryophyta) growing near the river banks in distances of up to 128 m downstream from the cave entrances. Our results showed that the water exiting caves with large bat colonies has higher levels of total Nitrogen, phosphates and nitrates than the same water before the contact with the bat guano. We further established that the nutrients from guano are assimilated by moss for more than 60 m from the cave entrances. Our study shows that cave bats provide additional ecosystem service, namely providing nutrients to surface aquatic ecosystems.

Linking Roosting Ecology and the Evolution of Bat Landing Mechanics

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Bat roosts are ecologically critical refugia that facilitate thermoregulation, enhance access to mates and food, and provide venues for social interactions. We hypothesize links between roosting habits and landing maneuvers because these maneuvers arrest flight for safe roost access. Specifically, we predict that the physical properties of roosts may have influenced the evolution and mechanics of bat landings. We tested this using high speed videography and impact force measurement to document landing kinematics and mechanics (video: 663 landings from 35 species, 21 genera, nine families; force: 405 landings, 17 species). We collected data in the lab and at sites in Belize, Bulgaria, China, and Costa Rica. We observed three landing styles: two-, three-, and four-point. In two-point landings, bats gained purchase using both feet, and performed multiple, complex body rotations before enacting low-impact landings. Bats using three- and four-point landings made additional contact with one or both thumb claws and performed simpler body rotations, resulting in higher impact forces. Phylogenetic comparative analyses demonstrate that two-point landings convergently evolved at least three times and are associated with stiff horizontal roosting surfaces (e.g., cave ceilings and tree hollows), where low-impacts could reduce injury.Three-point landings evolved primarily among stenodermatines, associated with roosting in leaf-tents and termite nests. Four-point landings are basal and are negatively associated with roosting on stiff horizontal surfaces. Our results suggest that bat ancestors performed simple landings using all four limbs, like those observed in gliding mammals, and that complex landing styles evolved in association with novel roost types.

Sex and the City: Reproductive Ecology in a Successful Urban Species, *Chalinolobus gouldii*

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Adaptive sex allocation hypotheses predict that parents should invest differentially in sons and daughters when sex-specific fitness returns vary with parental ability to invest. Maternal body condition is a common measure of ability to invest, reflecting energy stores and resource availability, and has often been associated with variation in offspring sex ratios. There is a distinct lack of research on the reproductive outcomes of Australian microbats, which is becoming increasingly imperative with urbanisation. Long-term monitoring of bat-boxes at two sites (one urban and one peri-urban) in greater Melbourne, Australia, provided a unique opportunity to recapture female Gould's wattled bats (*Chalinolobus gouldii*) at multiple time points. Here we use EchoMRI scans, a novel technique not yet used in Australian bats, to determine maternal body composition. We measured maternal condition at mating and conception, in 2017 and 2018, and related that to offspring sex ratios. Additionally, we were able to examine changes in body condition over the winter hibernation to identify the effects of stored resources. Maternal fat mass percent was greater at the urban site compared to the peri-urban site during mating, but not at conception, which suggests the urban bats are using more stored energy over winter. There was no offspring sex ratio bias at either population in relation to maternal body condition or change in condition, however mothers who had bred previously produced more daughters. Understanding the life-history strategies around reproduction is key to understanding the drivers associated with a species' success in changing environments.

AO5-144

Bats Pollinating Bromeliads: A Review

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Among the chiropterophilous flowering plants of the New World, Bromeliaceae is one of the most ecologically important families; however, information about the chiropterophilous interaction in this family is scarce. We carried out a comprehensive review of bat pollination in bromeliads, covering floral traits, rewards offered to pollinators, floral attractants and the identity of visiting bat species. We discuss traits shared among chiropterophilous bromeliads and present general trends in an evolutionary context. For this purpose, we constructed a phylogenetic tree to elucidate the ancestral pollination syndromes of the 42 extant bromeliad species (ca. 1% of total) known to be bat-pollinated. Most of the species within the ten genera reported belong to the Tillandsioideae subfamily, with three genera appearing to be exclusively bat-pollinated. Floral visitors include 19 bat species of 11 genera from the Phyllostomidae. Our analysis indicated that chiropterophilous floral features originated multiple times in bromeliad evolution, most probably from ornithophilous. The evidence for floral traits associated with bat pollination and the chiropterophilous syndrome presented by certain Bromeliaceae indicate the important role played by bats in the evolution of this plant family.

AO5-145

Multivariate Analyses Elucidate Drivers of Bat Ectoparasite Specificity from Brazil

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In the field of parasitology, host specificity is a fundamental property that describes the extent to which parasites associate with certain host species. Host specificity can be a product of coevolution, ecology of both parasites and their associated hosts, environmental factors, or a combination of all three. Obligate ectoparasitic bat flies (Streblidae and Nycteribiidae) have generally been considered highly host specific due to a history of coevolution with their bat hosts. Recent studies, however, indicate that cospeciation may not be as common between bat flies and their hosts and that factors such as host bat roost sharing, community network dynamics, and habitat structure may be more important in explaining patterns of bat fly specificity. We collected 848 individual bat flies from 16 bat species from the Atlantic Forest of Brazil, identified them morphologically and generated a RAxML tree from two amplified genes (COI, mitochondrial; CAD, nuclear). We calculated three metrics of specificity for each of the 20 bat fly species identified and created pairwise specificity distance matrices between each bat fly species. To evaluate the drivers of bat fly specificity, (e.g., fly phylogeny, fly abundance, fragment cooccurrence), we constructed a bipartite network depicting host/parasite associations and used multiple regression on distance matrices (MRM) to measure the influence of various host and parasite traits. Fly abundance and basic specificity significantly predicted both structural and phylospecificity at the entire community scale. Phylogenetic distance between flies did not significantly predict differences in host specificity, suggesting that bat flies may associate with bat hosts based on factors other than phylogenetic history. Analyses are currently underway to determine drivers of specificity for generalist and specialist flies separately, as host specificity may operate differently at separate ecological scales. Determining drivers of host specificity has important implications for modeling potential disease transmission in tropical communities.

AO5-146

Does Foraging Activity of Insectivorous Bat in Organic Rice Fields is Higher Than Conventional Rice Fields?

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Populations of many bat species have severely declined over recent years, and one of the main reasons of this depletion was possibly due to the impact from agricultural intensification. We compared bat activity in organic and conventional rice fields in Songkhla lake basin, Southern Thailand. Bat activity was quantified using acoustic surveys by ultrasonic detectors. Acoustic sampling took place in two periods, first period- 18 paired sites during November 2016 and February 2017 and second period- 30 paired sites during November 2018 and February 2019. Insect samples were collected in both rice field types to calculate biomass. The total bat activity during the first period was significantly higher in the organic rice fields than in the conventional rice fields. Significantly more passes of *Myotis* species were recorded on organic rice fields than on conventional rice fields. In addition, bat activity was positively associated with insect biomass only in organic rice fields. In contrast, the preliminary results from a second period demonstrated that the activities of bats and insect biomass were not significantly different between both rice fields. This study highlights the highly variation among sampling rice fields even within the same habitat. Further analyses of variation in surrounding landscape features are examined to verify if any landscape features affect prey availability thus consequently impact on bat activity.

AO5-147

The secret lives of Tube nosed-fruit bats – insights into the behaviour and ecology of *Nyctimene robinsoni*

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Although fruit bats (Chiroptera: Pteropodidae) play crucial roles in maintaining healthy forest dynamics by contributing ecosystem services such as seed dispersal and pollination, particularly the smaller and inconspicuous species remain considerably understudied. One such example is the little known subfamily of Tube-nosed bats (Nyctimeninae), comprising species listed as endangered, vulnerable or data deficient by the IUCN. This project investigated the ecology and behaviour of Eastern Tube-nosed Bats (*Nyctimene robinsoni*), a species occurring along the north eastern coast of Australia. Despite their presumably important function as seed dispersers, available information on these bats is dominated by anecdotal records rather than field studies, with confounding notes on their home range size and social behaviour. We employed a GPS tracking approach to study their habitat use and roosting behaviour. Key habitat features, foraging areas and characteristics of day roost sites as well as frequency of social roosting were identified to get a better understanding of movement patterns and social interactions. To clarify their role as seed dispersers and pollinators, Next Generation Sequencing of faeces and spats was used to create an overview of their food plants. Here we present first findings focussing on their habitat use, roost sites, diet and some observations of social behaviour in a study population in the Queensland Wet Tropics.

AO5-148

Factors Determining Roost Selection by Cave-dwelling Bats in a Karst Network Landscape in Meghalaya, India

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Bats exhibit a wide variety of roosting strategies in order to meet their ecological requirements. They are especially ubiquitous in cave ecosystems and understanding how these complex decisions are made is of utmost importance to effectively facilitate their conservation. In this study, we evaluated characteristics of the environment, cave substrate and human-mediated disturbance in order to understand major drivers of roost selection in cave systems. Roosting probability was expected to increase with cave size and decreasing disturbance. We recorded echolocation calls emitted by emerging bats at 47 cave sites across a karst rich landscape in Meghalaya, India. Temporal replication, achieved by visiting each cave site on three consecutive evenings, allowed the estimation of cave occupancy probabilities while accounting for imperfect detection. For the top model, the estimate for detection probability p was 0.868 (0.416 SE). Cave length had a positive effect on bat occurrence Ψ, whereby the slope estimate for small caves (corresponding to the intercept) was –2.04 (0.75 SE) while the same for medium and large caves were 2.07(0.94 SE) and 3.55 (0.98 SE), respectively. Results suggest that horizontal development of caves primarily influenced the probability of *Rhinolophus* bats occupying them. Bats from this genus actively chose caves that were longer than 30m in length, and this relationship strengthened with increasing cave length. Roost selection in this area can therefore potentially be explained as a function of thermal stability and large surface area provided by long caves, allowing different species to exploit multiple niches within a protected environment.

AO5-149

Roost selection in concrete culverts by the large-footed Myotis *Myotis macropus* in Brisbane, Australia

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The large-footed Myotis, *Myotis macropus,* is Australia's only fishing bat. This species has adapted to living and breeding in urban areas and has been recorded roosting in concrete culverts under roads. However, little is known about the roosting ecology of bats which use these unique roost sites in Australia. We investigated *M. macropus* roost selection in Brisbane, eastern Australia. We developed a stratified sampling design to test which landscape and structure attributes most likely account for the presence of a bat roost in a culvert. A total of 308 concrete culverts were inspected for the presence of roosting bats over the summers and winters of 2017 and 2018. A total of 23 roost sites were located comprising day, night and maternity roosts.

We analyzed roost selection at a landscape scale using generalized additive models. We found that roost sites are associated with box culverts 1- 2.1 m in height with multiple barrels, channels that are 1.5 - 2.5 m deep and are located within landscapes with a high density of waterways within 5 km from the roost site. Understanding the types of culverts that are likely to provide suitable bat habitat will prevent the disturbance to bat roosts during the breeding season and this will have greater conservation outcomes for this urban adapted bat.

AO5-150

New Technological Approaches to Study Sensory Aspects of Foraging Behavior in Wild Bats

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New technologies allow us to record the location (GPS), movement (accelerometer) and acoustic behavior (microphone) of bats while they are behaving freely in the wild. Here, we present two case studies where we use these technological advances to assess different aspects of bat foraging.

We compared GPS tracks and echolocation of five different bat species. Linking the movement with sound recordings, we evaluated not only the foraging behavior of individual bats, but also recorded the presence of close-by conspecifics. We found that species that search for ephemeral prey, which is hard to predict in space and time, fly together in a group. Listening to their conspecifics' echolocation calls increases their detection range of prey and therefore the likelihood of finding patchily distributed food resources.

For one of those species – the greater mouse-eared bat, *Myotis myotis* – we analyzed the foraging behavior in more detail. GPS tracks informed us on the nightly, stereotypical foraging routes and large-scale strategies that these bats employ. The analysis of body movement and echolocation behavior gave unprecedented fine-scaled insights into the actual foraging behavior of individual captures. Our acoustic recordings described the dynamics of this species' echolocation when listening for prey-generated sounds and hunting airborne prey. Finally, we could not only distinguish between different foraging modes (aerial vs. ground capture), but also evaluate the attack success rate and possible prey type. This kind of data can inform us on important basics of foraging and thereby open up possibilities to estimate optimal foraging strategies.

AO5-151

Food Limitation Slows Down Sperm Production But Not Torpor Use in Male Bats During Summer

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Bats, as small endothermic animals have high energy demands, due to high cost of locomotion, and unfavourable body mass to surface ratio. They can use torpor (i.e. reduce metabolic rate and body temperature) to save energy and/or allocate resources to fat deposition. However, torpor has also been suggested to slow down important processes, such as sperm production. In this study, we investigated the influence of food limitation on body condition, torpor usage, testes development and epididymides filling during the crucial period of spermatogenesis. We exposed captive male parti-coloured bats (*Vespertilio murinus*) to different feeding regimes and found a significant effect on sperm production. "*Ad libitum*"-fed males finished spermatogenesis up to half a month earlier compared to males under food restriction. Concurrently, all bats showed similar pattern of torpor usage regardless of feeding treatment. Torpor use increased towards the end of the experiment as spermatogenesis was being completed. Body mass remained constant during spermatogenesis. It, then increased only in "*ad libitum*"-fed males. Our results support a trade-off between the investment into reproductive tissue and the accumulation of fat. Ultimately, food availability might influence reproductive success by affecting sperm and fat reserves available during the mating season. The project was funded by the Polish National Science Centre grant: DEC-2013/10/E/NZ8/00725

AO5-155

The Costs of Flight-Getting to the Heart of the Matter

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If we are to effectively manage and conserve native populations it is crucial that we understand how individuals budget their energy in the wild. Advancements in technology have enabled us to gain fine time scale measurements of movement and energy expenditure in nature via accelerometers (ACC) and the heart rate (HR) method. However, both methods require calibration under controlled conditions and during various behaviours to be effectively applied to wild animals. Here, we investigated the relationship between metabolism and heart rate in 21 captive *Rousettus aegyptiacus*, while resting in a respirometry chamber or flying along a flight corridor. We measured ACC and HR via onboard tri-axial accelerometers and electrocardiogram (ECG) loggers, and correlated this to measures of metabolism via the sodium bicarbonate method (a proxy for CO_2 production). We also fitted 11 wild *R. aegyptiacus* with GPS, ACC and ECG loggers and tracked their movements, behaviour, and HR for up to 4 days of continuous recording. Our results show that during flight the HR of bats was similar to that expected from allometric scaling (650 bpm) with a daily HR range between 200 and 800 bpm in wild bats. We found that the best fit model for estimating $\dot{V}CO_2$ from HR was a curvilinear one. We also found that overall dynamic body action (ODBA) calculated from ACC showed a linear relationship with flight costs and could provide valuable data for energy expenditure in the field.

AO5-156

Synanthropic Bats as Potential Suppressors of Multiple Agricultural Pests: A Case Study From Madagascar

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The exceptional biodiversity of Madagascar is heavily impacted by slash-and-burn agriculture. Yet, some species, such as insectivorous bats, can explore agricultural ecosystems and potentially supress agricultural pest. Here, we i) assessed roost selection by synanthropic bats in villages around Ranomafana National Park; ii) conducted acoustic surveys of insectivorous bats in five habitats (irrigated rice, hillside rice, secondary vegetation, forest fragment and continuous forest) across an agricultural-forest frontier; and, iii) collected faeces from the six most common bat species to detect insect pest species in their diet using DNA metabarcoding. In 2015 we surveyed 180 buildings in ten villages and found bats roosting in 21 (12%). Of those, 17 were public buildings harbouring large molossid colonies. The acoustic surveys yielded 9,569 bat passes from 19 species. Total bat activity was higher over rice fields when compared to forest and bats belonging to the open space and edge space sonotypes were the most benefited by the conversion of forest to hillside and irrigated rice. Two economically important rice pests were detected in the faecal samples collected - the paddy swarming armyworm *Spodoptera mauritia* was detected in *Mops leucogaster* samples while the grass webworm *Herpetogramma licarsisalis* was detected from *Mormopterus jugularis* and *Miniopterus majori* samples. Samples from all bat species also contained reads from important insect disease vectors. We argue that Malagasy insectivorous bats have the potential to suppress agricultural pests. It is important to retain and maximise Malagasy bat populations as they may contribute to higher agricultural yields and promote sustainable livelihoods.

AO5-157

Genetic analyses reveal alloparental care in the carnivorous bat *Megaderma lyra*

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Alloparental care occurs in many vertebrate species, including some mammals, and may increase either indirect or direct fitness of the helpers. However, of the over 1,360 extant bat species, alloparental helping such as food provisioning or pup guarding has been reported only sporadically. We examined patterns of female infant support within four maternity colonies of the carnivorous bat *Megaderma lyra* in India. Using nine microsatellite loci we defined genetic relationships to infer patterns of female care towards pups. There were identified the mothers in 70% of 74 young aged 1 to 27 days. In two cases mothers nursed young of other mothers although their dependent young were still present in the colony. Non-maternal females babysat young pups less than 19 days old much more frequently than pups that were at least 19 days. Evidently, babysitting in *M. lyra* is pup age-dependent, indicating that this phenomenon is related to the guarding of pups, either assuring appropriate body temperature at the early stage of pups' development and/or avoiding predation during the period when pups are not able to fly. Thus, babysitting in *M. lyra* seems to be a form of alloparental care that follows the kin selection theory. The relatedness among nanny-pup pairs was significantly higher ($P < 0.01$) than among either randomly chosen female-pup pairs or pairs of adult females.

AO5-159

Trophic groups in a Mediterranean bat community: are echolocation and foraging behavior really important?

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Predator-prey interactions forge the behaviour and ecology of all organisms and are crucial in structuring ecological communities. In bats, several studies have emphasized the role of species morphology, echolocation, and foraging behaviour in prey acquisition and have tried to group bats accordingly in guilds. However, due to practical difficulties in studying entire communities and the constraints of morphology-based diet analysis, it is not clear how these guilds actually correlate to diet. To better understand this question, we used DNA metabarcoding to assess the diet of an insectivorous Mediterranean bat community located in Northeast Portugal composed by 19 different species.

Bat droppings were collected from 486 individual bats and DNA was extracted and amplified from 1206 individual pellets (up to three per bat). We used a canonical and ecological network analysis to assess the dietary guilds. Bats were structured in 4-5 diet groups, three of which were very distinct and fed on either noctuid moths, crickets, or spiders, respectively. The fourth and fifth groups were mainly characterized by not feeding on these taxa and ingesting more coleoptera, diptera and hemiptera. None of the diet groups corresponded to previously suggested echolocation or foraging guilds, with the exception of *Myotis myotis*, the only ground gleaning bat in our community, which formed a guild on its own. For the first time, we provide empirical evidence for the existence of dietary guilds in Mediterranean insectivorous bat communities and show that these do not correlate to previously proposed guilds based on echolocation signal or foraging behaviour.

AO5-160

Modelling Distributions and Habitat Relationships of Bats in Cambodia Using a Multi-method Occupancy Framework on a Country-wide Scale

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Identifying species habitat relationships are the first step in developing management strategies for bat conservation and disease surveillance. These relationships are relatively easy to determine with a well thought out study design within an occupancy framework that incorporates imperfect detection. Species are not detected perfectly, therefore accounting for imperfect detection leads to unbiased estimates of occupancy. We surveyed >200 stratified random sites in Cambodia for bats using mist nets, harp trap (when appropriate) and an acoustic detector. Combining data from multiple survey methods allows for a more complete survey of the bat fauna and hence a more accurate estimate of the bat community at each site. We were able to develop habitat relationship maps for several species of bats and to determine the probability of occupancy for each species among habitat types. The randomized study design allowed us to extrapolate our findings across the country of Cambodia. This information is not only the first of its' kind for Cambodian bat species, but it can set the stage for further research into the ecology of Cambodian bats. Interactive habitat maps can be used in many ways such as, informing stakeholders when talking about conservation strategies, identifying population trends in a changing landscape, and disease surveillance.

Survey Design and Occupancy Modelling Combine Multiple Survey Methods for the Development of Species-habitat Relationships on a Country-wide Scale in Cambodia

Survey design is a critical component of any scientific research effort. Here we describe a survey design for bats that combines data from multiple survey methods (mist net, harp trap, acoustic detector), incorporates imperfect detection and can be extrapolated at the country-wide level. We selected 250 stratified random sites across Cambodia. Sites were stratified according to large scale habitat type. The basic sampling interval that is the basis for occupancy modelling is the sampling occasion. We used temporal replication as a basis for our sampling occasion. We found that using multiple methods of survey at each site simultaneously, increases the probability of detection and the number of species detected. The occupancy framework can be used to estimate probability of occurrence in addition to, changes in occupancy over time when sites are surveyed repeatedly in different seasons/years. The flexibility and versatility of this analysis method is especially useful in answering many types of ecological questions and is well suited for bat surveys.

AO5-161

Competitors Versus Filters: Drivers of non-random Structure in Forest Interior Insectivorous Bat Assemblages along Elevational Gradients

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Non-random assemblage structure in species-rich resource-based assemblages are driven independently or simultaneously by competition and environmental filtering leading to trait dissimilarity or similarity respectively. Monotonic decline in bat species richness along forested Afrotropical elevational gradients is resource driven, yet the relative roles of competition and environmental filtering remains unclear. Ecomorphological traits such as bite force and wing morphology are essential for dietary resource partitioning, and respond to environmental conditions, providing opportunities to answer such questions. We hypothesize that if competition is driving assemblage structure along elevation gradients then species should be less similar in trait space, but conversely more similar under environmental filtering. Along two forested elevational gradients in southeastern Nigeria, we trapped bats using five harp traps set every 50 m along four 200 m long transects, at sites established on elevational strata ca. 250 – 400 m apart. We measured vegetation structure within four 2 m^2 plots around each harp trap and collected insects using light traps at each transect. For captured bats, we recorded forearm length and body mass, and measured bite force using bite plates attached to a Kitzler force transducer and photographed wings of bats restrained to a gridded board. Wing morphology parameters were measured from photographs of bat wings using imageJ and mean nightly counts of insect conducted. We examine trait-environment relationships, changes in trait volume and nearest neighbor distances between species in trait space. The result of these analysis will uncover drivers of non-random bat assemblage structure along elevational gradients.

AO5-162

Landscape and Microclimatic Drivers of Roost Selection in *Rousettus aegyptiacus* Across Southern Nigeria

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The Egyptian fruit bat (*Rousettus aegyptiacus*) is an obligate cave roosting species in Nigeria. The species is ecologically and economically important in southern Nigeria, where it is threatened by habitat loss (due to agriculture) and intense hunting where offtakes can reach 1500 bats per hunting effort at a single cave per day. Despite having disjoint distribution due to cave-dependence and limited cave availability, knowledge of roost selection is poorly understood. Cave microclimatic condition, landscape effects, and human disturbance are known to influence roost selection in other cave dwelling bats. Therefore, unraveling the influence of cave microclimate, landscape effects, and human disturbance on bat abundance is critical to understanding roost selection in *R. aegyptiacus*. We assessed bat abundance at cave roosts by conducting emergence counts across localities in southern Nigeria. We measured cave microclimate and dimensions, vegetation structure at cave entrances and recorded presence of water. Using high resolution landcover data, we measured proportion of major landuse/landcover types: forest, farmland and bare rock at multiple spatial scales. We will perform a random effects Conditional Inference Tree (CIT) in the R package REEMtree to unravel the drivers (cave microclimatic conditions, surrounding vegetation and landscape factors) of *R. aegyptiacus* abundance. The results will aid understanding of roost selection by an intensely hunted obligate cave roosting species in both native habitats and human modified landscape. The results will inform cave prioritization for the species conservation.

AO5-164

How Far Do Bats Take It? A Review of Home Range Studies

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Variation in home range sizes for terrestrial wild animals is attributed primarily to body size (larger body size increases home range size) although factors such as trophic level (species in higher trophic levels use larger home ranges), climate, breeding status, predator risk, and habitat quality (poor quality increases home range size) can influence home range use. Are home ranges for highly volant species such as bats also a reflection of animal size or trophic level? I reviewed publications to identify which peer-reviewed studies of bats focused on use of radio telemetry and identified home ranges. I categorized publications by location and decade that the study started, recorded bat species, home range sizes, method for describing home range, and focus of the study (habitat use, behavior, thermoregulatory patterns, energy balance, other). Of 516 publications, 40% used radio telemetry to study bats but only 53 of these specified home range sizes. Number of publications per decade increased dramatically following the development of transmitters small enough to be used on bats (number of publications work conducted in the 1970s, 1980s, 1990s, 2000s, 2010s were 4, 15, 30, 73, and 84, respectively) and occurred on almost all continents. Most used Minimum Convex Polygons to estimate home range size. Bats from a variety of families and feeding guilds were studied; however, home range sizes were not always related to mass of the bat studied or feeding guild.

AO5-165

Bats as Bioindicators? Evidence of Strong Associations between Bats, Climate and Vegetation along an Environmental Gradient

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Bats are acknowledged to be highly dependent of environmental conditions including strong associations to climate and habitats. Consequently, their potential as bioindicators is high but the use of bats as bioindicators is almost non-existent. This situation may arise from the lack of long-term studies focusing on species' associations to habitats or climate. In here, we present the results of 5 years (2014-2018) of mist-net sampling over an altitudinal gradient (from 357m to 1862m a.s.l.) at mountains of central Portugal. Sampling occurred between May and October of each year, totalising 200 sampling nights in 72 sites of which 32 sites were sampled seasonally. Environmental parameters (weather, vegetation) were registered every sampling night over a 100 meters buffer. During the 5 years of sampling we captured 1781 bats belonging to 23 species. Multivariate statistical analyses were performed to define the ecological gradients to analyse with bat data. Four biophysical altitudinal belts were identified mainly due to temperature and altitude variables though a marked vegetation gradient was also detected. We also detected a strong correlation between bats' species and the vegetation gradient especially between extremes of vegetation cover and climatic gradients. Notably, we found that bats' relationship with these gradients changed over the different seasons of their annual cycle. The finding of strong associations between bat species and a number of environmental conditions may constitute a baseline for further research on bats as bioindicators – a field that will most likely boom under the predicted threat of climate change.

AO5-166

Neighbors Matter! Stability of Roosting Patterns in a Laboratory Colony of *Carollia perspicillata*

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Social systems of animals are crucially shaped by the distribution of individuals in space and time which reflects their mating system, and sets the framework for individualized interactions. To test for sociality, rather than mere aggregation, in a laboratory colony of *C. perspicillata,* we explored roosting patterns focusing on group composition and its temporal stability, and related them to body condition, sex and age of the individuals involved. A social network analysis was performed on roosting data of the 23 to 25 bats of the colony monitored over eight months in the animal facility, using SOCPROG 2.8 to determine dyadic half weight association indices, to test for preferred or avoided associations, and to fit models based on standardized lagged association rate. The bats perched in stable, non-randomly associated groups of an adult male with several reproductive females (harems), of associated bachelors, and a group consisting mostly of juveniles of both sexes; in addition we found evidence that a female perching with two adult males gave birth. Stability of groups varied considerably; a “constant companions and casual acquaintances” model explained data best. Bats older than one year showed more stable associations than younger animals, had higher association rates, and were associated with more strongly associated individuals. This correlated with a higher “forearm-mass-index” as proxy for body condition. In contrast, the fact that females showed more stable associations than males was not correlated to differences in body condition. In sum, the bats displayed a complex and dynamic social structure in captivity.

AO5-167

Roosting Patterns of Kitti's Hog-nosed Bat

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As the smallest bat in the world, Kitti's hog-nosed bat *Craseonycteris thonglongyai* would have limited energy reserves and need proper energetic strategies to decrease energy expenditure. This bat has developed foraging strategy to lower the energetic costs of flight by having two short foraging periods at dusk and dawn, and spend most time roosting in the cave. In this study, roosting activity and time of Kitti's hog-nosed bat in two caves at Sai Yok district, Kanchanaburi province were observed using infrared video cameras. Although large colonies (ca.100-500 individuals) were found in the caves, these bats always roost solitary. Average temperature and relative humidity inside the caves were 26.5°C and 85%, respectively. During the day, bats spent most time resting at their day roost. Day roosting time started from sunrise until around 15 minutes after sunset. After their foraging flight at dusk, bats quickly returned to the cave for night roosting, but most bats did not roost at the same area where they roost in daytime. Night roosting started on average 1 hour after sunset and usually ended 30 minutes before sunrise. Few bats did not leave their night roost and kept roosting through the day. This study confirms the importance of their roost site inside the cave as their resting place, therefore roost disturbance from human activities including inappropriate cave tourism would have an adverse effect to this fragile bat species.

AO5-168

The Effect of Fire on Insectivorous Microbats and Their Resources in Cape York Peninsula, Australia

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Fire is a critical ecological force in Australia, causing a wide range of ecosystem effects from immediate wildlife mortality to long-term habitat changes. There is mounting evidence that inappropriate fire regimes are a key process driving the decline of small mammals in northern Australia. In Cape York Peninsula there are 27 species of insectivorous microbats, several of which are threatened, yet little is known about how fire affects these microbats. In this study, we examine the effects of different fire regimes on microbats and their habitat, as well as the short-term response of microbats and their insect prey to fire. We've used a range of methods including passive acoustic monitoring, habitat assessments, and insect trapping, in before-after-control-impact (BACI) experiments, and randomized block experiments to critically determine the effects of fire on microbats and their resources. Our results show that fire can have a significant impact on microbats and their resources, and that differing fire regimes are likely to have varied impacts. We've also demonstrated that site-specific characteristics can drastically influence ecological responses to fire. The findings from this study can be used to improve conservation strategies in northern Australia, and can aid in the interpretation of results from other fire and microbat studies globally.

AO5-169

Effects of Environment and Bat Ecology on the Microbiome of Ectoparasites

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Arthropod parasites, which generally have nutrient poor diets, are dependent on their bacterial symbionts for development, nutrient acquisition, and immune health. As the body of research on parasite-microbiome interactions continues to grow, it is becoming more apparent that the parasite is not a perfect island that physically and biologically constrains the microbiome. The composition and diversity of the microbiome and abundance of its members are influenced by both its immediate environment (the parasite) and broader environment (where the parasite lives). Habitat fragment size and distance from a source are important variables influencing community composition of plants and animals, but their role in microbial community composition and variation is unknown. It is hypothesized that evolution and ecology of the arthropod parasite would influence its microbiome more than broader environmental factors, but this hypothesis has not been tested. To compare the relative influence of broader environment to that of parasite constraint on its microbiome, we applied high-throughput sequencing of the V4 region of 16S rRNA from 217 obligate ectoparasitic bat flies (11 species) collected from 155 bats (6 species) from 10 habitat fragments in the Atlantic Forest of Brazil. Preliminary results suggest that habitat fragment size, bat fly species, and bat feeding guild influence diversity of the microbiome. Environmental changes resulting from habitat fragmentation have consequences for the diversity and abundance of bacteria in the microbiome of bat flies, which may be detrimental to their immune response against pathogens they vector to their host bat.

AO5-170

Hydrogen isotopes reveal complex seasonal migratory structure in at-risk tree-roosting bats in North America

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Understanding migratory patterns is essential to predicting the impacts of, and organismal tolerance to, global environmental change. Several species of bat migrate long distances within North America, exhibiting potentially complex migratory structure. These species have been negatively impacted by human development during migration, and some might be at risk of extinction. However, bat migration has thus far been very difficult to study by traditional means. Stable isotope signatures present a promising alternative, but bat movement patterns have thus far been too complex to summarize within the context of small regions or distinct management units. Understanding of bat abundance and habitat usage is also limited, so it is difficult if not impossible to identify distinct regions of seasonal habitat. We used stable hydrogen isotope analysis in conjunction with emerging methods of analytically comparing probabilistic assignment models of animal origin to examine migratory structure in three species of North American tree-roosting bat. Our results indicate a strong signal of migratory structure in two of the three species, and the presence of partial migration (year-round residency of some individuals, up to very long-distance migration in others) in all three species. These results have important implications for understanding the migratory ecology, evolutionary ecology, and conservation risks facing these species.

Bat Eco-Interactions Database

Cullen Geiselman

Bat Eco-Interactions Database Project, Houston, Texas, USA

With over 1300 species worldwide, bats are critical components to many ecosystems as pollinators, seed dispersers, and insect predators. Scientific studies of their interactions with plants and arthropods are increasing and continue to reveal the critical roles bats play in nature and the benefits they provide to human economies. We created a platform, the Bat Eco-Interactions Database (formerly the Bat-Plant Interactions Database), to catalog all published accounts of bat interactions with plants and arthropods to facilitate scientific research, reduce duplication of effort, and share and visual published data. For each interaction we include family, genus, and species of each interactor (bat, plant or insect), type of interaction (pollination, visitation, consumption, dispersal, transport, roost, host), details of the location (country, habitat type, elevation, GPS), and citation. Search results can be visualized in tables or geographically and are available for download. The database is open sourced, free, and updated by its users at www.batplant.org. Currently over 6,000 interactions are included from Latin America, Asia, and Africa and we are continuously adding regions and publications to the list. We invite students and researchers to become a part of this online community by submitting publications or adding data directly through the online portal.

AO5-172

The Bird Species Diversity in the Diet and Its Foraging Strategy of the Great Evening Bat

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Bat predation has probably influenced the evolution of bird migration strategies and behaviour. It's critical that acquire a integral knowledge about bird prey to our understanding the interactions between bats and migrating birds. However, there is no evidence of behavioral experiment to reveal the highlighted issue that bats prey on birds so far. We used DNA metabarcoding to ascertain bird species and diversity in the diet of the great evening bat *Ia io*, further performed a captive feeding experiment to verify feeding behaviour, and test two hypotheses involved in foraging strategy by mimicking behavioral experiments. We found a high bird prey diversity, with 22 species of seven families from Passeriformes. Moreover, the majority of species were migratory birds, and four species considered as local resident birds. We also found that bats tend to select small-size passerine birds for optimizing benefit trade-off, the ratio bird prey to bat size conform with new threshold for aerial-hawking bats. The captive feeding experiment verified that *Ia io* eating birds undoubtedly. Finally, the preliminary results from the first mimicking behavioral experiments showed that bats have capability of capture flying birds by using aerial-hawking strategy. This presents a empirical evidence supporting the hypothesis that several temperate-subtropical species of aerial-hawking bats prey on migrating songbirds. Our results indicate that the great evening bat is a opportunistic bird-eating predator, and predation on birds which as an ecological opportunity may subjected to intense natural selection pressure, making them access to the new diet-defined adaptive zones.

AO5-176

Understanding *Mystacina*: Ten years of research into the biology and behaviour of 50% of New Zealand's bat fauna

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Over the past 10 years our team have sought to increase understanding of the behaviour and biology of the enigmatic New Zealand lesser short-tailed bat, *Mystacina tuberculata*. In particular, we have focused on the role of *M. tuberculata* in plant pollination, its use of non-pristine habitats, and its mating behaviour. In this talk I will outline: how flowering phenology may be adapted to minimise competition for the pollination services of the short-tailed bat; that although *Mystacina tuberculata* generally prefers native forest, in fragmented landscapes some individuals prefer exotic plantation and open space; and that this species exhibits a fascinating lek mating system with social vocalisations playing a central role in their breeding biology. Finally, I will conclude with an update on our latest results focusing on phonological analysis of short-tailed bat song which aims to determine if the bats possess a shared linguistic framework and if there are individual variation in syntactic expression.

AO5-177

Impacts of an Invasive Ant Species on Roosting Behaviour of an Island Endemic Flying-fox

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The introduction of alien species into ecosystems is considered a major contributor to species extinctions worldwide, particularly on islands. The yellow crazy ant (*Anoplolepsis gracilipes*; YCA) is one of the most harmful invasive ant species, and has detrimental effects on many animals on Christmas Island. However, the full extent of the effect of YCAs on Christmas Island's fauna is not yet known. In this study, we investigated the impacts of the YCA on the last endemic mammal of Christmas Island: the Christmas Island flying-fox (*Pteropus natalis;* CIFF). This species has been described as a keystone species, but has recently experienced a population decline to the extent that it is now listed as Critically Endangered under the Commonwealth Environment Protection and Biodiversity Conservation (EPBC) Act 1999. We examined the impacts of the YCA on the roosting behaviour of the CIFF, and on its local and island-wide distribution patterns. We showed that YCAs increased behaviours in CIFFs that were associated with avoidance of noxious stimuli, and decreased behaviours associated with resting. Roost tree selection and roost site location, on the other hand, were not related to variation in the abundance of YCAs on the island. Our results indicate that YCAs interfere with the activity budgets of CIFFs. However, CIFFs failed to relocate to YCA-free roost trees or roost sites when confronted with the noxious ant, suggesting that CIFFs are either not sufficiently disturbed to override strong cultural attachment to roosts, or are behaving maladaptively due to ecological naïveté.

AO5-178

Landscape Context Matters for Effective Use and Attractiveness of Road Underpasses by Bat Communities

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The worldwide expansion of road networks is a major concern in biological conservation because of its predominantly negative effects on terrestrial fauna, and especially on bats, for which roads act as barriers to movements and increase mortality caused by vehicle collisions. Among wildlife crossing structures existing to maintain landscape connectivity, road underpasses are considered as the most effective mitigation measure for bats. While a few studies assessed the effects of local underpass attributes on bat use, none to date has yet assessed the impact of landscape context on underpasses use and attractiveness, although underpass efficiency is expected to depend on both local and landscape characteristics. To investigate this, we monitored bat activity during three consecutive nights around 24 underpasses selected along a gradient of forest cover (N = 114 618 bat passes). We compared bat activity under and above underpasses (i.e., underpass use), at road sections with and without underpasses and at habitats adjacent to roads (i.e., underpass attractiveness) using GLMMs. We found a significant positive effect of forest cover for *Myotis* spp and *Barbastella barbastellus*, significant negative effects of distance to the nearest forest patch for *Rhinolophus* spp and hedgerow length for *Myotis* spp, on both underpass use and attractiveness. Our study highlights the key influence of landscape context on road underpass efficiency to maintain landscape connectivity for bats. We advocate for incorporating a landscape-scale approach in the decision-making process of underpass location during road project planning in order to enhance efficiency of such costly crossing structures.

AO5-179

Pest Consumption in a Vineyard System by *Rhinolophus hipposideros*

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Herbivorous arthropods cause immense damage in crop production annually. Consumption of these pests by insectivorous animals is claimed to be crucial to counteract their adverse effects. Bats are considered amongst the most voracious predators of arthropods, of which some species are known to consume pests. In vineyard dominated Mediterranean agroecosystems, multiple crops are damaged caused by the attack of insect pests, thereby in this study, we aimed 1) to explore the diet and pest consumption capacity of the lesser horseshoe bat *Rhinolophus hipposideros* and 2) analyse whether the occurrence of pest species in its diet is influenced in time by season. For that, we employed a dual-primer DNA metabarcoding analysis of DNA extracted from faeces collected in three bat colonies of a wine region in Southwestern Europe during the whole active period of most pest species. Overall, 395 arthropod prey species belonging to 11 orders were detected; lepidopterans and dipterans were the most diverse orders in terms of species. Altogether, 55 pest species were identified and 24 of them are considered major pests. Occurrence of pest species in faeces changed significantly through time. In view of the results, it can be asserted that *R. hipposideros* may act as a suppressor of a wide array of agroforestry pests in Mediterranean agroecosystems. Therefore, appropriate conservational measurements to favour the growth of its populations should be considered.

AO5-180

Seasonal Diet Variation of Sympatric Insectivorous Bats Revealed by Stable Carbon Isotope

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Sympatric bats partition their resources using various strategies such as microhabitat use. Sometimes sympatric insectivorous bats may share the same habitat, but select different prey insects to reduce the degree of competition. For conservation efforts, it is essential to improve our understanding about the mechanisms underlying the coexistence of bat species. In this study, we used stable carbon isotopes to delineate the food web memberships of a previously understudied bat ensemble; open-space foraging bats of Southeast Asia. Based on stable carbon isotope ratios of wing tissues, we found that sympatric open-space foraging bats varied in isotopic composition between the dry and wet seasons. *Taphozous melanopogon*, *T. theobaldi* and *Chaerephon plicatus* fed more on a C_3 food web during the dry season whereas all fed equally on both C_3 and C_4 food webs during the wet season. In contrast, *Hipposideros larvatus,* an edge-foraging specialist bat, fed on both C_3 and C_4 food webs during the dry season while they fed mainly on insects from C_4 food webs during the wet season. The differences in isotopic ratios of wing tissues may indicate seasonal changes in their diet which may reflect changes in resource abundance caused by growing season and agricultural practice.

AO6-101

Burning Fat by Inducing Beige Adipocytes: Insights from a Bat Study

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Beige adipocytes can be induced from white adipocytes and precursors upon stimulation by cold temperatures and act like brown adipocytes to increase energy expenditure. Most *in vivo* studies examining the mechanisms for the induction of beige adipocytes have focused on subcutaneous white adipose tissue (sWAT; benign fat) in the mouse. How intra-abdominal WAT (aWAT; malignant fat) develops into beige adipocytes remains obscure, largely because there is a lack of a good animal model for the induction of beige adipocytes from aWAT. To better understand the development of beige adipocytes from mammalian WATs, especially aWAT, we induced beige adipocytes from bat aWAT and mouse sWAT by exposure to cold temperatures and analyzed their molecular signatures. RNA sequencing followed by whole genome-wide expression analysis shows that beige adipocytes induced from bat aWAT, rather than sWAT, have molecular signatures resembling those of mouse sWAT-induced beige adipocytes and exhibit dynamic profiles similar to those of classical brown adipocytes. In addition, we identified molecular markers that were highly enriched in beige adipocytes and conserved between bat aWAT and mouse sWAT, a set that included the genes *Uqcrc1* and *Letm1*. Furthermore, knockdown of *Uqcrc1* and *Letm1* expression shows that they are required not only for beige adipocyte differentiation but also for preadipocyte maturation. This study presents a new model for research into the induction of beige adipocytes from aWAT in vivo, which, when combined with models where beige adipocytes are induced from sWAT, provides insight into therapeutic approaches for combating obesity-related diseases in humans.

AO6-102

Determining Torpor and Emergence Behaviors of Four Cavernicolous Bat Species in Relation to *Pseudogymnoascus destructans* Susceptibility

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Bat species exhibit varying susceptibility to *Pseudogymnoascus destructans* (*Pd*), the causative agent of white-nose syndrome. The influence winter activity (i.e., emergence and torpor behaviors) may have on susceptibility has yet to be investigated. We deployed temperature-sensitive transmitters on three bat species (*M. grisescens*, *M. leibii*, and *M. sodalis)* to monitor torpor bouts, and implanted these same *Myotis* species, plus *Perimyotis subflavus,* with passive integrated transponder (PIT) tags to monitor cave emergence. PIT tags were detected by antennae surrounding cave entrances. We deployed 12 transmitters and implanted 1,271 PIT tags. Mean torpid body temperature was lowest for *M. grisescens* at 13.33°C, and highest for *M. leibii* at 18.73°C. Mean torpor bout length (TBL) was lowest for *M. leibii* at 2 days (range: 1-4 days), and highest for *M. sodalis* at 9.85 days (range: 4-5 days). *Myotis grisescens* had the greatest range in TBL (range: 0.5-18 days). PIT tag detections indicated *M. leibii* were active throughout the hibernation period (November–February), with an average of 42.35% of tagged individuals detected at cave entrances each month (range = 6.06%-72.7%; $P < 0.001$). Of the 111 PIT-tagged bats active during winter, only 29.7% (n = 33), the majority of which were *M. leibii* (69.6%, n = 22), were detected at a cave entrance more than once/night. The length of time between detections in the same night ranged from 11.5 to 399 min (6.65 hrs). Our findings are being used to develop conservation strategies of benefit to *Pd* susceptible bat species.

AO6-103

Molecular and Evolutionary Studies of Bat Viruses and Functional Gene Adaptation

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My lab has studied bats for about 20 years and over 100 graduate students published papers on bats involving in various subjects. In this talk, I would like to summarize our important research findings in the past two decades. For example, we found bats were the natural reservoirs of SARS coronaviruses and an evolutionary relationship existing between bat coronaviruses and their hosts. Then, we conducted a virome analysis based on pharyngeal and anal swab samples of 40 major bat species to investigate the presence of potential bat-borne zoonotic viruses and to evaluate the impacts of these viruses on public health. The data obtained revealed an overview of the viral community present in bats. Many novel bat viruses were reported for the first time and some bat viruses closely related to known human or animal pathogens were identified. This genetic evidence provides new clues in the search for the origin or evolution pattern of certain viruses, such as coronaviruses and noroviruses. Besides, bats are an excellent group in which to study adaptive changes. We studied the AGT (The enzyme alanine-glyoxylate aminotransferase 1) and detected positive selection in ancestral fruit bats, which supports adaptations related to evolutionary changes in diet. Furthermore, we found that chicken-type lysozyme has undergone multiple duplication events in a major family of insect-eating bats (Vespertilionidae) and that new duplicates have undergone molecular adaptation. More results will be presented in the conference, and all these findings will give us much better understanding on this amazing group of mammals.

AO6-104

Stressors Compromise the Bat-Virus Relationship Leading to Increased Virus Replication and the Potential for Spillover

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We have tested the hypothesis that bats have benign long-term associations with their viruses, and disruption of these relationships lead to virus shedding and potential spillover to other species. We tested this hypothesis in cultured *Eptesicus fuscus* cells infected with *E. fuscus* herpesvirus (EfHV) or with a coronavirus. These experiments were complemented with observations of field-captured and hibernating *E. fuscus* or *Myotis lucifugus* bats. Infection of bat cells with the human-derived middle eastern respiratory syndrome (MERS)- coronavirus caused rapid adaptive changes in a viral gene responsible for modulation the innate response, and the establishment of long-term, non-lethal persistent infection. Artificial suppression of the bat innate-response led to increased virus replication in these cells. These results were supported by an observed suppression of anti-viral innate responses in the intestines, the anatomical site of coronavirus persistence, of bats infected with the white nose syndrome (WNS)-causing fungus, and an accompanying increase in the replication of a coronavirus. Bats latently infected with EfHV and immunosuppression associated with hibernation and the stress of arousal led to reactivation of virus. Our results show that many individuals of two north American bat species are latently or persistently infected with herpes and/or coronaviruses, and stressors that suppress innate host anti-viral responses lead to recrudescence or an increase in viral replication.

AO6-105

Acquisition of Antibiotic Resistant Bacteria by Australian Fruit Bats (*Pteropus poliocephalus*) in Urban and Captive Environments

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Antimicrobial resistance (AMR) is a global issue that also impacts wildlife, in addition to human health. The spread of human-associated AMR to wildlife has been facilitated by increased human-wildlife contact and acquisition of resistance genes via mobile genetic elements. Over recent decades, the number of Grey-headed Flying Foxes (*Pteropus poliocephalus*), an Australian fruit bat species, roosting in urban environments has increased. Each year, several thousand sick, injured and orphaned Grey-headed Flying Foxes (GHFF) enter wildlife rehabilitation facilities. In urban and captive environments, GHFF encounter human-associated bacteria which may carry antibiotic resistance genes. A survey of GHFF fecal samples detected class 1 integrons, a mobile genetic determinant of antibiotic resistance, in wild GHFF (5.3%) and captive GHFF (41.2%) undergoing rehabilitation. Bacterial culture of wild and captive GHFF fecal samples detected ß-lactam (amoxicillin) resistant *Escherichia coli* in 1.95% of wild GHFF and 22.2% of adult and orphan GHFF undergoing captive rehabilitation. All ß-lactam resistant *E. coli* isolates were multidrug-resistant, exhibiting resistance to between two and eight classes of antibiotics. Of greatest concern, was the detection of a carbapenemase producing *E. coli* isolate, which exhibited resistance to imipenem and meropenem, two carbapenem antibiotics of last resort. The detection of antibiotic resistant bacteria, particularly in captive GHFF, may negatively impact sick and injured GHFF requiring veterinary treatment. Additionally, released individuals may spread antibiotic resistant bacteria to other GHFF and wildlife species. This presentation will discuss these findings and their implications on the management and conservation of the endangered Grey-headed Flying Fox.

AO6-106

Coordinated change at the colony level in fruit bat fur microbiomes through time

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The host-associated microbiome affects individual health and behavior, and may be influenced by local environmental conditions. However, little is known about microbiomes' temporal dynamics in free-living species compared to those of humans and model organisms, especially in body sites other than the gut. Here, we investigate longitudinal changes in the fur microbiome of captive and free-living Egyptian fruit bats assessed using 16S rRNA gene amplification. We find that in contrast to patterns described in humans and other mammals, the prominent dynamics are of change over time at the level of the colony as a whole. On average, a pair of fur microbiome samples from different individuals in the same colony collected on the same date is more similar to one another than a pair of samples from the same individual collected at different time points. This pattern suggests that the whole colony may be the appropriate biological unit for understanding some of the roles of the host microbiome in social bats' ecology and evolution. This pattern of synchronized colony changes over time is also reflected in the profile of volatile compounds in the bats' fur, but differs from the more individualized pattern found in the bats' gut microbiome. As a continuation of this study we are now looking at microbiome changes in times of sickness; how might physiological and social behavior alterations due to pathology reflect in the fruit bat fur and gut microbiome.

AO6-107

Into the Wild: Integration of Human-associated Parasites into *Pteropus* Microbiomes

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Spillover of zoonotic viruses from bats to humans is well known. In contrast, reverse transmission (zooanthroponosis) whereby pathogens move from humans into bats remains largely unexplored. In Australia, increasing urbanisation and habitat loss are driving bats into urban and regional centres, creating a conduit for microbial traffic between bats, humans and domesticated animals. This urbanisation creates high connectivity to humans and the pathogens they carry, and increases the risk of zooanthroponosis. Flying foxes may also undergo rehabilitation in wildlife care settings where they have very close contact with carers. Animals in care are at risk of exposure to micro-organisms atypical to those found in their natural habitats. How such exposure impacts flying fox health and their microbiomes are unknown. There is also the risk of spreading acquired organisms to wild populations through release programs. This presentation will showcase examples of zooanthroponoses in bats through the integration of human-derived protozoan parasites, *Cryptosporidium* and *Giardia,* in flying foxes in Australia. The impacts of dissemination of these parasites to flying foxes, as well as risk of flying foxes becoming reservoirs of non-viral zoonotic agents as a result of zooanthroponosis will be discussed.

AO6-108

Microbats of the South West Botanical Province of Western Australia: Pathogen Diversity and Host Genetic Connectivity

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Microbats in Western Australia are an important component of local biodiversity. However, baseline data necessary for species management is lacking, including information on genetic diversity, population connectivity, and potential infectious disease risks. Characterising viral diversity within healthy bat communities is crucial to detect changes in pathogen dynamics that may hamper their survival or constitute a public health risk. We used targeted methodologies (PCR, qPCR, serology) to describe the diversity of adenoviruses, coronaviruses and paramyxoviruses in 571 faecal samples representing 12 species of insectivorous bats within the region. Next generation sequencing was employed for the discovery of unknown viral agents. In addition, we tested 662 blood samples for reactivity to paramyxovirus-like, beta-coronavirus-like and lyssavirus-like antigens. In general, we observed a strain-host association across all viral families. Results indicate that divergent viral strains circulate concurrently within bat populations and viral burden does not appear to be equally carried by all species in a community. Additionally, oral shedding of lyssavirus was not detected, however serological results identified previous exposure to this virus supporting the existence of additional lyssavirus reservoirs.

AO6-109

High Risk Excretion Periods of Diverse Coronaviruses in the Egyptian Rousette Bat in South Africa

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The ecologically important Egyptian rousette fruit bat species (*Rousettus aegyptiacus*) is known to host high risk viral species, including Marburg virus and *Henipavirus*-related paramyxoviruses. Such viral agents have been identified from South African rousette bat populations, with apparent seasonal increases that may be linked to reproductive cycles. Coronaviruses are known for their potential to cross-species barriers and are a concern as emerging zoonotic agents. This is exemplified with the emergence of three novel coronaviruses of public and veterinary health importance in the last 16 years, including Middle East respiratory syndrome coronavirus. Coronavirus surveillance within rousette bat populations in Southern Africa is limited. The project focused on identifying the coronavirus diversity present in a rousette roost at the Matlapitsi cave (Limpopo province, South Africa), with the further aim of determining excretion cycles throughout the year. Fecal samples (n=371) were collected on a monthly basis throughout 2017-2018 from underneath roosting bats. A conserved region of the RdRp gene was amplified with RT-PCR and phylogenetically analyzed using Bayesian approaches. Monthly excretion frequencies were investigated for possible seasonality. Sequences of *Alpha*- and *Betacoronavirus* genera were detected, indicating maintenance of diverse coronaviruses within the colony. Viral shedding was seen to span the winter to spring months, coinciding with the early breeding period and overlaps with high risk excretion times of viruses like *Henipavirus*-related paramyxoviruses in urine. High risk periods can be identified and be used to develop mitigation strategies to prevent spillover and emergence of novel coronaviruses in humans and other animals.

AO6-110

Diversity and Excretion Dynamics of *Henipa-*, *Rubula-* and Related Viruses in *Rousettus aegyptiacus* from South Africa

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A significant diversity of viruses has been described from bats within the last 80 years. A number of these viruses are associated with zoonoses and include members from the *Paramyxoviridae* family such as Hendra and Nipah viruses (*Henipavirus* genus) and Sosuga virus (*Rubulavirus* genus). Pteropid bats have been identified as the natural reservoirs for the zoonotic henipaviruses in Australia and Southeast Asia. The natural host for Sosuga virus is the Egyptian rousette bat (*Rousettus aegyptiacus*) with a fragmented distribution across sub-Saharan Africa and parts of North Africa, Southwest Asia and the Middle-East. However, the association of paramyxoviruses with *R. aegyptiacus* host species has only been studied to a limited extent. This study aimed to determine the diversity of *Henipa-, Rubula-* and related viruses within a population of this bat species in South Africa and to conduct a longitudinal excretion analysis of the viruses at population level. Spleen (n=302) and population-level urine samples collected on plastic sheets underneath the roosts (n=255, pools of 10) were tested for the presence of viral nucleic acids with the use of two broadly reactive RT-PCR assays. A large diversity of viruses related to both genera were detected. A winter excretion peak was observed for both *Henipa-* and *Rubulavirus*-related viruses. For the latter viruses, an excretion peak was also observed during the late gestation period of *R. aegyptiacus*. This study reports the first evidence of *Henipa-* and *Rubulavirus*-related viral sequences in *R. aegyptiacus* from South Africa and identified periods of high-risk for virus transmission and spill-over.

AO6-111

Effect of Fitness Traits and Weather Condition on the Infection of Coronavirus of Lyle's Flying Fox

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Lyle's flying fox is natural reservoir for zoonotic coronaviruses. The influential factor associated with coronavirus infection in natural host populations is not well understood. In this study, we hypothesized that fitness-related traits, and temporal environmental stress, represented by monthly weather condition, were associated with the infection rate of coronavirus. Sample of 352 individuals were captured monthly during January - December 2012 at three sites in Chonburi province. To detect the infection of coronavirus, nested RT-PCR of RNA-dependent RNA polymerase gene from rectal swab samples was used and the infection was affirmed by phylogenetic analysis. Data analysis was done by generalized linear model regressing on infection by exploratory variables composed of weight, body mass index, and body condition index representing individual fitness of individual bat; and environmental stress variables consist of monthly average temperature and rainfall. The best subset model selection procedure was used to define the best model based on AIC. The best model composed of negative effect of body condition index, the negative effect of first-order lag average temperature, the negative effect of second-order lag rainfall, and the positive effect of second-order lag average temperature. The most frequent variable that occur in the best models were second-order lag average temperature, while body mass index and body condition index were complementary. The partial model showed that weather condition and body condition index independently associated with the infection. This study could support the prevention effort of coronavirus by providing insight of population and temporal level of influential factors.

Detection of Influenza A Viruses (IAV) in Diverse Bat Species in Bangladesh

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Background: Recent discovery of novel bat influenza A viruses (IAV) raises questions regarding host range and the role of bats in the evolution of IAV. The ability to infect wide range of host species makes the ecology of these viruses both interesting and critically important.

Methods: We conducted longitudinal surveillance in bats from 2015 to 2018 to detect and characterize IAV. We sampled 1189 individual bats representing 13 species and 6 families across 23 sampling sites. Oral and rectal swab samples were tested using PREDICT's pan-influenza consensus PCR to detect novel influenza subtypes targeting different regions of polymerase basic (PB1) gene and Matrix (M) gene.

Results: Prevalence of IAV in bat was 5.2% (62/1189; 95% CI: 4.2-7.0); 4.8% (40/839) of fruit bats and 6.3% (22/350) of insectivorous bats were positive respectively. Among 13 species of bats, IAV was found in 8 species; *Cynopterus sphinx* (n=24; 6.9%), *Hipposideros cineraceus* (n=2; 22.2%),

Macroglossus sobrinus (n=3; 18.7%), *Megaderma* sp. (n=9; 4.6%), *Pteropus medius* (n=11; 3.3%), *Rhinolophus lepidus* (n=2; 5.3%), *Rousettus leschenaultii* (n=2; 1.7%) and *Tylonycteris pachypus* (n=9; 16.1%). Wet season (OR=0.55; p=0.02) and male bat (OR=0.6; p=0.07) had significantly less IAV than that of dry season and female bat respectively. Deep sequencing and subtyping of positive samples are ongoing.

Conclusion: The study suggests that IAVs are circulating in diverse bat species across Bangladesh. Further surveillance for IAVs in bats is recommended to determine evolutionary, spatial and temporal dynamics of IAV circulating in bats, and the role of bats in the natural host ecology.

AO6-113

Learning from bats: studying inflammation and its implications for health

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The unique physiology of bats allows them to raise their metabolism drastically during flight, including heartbeats of up to 1200bpm, and rapidly turn over their energy reserves without any obvious consequence of metabolic disease or accelerated aging. Additionally, they can endure infection with multiple pathogens, normally deadly to humans, with minimal consequence of infection and no obvious disease. Through *in vitro* and *in vivo* stimulation, deep sequencing analysis, molecular characterisation of Pattern Recognition Receptors (PRRs), proteomics profiling and comparative biology to other mammals we have uncovered several pathways that dampen their inflammatory response to pathogens. Stress sensors such as NLRP3, AIM2, STING and the TLR's are all affected, along with several downstream molecules. How much these pathways overlap with metabolism or longevity is now under investigation. Using our research bat colony of *Eonycteris spelaea* and comparisons with wild bats we can interrogate these pathways for a better understanding of global health and how this can be applied to other animals and humans.

AO6-114

Bats, disease, and dynamic densities: Investigating community structure as a driver of viral dynamics in flying-foxes

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Bats are highly gregarious mammals, with some species roosting in dense, seasonal colonies that can range from hundreds to hundreds-of-thousands of animals. This creates frequent opportunities for direct and indirect contact between large numbers of individuals, and contributes to the propensity of bats to be important disease reservoirs. Understanding the roosting dynamics of bats is important in the context of infectious disease, as spatio-temporal patterns in abundance and density will influence infectious contacts between individuals, and thus the propensity for infection and spread of disease. We investigated the roosting structure of three sympatric species of flying-fox (*Pteropus alecto*, *P. poliocephalus* and *P. scapulatus*), using high-resolution spatial mapping techniques. Preliminary analyses show dynamic patterns of animal clustering through space and time, driven by underlying roost tree structure and dramatic fluctuations in total bat abundance. Future analyses will integrate roosting dynamics with matched data on Hendra virus excretion to mathematically explore the plausibility of hypothesised but unobservable mechanisms of virus circulation in bats. We will also explore the potential for "dilution" of infectious contacts within bat populations with infiltration of nomadic, dead-end hosts (*P. poliocephalus* and *P. scapulatus*) to primary reservoir host communities (*P. alecto*). Simulations of virus invasion and spread within bat populations will be important for inferring disease dynamics in species with highly unstable, periodically fluctuating densities. As one of few studies to systematically evaluate roosting patterns in flying-foxes, this study will also provide valuable ecological information on bat habitat preferences, with practical applications for flying-fox conservation and conflict management.

AO6-116

Pathogen Detection in Bat Flies (Diptera: Nycteribiidae) and Their Potential Utilization in Host Conservation

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Bats are known as `keystone species` since they perform important ecosystems services. Nevertheless, their importance is also significant as reservoir species of zoonotic diseases. We evaluate the utility of dipteran hematophagous ectoparasites in pathogen detection and potential importance in avoiding invasive sampling and voucher collection. We tested both bat blood and ectoparasites to detect three distantly related pathogenic groups using molecular methods (*i.e. Bartonella* Strong et al., *Polychromophilus* Dionisi and *Trypanosoma* Gruby) and we compared the detection rate between hosts and ectoparasites. We sampled and tested two bat species, *Miniopterus natalensis* Smith (South Africa) and *M. schreibersii* (Kuhl) (Hungary, Italy and Spain) and their highly specific ectoparasites, *Nycteribia schmidlii scotti* Falcoz and *N. schmidlii* Schiner, respectively. We found that depending on the pathogen, the detection rate was different but it can be useful in determining pathogen presence and diversity. Future perspectives on host conservation and zoonosis monitoring are discussed.

Origins of bat protozoan parasites of the *Trypanosoma cruzi* clade

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Understanding patterns of interactions between hosts and parasites can provide useful insight into the evolutionary history of the organisms involved. Species in the *Trypanosoma cruzi* clade include the infamous parasite infecting humans (*T. cruzi cruzi*) and responsible for the American Trypanosomiasis. Diversity in this clade has been recently expanded by newly discovered species, but the common ancestor and geographical origins of this group of blood parasites are still debated. We present here results based on the molecular characterization of trypanosome isolates issued from 1495 bat representing 77 species and sampled over 16 countries from Europe, Southern Africa, East Asia and Central America. Among the eight *Trypanosoma* species detected in our samples, two species were newly discovered and parasitized the genus *Miniopterus* both in Europe and Africa. These parasites were found in an unexpected position in the global phylogeny of the *T. cruzi* clade. We discuss the impact of these findings on the biogeography and taxonomy of this important clade of parasites and question the role played by bats, especially by the *Miniopterus* genus, on the dispersal and diversification of this protozoan parasites across continents.

AO6-118

Did you wash your caving suit? Cavers' role in the transport of White Nose Disease

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White Nose Disease (WND) is a mycosis that has killed millions of hibernating bats in America. Its causative agent *Pseudogymnoascus destructans* is introduced to North America but native to Europe and Asia, where it does not cause mortality. Although it is not possible to completely eradicate it, research on WND means of distribution can help us prevent its introduction to new places or take measures against similar emerging diseases. It is of particular importance to quantify the role of cavers in transporting *P. destructans* spores on their clothes and equipment, and to raise awareness of the problem within the caving community. In the course of two consecutive filed seasons, we collected samples from our clothes and equipment before and after work in Bulgarian caves known as sites of white-nose fungus occurrence. Results show the presence of viable *P. destructans* spores on our caving clothes in almost 100% of the cases where we have visited white-nose positive bat hibenacula, disregarding the time of year. Consecutive lab experiments showed that pathogen's spores can survive on pieces of dirty clothes and equipment under room temperature for 25 days, which is more than enough for cavers to move from one expedition to another. So far, it seems that regular washing (with brush, soap, and water) can successfully remove *P. destructans* spores but having in mind that many recreational cavers do not bother to wash or that many bat workers visit several caves per day during monitoring activities, more education on the subject is needed.

AO6-119

Non-lethal Longitudinal Viral Monitoring in European Bats

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Bats are well-recognised as a source of zoonotic viral infections, with several causative agents of severe human diseases identified as having a chiropteran origin, including *Marburgvirus*, *Nipahvirus*, SARS-like *Coronavirus* and several *Lyssaviruses*. However, most work on monitoring and identifying viruses in bat populations has taken place in Asia, Africa and the Americas; European laws protecting bat species has reduced screening efforts in native populations. These laws limit interaction with populations and prevent lethal sampling, making effective sampling of these small species challenging.

In this study, we have used RNA-sequencing of low volume blood samples taken from a cohort of over 600 *Myotis myotis* bats non-lethally sampled in Brittany, France over a 7-year period. This unique cohort of microchipped individuals in a monitored population has enabled determination of temporal viral changes within individuals over a multi-year period, in addition to detecting changes by age cohort and year across the population.

We have found that there is significant variation in viral diversity across age cohorts, with changes in viral ecology evident between juvenile and adult bats. We have identified some viral infections which appear to be persistent within the individuals, and others able to be rapidly cleared. Monitoring of physiological measures and recapture data has revealed no evidence of detriment to fitness from any virus.

Through these analyses, we have identified endemic viral species in European bat populations which are of potential consequence to human health. Further analysis is required to fully characterize these novel viruses.

AO6-120

Global Host and Pathogen Dynamics of White-nose Syndrome

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The introduction of novel pathogens to naïve host populations has caused catastrophic impacts and species extinctions. However, the mechanisms allowing hosts to persist with these same pathogens in disease endemic regions are poorly known. We examined the global dynamics of white-nose syndrome (WNS) on bats and in the environment to determine how species and populations in endemic regions persist with this disease. In Eurasia, for species with high fungal prevalence, we found that infection dynamics during winter were similar to the first year of pathogen invasion into North American hibernacula, with prevalence increasing from near zero to higher levels (50-100%). These dynamics differed substantially from infection patterns during the mortality-phase of WNS in North America, when most North American bats have sustained high infection prevalence (100%) over winter. Although *P. destructans* has been present in hibernacula across Europe and Asia for thousands of years, we found that *P. destructans* in the environment was low. We explore the causes and consequences of differences in bat infection dynamics between Eurasia and North America to provide insight into the steady-state dynamics of North American bat populations.

AO6-121

The effects of temperature on the white-nose syndrome bat population dynamics

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White-nose syndrome (WNS) has had dramatic impacts on North American bat populations, and threatens several bat species with local extinction. Growth of the fungus that causes WNS (*Pseudogymnoascus destructans*) is strongly influenced by temperature, and therefore temperature is predicted to be a key factor determining disease outcome. However, linking variables thought to be important in determining population-level persistence (e.g. temperature and fungal loads) to individual bat outcomes is a significant challenge in free-ranging bats. Here, we use recapture data from marked individuals and mathematical models to examine the effects of roosting temperature on infection and survival to assess their importance in population persistence. We find that individuals roosting at warmer temperatures in early winter have significantly higher fungal growth than individuals roosting at colder temperatures. Warmer hibernation temperatures also resulted in a lower probability of recapture, suggesting that bats that roost at warm temperatures are more likely to die from WNS. Using mathematical models parameterized with *in vitro* fungal growth at different temperatures, we found that bats dying of WNS roosted at warmer temperatures which and had higher fungal loads than bats that survived. Roosting temperature alone predicted overwinter bat survival with greater than 65% accuracy, suggesting that roosting temperature is a critical factor determining bat population persistence. Our data suggest that temperature is important factor determining long-term persistence of North American bat populations.

AO6-122

Serological evidence of Filovirus in bats and bat-hunters in the Northeastern states of India

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Despite being known reservoirs of several medically-important viruses, there has been little research on bats and bat borne viruses in India. The northeast of India is a mountainous region where bushmeat is still an important source of protein in rural areas. Some local groups in these areas engage in harvesting of cave dwelling bats- *Rousettus leschenaultii*, *Eonycteris spelaea* and *Hipposideros armiger* are particularly targeted, providing a possible junction for cross-species transmission. Our work examines traditional bat harvests in two North-eastern states of India- Nagaland and Arunachal Pradesh. We collected serum and tissue samples from bats killed at the harvest sites. Furthermore, we also collected serum samples from the harvested bats and from human that participated in the harvest. Sera was screened with a multiple serological assay for antibodies against medically important members of the virus family Filoviridae. Bat kidney, lung, and spleen tissues from an individual were pooled and screened with a pan-filovirus PCR. Harvested species of bats were sero-positive for filoviruses, while a few human sera samples were sero-positive for filoviruses. This study demonstrates the need for nation-wide surveillance of medically-important viruses in bats in order to understand the transmission pathways and to ultimately address disease and conservation management strategies.

AO6-123

Life history variation in immune and metabolic gene expression in free-ranging little epauletted fruit bats

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Bats are ecologically and physiologically unique. The evolution of flight in these long-lived mammals is hypothesized to have exerted strong selection on immune and metabolic processes. Bats appear to be able to host diverse viral pathogens with little pathology. Furthermore, they not only survive, but rather thrive in challenging, highly seasonal environments. Despite their global prevalence and their documented status as reservoir hosts of emerging infectious diseases, we have limited understanding of their immune and metabolic physiology in their natural habitat. Our studies harness the power of transcriptomics and veterinary diagnostics to explore bat physiology in their "real world". Using the study species *Epomophorus labiatus* (little epauletted fruit bat), which is a highly social and adaptable 'peri-domestic' African Pteropodid, we examine both intrinsic and extrinsic factors that may contribute to gene expression heterogeneity. These factors include age, sex, reproductive state, season, body condition, and the influence of active or previous infections. We present evidence that some of these factors, such as reproductive state and parasitic infection, influence bat health and immune and metabolic gene expression in a way that may affect fitness and survivorship. Furthermore, heterogeneity in the regulation of metabolic and immune processes due to intrinsic and extrinsic factors may mediate the ability of bats to serve as reservoir hosts by controlling viral prevalence under some conditions. This may then contribute to seasonal infection dynamics by affecting viral load and the viral shedding that may lead to spillover under specific ecological conditions.

AO6-124

Bat Research Networks and Viral Surveillance: Gaps and Opportunities in Western Asia

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Bat research networks and viral surveillance are assumed to be at odds due to seemingly conflicting research priorities. Yet human threats that contribute to declines in bat populations globally also lead to increased transmission of bat-associated viruses, which may pose a threat to global health. We discuss the importance of multidisciplinary collaborations between bat research networks and infectious disease experts to tackle shared threats. We assess research effort on bats and bat-associated viruses globally, and demonstrate that Western Asia has limited published research and represents a gap for coordinated bat research. The lack of bat research in Western Asia severely limits our capacity to identify and mitigate region-specific threats to bat populations and detect interactions between bats and incidental hosts that promote virus spillover. We detail a recent initiative to establish the first bat research network in the region (Western Asia Bat Research Network, WAB-Net), with the aim of integrating ecological research on bats with virus surveillance to find “win-win” solutions that promote bat conservation and safeguards global health. Since project inception (Oct 2017), we developed standardized protocols for non-lethal bat sampling, site characterization, and screening bat-associated coronaviruses; identified sites and collected diagnostic samples from >10 bat species in Georgia, Jordan, and Turkey; and hosted the first annual WAB-Net meeting. Additional sampling in Pakistan, Armenia, Oman, and Azerbaijan is to be completed by July 2019. WAB-Net leverages existing, regional expertise in wildlife research and laboratory diagnostics for One Health surveillance, allowing WAB-Net to be sustained beyond the 5-year funding period.

AO6-125

Maybe She's Born with It: Big Brown Bats Show Physiological Resistance to White-nose Syndrome

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Wildlife pathogens can cause population declines and extinctions, and understanding species differences in susceptibility is important for conservation. White-nose syndrome (WNS), caused by the fungus *Pseudogymnoascus destructans* (Pd), is a skin disease devastating populations of North American hibernating bats. Two of nine WNS-impacted species (i.e., little brown myotis and big brown bats) both hibernate in conditions favoring Pd growth. However, little brown bats have faced significantly steeper declines. Two competing hypotheses could explain this difference in impacts. Big brown bats could be: (i) resistant to *Pd* (i.e., maintain low pathogen loads); or (ii) tolerant of *P. destructans* (i.e., exhibit limited disease and morbidity despite high pathogen loads). The resistance hypothesis predicts that big brown bats should maintain lower fungal loads than little brown bats when hibernating in identical conditions that favour growth of *Pd* while the tolerance hypothesis predicts that big brown bats will exhibit high fungal loads without evidence of disease. We tested these hypotheses using a replicated inoculation-challenge experiment. We housed Pd-inoculated and sham-inoculated groups of both species in separate cages within two identical incubators both maintaining 8 °C and 98% relative humidity. Consistent with the resistance hypothesis, inoculated big brown bats in both incubators had significantly lower prevalence and intensity of infection based on qPCR after 60 days. Although big brown bats appear to be physiologically resistant to the disease, management actions that reduce loads for this species could be important for conservation by reducing potential inter-species transmission within and between hibernacula.

AO6-126

Staphylococcus aureus Outbreak Following Introduction of Wild-caught Bats into a *Rousettus aegyptiacus* Research Colony

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Several zoos and research institutes keep *Rousettus aegyptiacus* colonies. Introduction of wild-caught bats poses health risks to the colonies, and requires preventive treatment. On January 2018 we captured 22 healthy bats in Jaffa, Israel, and quarantined them in our bat facility for 4 weeks. Within the first two weeks of quarantine, five pregnant or post-partum females from the adjacent main colony of 51 bats, developed severe pyoderma of scruff and vulva and ulceration of the wings. *Staphylococcus aureus* was isolated from the lesions. Three bats with the most severe lesions were euthanized and examined post-mortem. The main findings were bacterial skin infection with extensive necrosis of skin and wings, and myocardial fibrosis, compatible with stress-induced lesions. Because there was no direct contact and no air-exchange between quarantined bats and main colony, we think the voices of the adjacent wild-caught bats increased stress to the pregnant females – which led to outbreak of resident *Staphylococcus aureus*. Four weeks post-capture, the quarantined bats were introduced into the main colony. After 4-5 weeks, sixteen bats from the original colony developed abscesses; thirteen of them were young bats born in captivity. *Staphylococcus aureus* was isolated from abscesses. To prevent spread to the other bats, the entire colony was treated with amoxicillin-LA for two weeks. Two bats developed sepsis complications, but the rest healed completely, and no further cases appeared. Following this experience, we added amoxycillin to the routine preventive treatment for wild-caught bats. No disease incidents occurred in the two captures performed since then.

AO6-127

Molecular investigation of *Polychromophilus* infection in the bat-fly *Basilia nana* from *Myotis bechsteinii* bats across Europe

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Haemosporidian parasites infect diverse vertebrate hosts and include *Plasmodium*, the causative agent of malaria. Bats host a high diversity of malaria parasites, including the genus *Polychromophilus* that is exclusive to bats. *Polychromophilus* parasites commonly infect vespertilionid/miniopterid bats and are transmitted by different species of bat flies (Nycteribiidae), highly specialized ectoparasites. One species, *Polychromophilus murinus*, has been recorded from European vespertilionid bats. Here we investigated *P. murinus* infections in the bat fly *Basilia nana*, collected from its primary host *Myotis bechsteinii* at locations across its distribution range in Europe, the Caucasus and Iran. Additionally, a subset of other bat fly species/genera from *Myotis* spp. were included in the molecular analysis. Extracted DNA of 190 bat flies was screened for *Polychromophilus* infections via PCR of *cytochrome b*. Other markers were subsequently amplified for the positive samples. *P. murinus* infections were detected in flies of every sampled region and seven haplotypes were recovered. Strikingly, two sets of distinct *P. murinus* haplotypes are present in *B. nana/M. bechsteinii,* which however are both distributed across Europe and the Caucasus. This might be explained by the apparent recent contact in the two populations of *B. nana* regardless of the complete isolation in the bat host genetics. Despite this deeper split, very low overall *P. murinus* diversity was found across Europe. However, we recovered a clear split of *P. murinus* haplotypes between the *B. nana/M. bechsteinii* and those found on other bat/fly associations, pointing to long-term host-specific associations between *P. murinus* and its various host species.

AO6-128

Population Genetic Structure and Movement of the White-nose Disease Fungus, *Pseudogymnoascus destructans*, within and between Continents

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The longstanding utility of fungi to all life on earth has often been matched by the ability to cause devastating diseases in humans, animals and plants. In animals, an unprecedented number of fungal diseases have caused some of the most severe die-offs and extinctions ever recorded in wild species, with chytridiomycosis in amphibians and White-Nose Disease in bats. Given that emerging fungal infectious diseases pose serious threats to wildlife health, food security and ecosystem stability, understanding the factors leading to their emergence has never been more urgent. North American bat species are now faced with extinction from a devastating disease caused by a fungus, *Pseudogymnoascus destructans*, recently introduced in North America from Europe, which is continuously expanding its North American range. The aims of the present study are (i) to better understand the movements of the fungus between and within continents and (ii) to characterise population structure of the fungus across Europe and evaluate whether intra-European movements of the fungus are of concern (e.g. if different geographically separated lineages exist). An extensive dataset of more than 3,000 samples from 26 countries in Europe was generated thanks to the efforts of 170 bat researchers, conservationists and other volunteers. These samples were genotyped for a set of 18 variable microsatellites in addition to mating type loci. This large genetic dataset clearly supported a European origin of the fungus but also revealed a surprisingly strong population structure of the fungus across Europe. Although our study did not specifically address the mechanisms of fungal movement, the general patterns observed are consistent with movements via bats with some exceptions that support long distance anthropogenic movements.

AO6-129

Investigating the Control and Clearance of Filoviruses and Paramyxoviruses by Egyptian Rousette Bats

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Although bats are increasingly being recognized as natural reservoir hosts of emerging zoonotic viruses, little is known about how they control and clear virus infection in the absence of clinical disease. In this study, we tested more than 50 convalescent sera from Egyptian rousette bats (ERBs) experimentally primed or prime-boosted with Marburg virus, Ebola virus or Sosuga virus for the presence of virus-specific neutralizing antibodies using homologous infectious reporter viruses. After serum neutralization testing, we concluded that antibody-mediated virus neutralization does not contribute significantly to the control and clearance of Marburg virus, Ebola virus or Sosuga virus infection in ERBs. The results of this study suggest that ERBs may rely on other antibody-mediated functions (i.e., phagocytosis or antibody-dependent cellular cytotoxicity) and/or the innate immune response to modulate infection with these viruses that are otherwise pathogenic to humans.

Advancing Bat Research in Southern Africa through Interdisciplinary Collaboration

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Globally, viruses have been identified in several bat species. However, detection in bat species does not constitute a spill-over risk, and several factors influence this. These factors are not unique to understanding emerging infectious diseases but also overlap with conservation priorities. Here we examine how interdisciplinary research and collaboration (taxonomy, ecology, virology, biology and geology) is aiding biosurveillance and conservation at two sites in South Africa, Madimatla and Matlapitisi caves. These caves are also key maternity roost for the Natal long-fingered bat (*Miniopterus natalensis*) and the Egyptian Rousette bat (*Rousettus aegyptiacus*). Longitudinal biological sampling focused on the non-destructive sampling of oral, urine and blood specimens started in 2012. Data on the bat population size, composition, age class, sex and reproductive condition were collected. Tattooing and Pit tags were used to mark and identify individuals, caves were mapped using laser technologies, and environmental data were collected. Surveillance indicated that changes in viral shedding and seroconversion patterns are driven by sex, age and reproductive condition of female bats. Population size and structure fluctuations over time, bat biodiversity, movement data and timing of reproductive seasons are used to compile conservation management plans in collaboration with AfricanBats and the landowners. This research approach highlights the complexity of infection dynamics in bat species and the importance of interdisciplinary longitudinal studies. It therefore not only generate data on the presence and risk of viral spillover but also aid in conservation management, ultimately complimenting both.

AO6-131

A target on their backs? Deriving bat conservation strategies from Marburg virus surveillance activities of Egyptian rousette bats

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Field investigations over the past 20 years, together with bat experimental infection studies, have established that cave-dwelling Egyptian rousette bats (ERB; *Rousettus aegyptiacus*) are a major natural reservoir for Marburg virus. We have consistently found 2-5% of wild-caught ERBs to be actively infected (PCR+) and have isolated more than 20 genetically diverse Marburg virus strains directly from ERB tissues. Marburg virus, closely related to the better-known Ebola virus, is associated with large human outbreaks with high case fatality. The linkage of ERBs to a deadly human virus could be perceived as being at odds with ERB conservation efforts. However, deeper knowledge of bat-virus interactions can lead to improved understanding of the public health threat and reduced destruction of ERB populations. Indeed, we have documented that unwise mining company efforts to minimize virus spillover potential by eliminating ERB populations can have opposite effects and increase virus circulation during natural bat repopulation. Such data provide critical evidence that can be effectively used by local communities and government authorities to develop evidence-based policies that will help conserve bats, such as promoting bat avoidance in domestic and peridomestic settings, encouraging safe tourism practices, and adopting anti-extermination postures when faced with a bat-borne public health concern like Marburg virus. ERBs are the only known reservoir of a human-pathogenic filovirus. Since Ebola virus, and the newly discovered Bombali virus found in bats in West and East Africa, are also likely bat-borne, conservation-minded strategies for living with Marburg virus may have universal applications to other filoviruses.

AO6-132

Coupling conservation with public health: Developing public health messaging and interventions that limit human exposure to bat-borne viruses and protect bats

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Viruses with significant human health impacts such as SARS coronavirus, Marburg virus, and Nipah virus have been linked to bat reservoirs. Human or domestic animal infection is frequently the result of activities that promote contact with bats. SARS coronavirus emerged through the wildlife trade which brought bats into wet markets in southern China and Nipah virus emerged in Malaysia and Bangladesh through wildlife resource provisioning (e.g. mango cultivation next to pig enclosures in Malaysia and date palm sap harvesting in Bangladesh). When emerging zoonoses are associated with bat reservoirs, there is the potential for government interventions or public reaction to focus on removing or exterminating bats rather than identifying and disrupting routes of spillover. In instances where disease investigations include host ecology, epizootiology, and bat-human interactions, more balanced recommendations that reduce the risk of spillover and avoid damaging actions towards bats or other wildlife can be achieved. Here we discuss two examples where surveillance and ecological research of bat-borne zoonotic viruses: Nipah virus in Bangladesh and Ebola virus in Liberia, in partnership with government ministries under a One Health framework, has led to public health messaging that included positive messages about bats and promoted interventions that reduce the risk of exposure and avoid harming bats or their habitat.

AO6-133

Linking Biodiversity Loss Mitigation and Infectious Disease Prevention

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As people, we modify our environments continuously. Mitigating the biodiversity crisis is one of the largest challenges we face. The interactions between people and biodiversity, including bats, is potentially complex. Disease causing microorganism diversity likely correlates with the host diversity, but similarly possible dilution effects may help mitigate the actual disease risk from species rich environments. Among the trillions of microbes on Earth, which exceeds all other diversity, a tiny number of these can cause disease in us, and even fewer of these have bats as hosts. Here, I will discuss how bats and emerging infectious diseases from bats can be linked to habitat fragmentation and other pressures, such as hunting. I will present an overview of current theories, along with a recently developed model that links the species–area relationship to novel infection emergence from forests and studies linking forest changes and Ebola virus emergence, in order to provide a framework that might provide win-win scenarios for human health and biodiversity conservation.

Molecular Adaptations Underpin Dietary Diversification and Specialisation in New World Bats

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The molecular adaptations underpinning dietary specialisations are poorly understood. Among mammals, the bat family Phyllostomidae (New World leaf-nosed bats) has undergone extreme diversification linked to diet, with different lineages specializing on fruit, nectar, insects and blood. To determine whether these evolutionary transitions have involved molecular adaptation in different sets of loci and pathways underpinning metabolism and morphology, we performed genome-scale screens across 66 bat species. We find that genes under selection in branch leading to the ancestral phyllostomid encode proteins with diverse roles in carbohydrate, protein and lipid metabolism, consistent with adaptation for a generalised diet. At the same time, we detect surprisingly little subsequent selection in the branch leading to frugivores, but a second burst of molecular adaptation for carbohydrate metabolism in the nectar-feeding bats. Vampire bats, on the other hand, show strong selection for the excretion of waste products. Our findings open up new opportunities for studies of metabolism in bats and other mammals.

Rapid changes in bat demography and social structure following large-scale habitat disturbance: the case of hydroelectric dam flooding

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Growing energy demands and its consequences on global climate led to a worldwide increase in the investment towards ‘clean’ energy, with hydropower still dominating the market. The later causes rapid and permanent habitat loss due to flooding of upstream terrestrial and riparian areas. Studies on the potential impacts of hydroelectric dams usually address changes in species presence/absence and abundance, but they fail to quantify the demographic processes underlying population declines. Focusing on the European free-tailed bat (*Tadarida teniotis*), we provide for the first time insights on the immediate effects of a hydroelectric dam on species demography. We monitored five roosts in road bridges before, during and after habitat alteration caused by the dam filling. We captured and marked 3821 individuals while also taking genetic samples. Using Capture-Mark-Recapture models, we estimated annual population size, individual survival and movement probability. We genotyped 1407 individuals to compare relatedness among years and roosts. Our results showed an overall increase in the number of bats using bridge roosts after dam filling along with a decrease in relatedness at the breeding roosts located at the centre of the flooding area, but not upstream. Movement probability between roosts was low suggesting high roost fidelity. Apparent survival was not affected by flooding confirming that long-lived species maximize adult survival during stressful periods. Taken together, these results suggest a change in the dynamic of *T. teniotis* population with unpredictable medium to long-term consequences on the reproductive success and survival of individuals forced to switch roosts after flooding.

AO10-100

Attitudes and Behaviors of Indigenous People Toward Flying Fox Hunting in Agusan Marsh Wildlife Sanctuary

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Protected areas like the Agusan Marsh Wildlife Sanctuary (AMWS) in Mindanao, Philippines are vital to conserve and protect wildlife and their habitats for ecological balance and sustainability. However, illegal activities such as flying fox hunting within and around AMWS may undermine its conservation goals. Despite the existence of the National Protected Areas System (NIPAS) Act (RA 7586) and Wildlife Act (RA 9147), flying fox hunting is still rampant in the AMWS. We used information from 120 direct interviews with flying fox hunters in order to understand the factors affecting illegal behaviors related to flying fox hunting in two hunting hotspots within the sanctuary. We explored correlations between demographic and socio-economic factors, knowledge and awareness, attitudes, norms, perceived behavioral control and behaviors toward different motivations for hunting (consumption and trading) and behaviors towards hunting quantity based on insights from the Theory of Planned Behavior. Our results suggest that knowledge, socio-economic and demographic factors influenced hunter's attitudes, perceived norms and behavioral control. We also found that the Theory of Planned Behavior components such as attitudes, norms, perceived behavior control and behavioral belief strength may be good predictors of the studied flying fox hunting behavior. Increasing the knowledge of local people regarding the ecological importance of flying foxes and improving Wildlife Act enforcement is essential for more efficient flying fox conservation in AMWS. Findings imply that to change hunting behavior toward flying fox conservation in AMWS, management interventions to reduce hunting threats should consider hunter's knowledge, awareness, attitudes, norms and background factors and their interrelationships.

AO10-101

An island wide effort to understand and address flying fox trade in Sulawesi, Indonesia

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Flying foxes have been hunted intensely in Sulawesi to satiate demand for bushmeat in the north. Lack of protective status for two commonly traded species, *Acerodon celebensis* and *Pteropus alecto*, causes overexploitation that threatens species persistence. A project to understand and address flying fox trade was conducted from 2018 to 2019 involving universities, research institutions, local communities, and conservation NGOs. We focused demand-oriented actions on North Sulawesi, where the bushmeat markets are, and supply-oriented actions on South Sulawesi, where most hunting occurs, and brought together stakeholders from both provinces to gain insight on trade and hunting, roosts, and important cultural and religious factors to consumption. We then designed activities to address these findings, including hunting surveys, social surveys, community-based roost protection, and demand reduction. Students conducted hunting and social surveys and found an expansion of hunting to Southeast Sulawesi and West Nusa Tenggara, neutral to negative attitudes about flying foxes, and hunting being tightly linked to livelihoods, while consumption was affected by cultural beliefs. The constant supply to the markets masked the impact of intense trade and lack of regulation meant there were no legal deterrents to consumption. The level of consumption among students was low, and they showed increased knowledge and awareness about flying foxes. We also supported the local community in South Sulawesi in establishing their flying fox ecotourism program by providing information boards and guidance. These project outcomes may act as a model for other flying fox conservation programs in Indonesia.

AO10-102

How to tell kids to not eat bats? A case study of outreach programs in North Sulawesi, Indonesia

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North Sulawesi has extensive bushmeat markets with flying foxes as one of the most commonly traded animals. High demand for flying foxes puts pressure on wild populations as hunting activities are now pervasive in many parts of Sulawesi and expanding to nearby islands. Lowering the level of consumption through outreach programs is one potential way to reduce this demand. We conducted an outreach program from March to April 2019 using storytelling targeting seven to ninth graders at schools in four districts in North Sulawesi, with a total of 113 students involved in this study. The story contained two key elements: 1) the intertwined relationship of forests, people, and bats to increase student knowledge, and 2) similarities between bats and people (*e.g.* moms raising their children) to improve student attitudes. To determine the success of the programs, we conducted pre- and post-assessments and tracked bushmeat consumption of each student for over a month. Every Monday, students placed stickers (egg, tofu, chicken, monkey, bats, etc.) about their meals for a week on a board in their classes. Flying foxes were the most frequently consumed by the students (6-10%) compared to the other wild meats. We compare student knowledge before and after the storytelling using cumulative link mixed models and found that there was an increase in understanding about flying foxes as beneficial to forests and people [(x^2=196.62, $p<0.05$ (forests), x^2=118.75, $p<0.05$ (people)]. The level of consumption gradually decreased after the outreach, indicating a changed behavior among the students.

Indigenous Children and Flying Foxes: their hunting attitude and behavior in Agusan Marsh Wildlife Sanctuary, Philippines

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The Agusan Marsh Wildlife Sanctuary (AMWS), like many other protected areas in Mindanao Island, Philippines harbors many threatened species. However, the near-threatened *Pteropus vampyrus* is known to be threatened by hunting in the sanctuary despite its protected status. Surprisingly, indigenous kids from 9-15 years old were involved in this illegal activity in the sanctuary using the kite-trapping technique. We conducted semi-structured interviews with 50 kids in two flying fox hunting hotspots in AMWS through the help of Key Informants. The socio-demographic and economic background of the young hunters and their knowledge and awareness of flying foxes were determined. We assessed their perceived norms, perceived behavioral control, behavioral belief strength, intentions and hunting behavior (hunting quantity) based on the Theory of Planned behavior. Their trading attitudes and behavior were also determined. Results showed that poor indigenous kids were mostly involved in illegal flying fox hunting as kite trapping assistants to adult hunters for consumption. They were also involved in trading for quick cash or allowance in school. Most of them revealed that they were aware about the hunting restrictions but the majority of them were not aware of the ecological services of flying foxes and the effects of unsustainable hunting. Most of them found kite trapping as risky but fun and exciting activity. More rigid monitoring, stricter law enforcement, information campaign with emotional appeal to kids and integration of flying fox conservation in elementary education curricula will change the hunting behavior of the young generation towards flying fox conservation in the AMWS.

AO10-104

Flying fox hunting and conservation in northeast Luzon, Philippines

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Three species of flying foxes are found in northeast Luzon: the solitary-living *Desmolopex leucopterus* (endemic, not threatened) and the colony-roosting *Pteropus vampyurus* (Southeast Asia, near-threatened) and *Acerodon jubatus* (endemic, Endangered). Three large roost sites were identified with the latter two species in the northern Sierra Madre Mountains where *P. vampyrus* and *A. jubatus* roost together. All three species are nationally protected. Nevertheless hunting is a threat to all three species, both near fruiting trees in the foraging area and in roost sites. Roost site counts have been conducted irregularly since 2000 and annually since 2015. Interviews were conducted in communities near the three roost sites. Here we report on the characteristics of the roost sites, the roost site counts and on hunting methods and locations, hunting volumes and trade in flying foxes. In addition we tried to understand the motivations, beliefs, norms and intentions that all influence hunters behaviors by using Theory of Behavior inspired questionnaires. The interview surveys led to the development of a theory of change and to specific activities to influence hunters and traders to decrease hunting pressure on and enhance conservation of flying foxes in northeast Luzon.

AO10-105

Understanding flying fox hunter motivations in Southeast Asia as a basis for conservation

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Hunting of flying foxes or giant fruit bats for food, traditional medicine and sport is widespread in Southeast Asia, and species are traded in markets across the region. Intense hunting pressure in combination with a limited capacity for recovery threatens species persistence, and hunting is identified as a threat to two-thirds of the 31 species of flying foxes in Southeast Asia. Flying fox declines are of intrinsic concern, but they are also of great environmental and economic importance because flying foxes provide regionally important ecosystem services as local, transregional and even transoceanic seed dispersers and pollinators. Hunting of flying foxes disrupts these ecological services, and flying foxes can lose their ecosystem functionality even before becoming rare if their numbers drop below a density threshold. Although some information is available about hunting intensity and trade in flying foxes, the full extent of the problem in Southeast Asia is not well understood. Flying fox conservation measures to reduce hunting have been implemented in several countries, but their success or failure has often not been evaluated. Flying fox conservation must target human behavior, but comprehensive information on the drivers, extent and consequences of hunting that can inform intervention and change behavior is lacking. This presentation presents a pilot project that is currently underway in Indonesia, Malaysia and the Philippines to better understand flying fox hunting and hunter's attitudes, subjective norms and perceived behavioral control towards flying fox hunting with the goal to be able to influence hunter's behaviors and reduce flying fox hunting.

AO10-106

Addressing flying fox hunting in the philippines through empowerment of local governments and communities

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A total of 84 species of bats occur in the Philippines of which 27 are endemic to the country and 10 are flying foxes. Among the 10 flying foxes, six are endemic to the country. The recent assessment conducted by the Biodiversity Management Bureau of the Department of Environment and Natural Resources (BMB-DENR) and Philippines Biodiversity Conservation Foundation Inc. (PBCFI) showed that of the 103 known roosting sites only seven roosts are inside Protected Areas and the rest are either in timberland areas, private land or mineral reservations.

Flying foxes are protected species in the Philippines as mandated under Republic Act 9147 or the Wildlife Conservation and Protection Act of the Philippines. Despite this and other national laws, hunting of flying foxes still occurs in a number of sites in the country. It is noteworthy to also mention that in the last 10 years, local government units in partnership with local organizations, communities and DENR have initiated conservation programs directed towards flying foxes conservation. This paper presents experiences of local government units in taking the lead in integrating the conservation of flying foxes in the local development programme. Challenges and development impacts on the population of the flying foxes, local communities and the habitats are also presented.

AO10-107

Severe declines in *Pteropus* spp. sightings throughout peninsular Malaysia – an effect of intense hunting and persecution?

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Only two species of flying fox (*Pteropus* spp.) are found in peninsular Malaysia: *P. hypomelanus* and *P. vampyrus*. Both are in severe decline, with hunting pressure and habitat destruction thought to be the main drivers. Both species are accordingly classified as 'Endangered' on the Red List of Mammals for Peninsular Malaysia. In order to formulate appropriate conservation action, current and accurate data on the occurrence and abundance of populations across the landscape is crucial. As such, we conducted a flying fox roost and population survey across the Peninsula. Previously known roost sites were visited from October 2018 to July 2019 to determine whether flying foxes were roosting and/or foraging in the area. We were successful in locating and quantifying populations of *P. hypomelanus*, which were only found on islands. However, we were unable to verify or access any *P. vampyrus* populations on the mainland, even in areas with previous presence and remaining habitat, although occasional foraging in villages was reported by local people. *Pteropus vampyrus* is thought to still roost in available mainland habitat such as forests, mangroves, and swamps, but specific locations were unknown, and difficult to access. Hunting was commonly reported as happening whenever flying foxes were sighted by locals on the mainland. This suggests that the remaining flying fox populations in Peninsular Malaysia are deliberately avoiding humans as a behavioural response to hunting and persecution. Apart from inaccessible wetlands, small offshore islands also appear to be the last remaining refuges for flying foxes across peninsular Malaysia.

AO10-108

Drivers of Human Behaviors: The Theory of Planned Behavior and Flying Fox Hunting in Southeast Asia

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Although many threats to bat populations derive from the degradation and loss of foraging and roosting resources, direct mortality from hunting and/or persecution threatens 10% of bat species globally and more than a third of Old World fruit bats (Pteropodidae) (IUCN 2018). Sensitization and outreach campaigns that vaunt the importance of bats may change values over generations, but effective real-time interventions need detailed insight into behavioral drivers of the action of concern. The Theory of Planned Behavior (TPB) provides a conceptual framework to interrogate the motivations of human behavior that has been used in psychology for more than 30 years. The TPB posits that human behavior is guided by beliefs about: the likely consequences of the behavior (behavioral beliefs); social pressure to perform or not perform the behavior (normative beliefs); and whether people feel they have the resources, opportunities, or abilities to perform the relevant behavior (control beliefs). More recently, the TBP has been applied to environmental and conservation behaviors that range from littering to illegal hunting of tigers. Here we introduce the TPB and detail its use as a conceptual framework to understand the diverse drivers of flying fox hunting across Southeast Asia.

AO10-109

Bat Hunting Overview: Which bats are hunted and how can we measure population-level impacts?

Tammy Mildenstein

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Bat hunting for consumption (bushmeat and medicine) is widespread and affects at least 167 species of bats (13% of the world's bats). Hunting is particularly prevalent among the large-bodied fruit bats of the Old World tropics. Half (50%, 92/183) the extant species in the family Pteropodidae are hunted, and these are six times more likely to be Red Listed as threatened than non-hunted pteropodids. However, there still appear to be knowledge gaps at the international level. One third of hunted bat species on the Red List are not considered threatened by hunting, and nearly 1/4 of the hunted species in this review are not listed as hunted in IUCN's species accounts. Research methods for understanding population impacts of hunting should include comparing rates of hunting mortality to population growth. However, the data required for this type of analysis are difficult to obtain. Other methods include using indices to population growth and/or hunting mortality, market and hunter surveys, and comparing hunted to non-hunted populations. In the Philippines and the Mariana Islands, I have been comparing bat population sizes to hunting pressure for three commonly-hunted species of large fruit bats. Results across 27 colonies (23 islands) suggest hunting pressure reduces the carrying capacity of roost sites by 10-85 times. A local non-profit awareness campaign in the Philippines responded to these results by promoting community-based roost site protection programs for threatened fruit bats. This conservation approach has proved successful and has gained endorsement by the national government.

AO11-105

Attitudes and emotions towards bats in northwestern Cambodia

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Bat populations are declining worldwide because of a variety of human activities, including habitat destruction and bushmeat harvest. Bats provide critical ecosystem services, such as agricultural insect pest suppression, pollination, and guano for fertilizer. Cambodia represents an important case study for exploring stakeholder relationships with bats, as Cambodians have a long-established relationship with caves, and have a history of the consumption of bats as bushmeat. Cambodia contains approximately 20,000 km^2 of unprotected and largely unexplored karst. These karst habitats, and the bats that inhabit them, are under imminent threat because of increased limestone mining operations. To effectively conserve bats, it is essential to understand human attitudes and perceptions of this taxon. We interviewed 60 key informants around karst areas in northwestern Cambodia to determine the following: 1) people's attitudes and emotions towards bats, 2) people's knowledge of bat ecosystem services, 3) the cultural importance of bats, and 4) perceived zoonotic disease risk associated with bats. Most respondents (70%) held positive attitudes towards bats and listed guano production, pest control, and tourism as common ecosystem services. Additionally, all informants believed that bats should be protected and stated that they would feel sad if bats were extirpated. Conversely, respondents noted that many people eat bats despite knowing the disease risks associated with the activity. The well-recognized ecosystem services bats provide Cambodians indicate they would support bat conservation policy and may be interested in developing robust, community-based conservation plans around local karst outcroppings.

AO11-106

Gauging attitudes of residents living close to flying-fox camps to inform conflict management

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Australian flying-foxes are becoming increasingly urbanised, and camps (roosts) are a source of mounting tensions with human communities. Local government agencies manage camps in response to complaints from residents, but acknowledge that it is difficult to capture the full range of views that are present in their communities. We conducted 49 semi-structured interviews, and sent 5000 surveys to residents living close to flying-fox camps across south-east Australia. These covered perceived impacts of camps, resident's values around nature, and their perceptions of management agencies. We found that sensory impacts and fear of diseases were the key concerns for residents. Some perceived the bats to be destructive and messy, and felt they impacted on their quality of life. Yet, positive associations were also common, such as appreciation of the ecological role that flying-foxes play, and a sense of awe and wonder from viewing them. Almost everyone stated that they loved wildlife, but in some cases this did not extend to the bats. Residents with strong opinions were divided between those that felt the rights of humans should take precedence, versus those who thought humans had to learn to live in harmony with wildlife. Many acknowledged that long-term dispersals of flying foxes are costly and associated with substantial risks. Management of contentious flying-fox camps in ways that satisfy community concerns is likely to remain a difficult and complex task.

AO11-107

Understanding Cultural Symbolism and Use of Bats in Southeast Asia for Conservation Interventions

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Modern-day chiropterophobia can trace its roots to medieval European mythology, while the East Asian regard for bats as symbols of luck and blessing has only been given recent recognition after years of neglect from global mainstream culture. In an attempt to understand local beliefs and practices surrounding bats, we investigated the cultural symbolism and use of bats in Malaysia and the rest of Southeast Asia. Particularly, we explore the intersections between conservation strategies and local belief systems with implications on designing appropriate conservation interventions for bats and their habitats. Through a preliminary desktop review and informal interviews with different stakeholders, we collated cultural information involving bats throughout the region and found a wide spectrum of perceptions ranging from negative to neutral to positive. Building upon these cultural profiles, we suggest employing targeted and locally contextualized outreach strategies that are culturally appropriate in order to carry out more effective bat conservation and awareness-raising in Southeast Asia.

AO11-108

Using social marketing approaches to improve attitudes towards the Mauritian fruit bat

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Understanding people's behaviour, and the attitudes that influence their actions, is an underappreciated prerequisite for wildlife conservation, and it is frequently necessary for conservationists to seek to influence people's behaviours in a pro-conservation direction. To succeed, conservation must ensure that it engages collaboratively with local communities to develop sensitive and effective behaviour change interventions. The disciplines of marketing, consumer psychology and behavioural economics have extensive practical expertise in understanding and influencing people's attitudes and behaviours – This talk will explore the effectiveness of social marketing approaches in the context of wildlife conservation ask how these disciplines can be used to improve people's attitudes towards the endangered Mauritian fruit bat in the face of wide spread government culls of the species.

AO13-100

Education and sensitization of Mauritians to conserve the Mauritius fruit bats, *Pteropus niger*

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Ecosystem Restoration Alliance Indian Ocean

The Mauritius flying fox, *Pteropus niger* (Chiroptera, family – Pteropodidae) is threaten by numerous factors but its survival chances are further imperiled by human behavior towards the species. With continuing loss of their natural food sources, as forested areas are cleared, bats are damaging commercial fruit crop. As such, they are considered as pest and lethal approaches like culling was implemented thrice since 2015. In addition of research for damage mitigation by bats, there is an urgent need to educate and sensitize the local population and mainly the youth regarding the vital ecosystem services namely pollination and long distance seed dispersal provided by this keystone species. Owing to that, a minimum of 30 % of both primary and secondary schools in Mauritius was targeted for educational talks pertaining to the ecological importance of pteropodid bats. Each school was visited once or several times, depending on the number of students. Moreover, in order to test knowledge and attitude of Mauritians towards the fruit bats, specifically age-targeted questionnaires were distributed to each participants. Following this, a presentation was given on the vulnerability of Mauritian fauna and flora, the disproportionate role of bats in ecosystems, the ongoing conflict with fruit growers and measures to effectively mitigate bat damage. Subsequent to the talk, each participants was given the same questionnaire again. Educational posters in both English and Mauritian creole were also distributed to all schools. Same methodology was applied to community and social welfare centers across the island, where most orchard owners and backyard fruit growers are gathered. Data collection from the surveys is still ongoing and a thousand questionnaires per age group is targeted by the end of the year. So far, of 516 (n = 516) questionnaires that were distributed, 481 were returned fully completed. These surveys will help predict human attitude which will be measured using the Theory of Planned Behaviour since it is the most widely used means of measuring attitudes towards an attitude object. Conclusively, the project's main goal is ensuring that local communities at different age classes are exposed to conservation issues in Mauritius and importance of ecosystem and biodiversity as well as appreciate natural heritage.

Key words: Theory of Planned Behaviour, human-wildlife conflict, human behavior, beliefs, conservation

AO14-101

Using GPS Tracking Research for Applied Conservation in Livingstone's Fruit Bats

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The Critically Endangered *Pteropus livingstonii* has a population of around 1200 individuals spread between 22 roost sites on two islands of the Comoros archipelago in the Western Indian Ocean. This large-bodied species is primarily threatened by ongoing forest habitat loss: out of the 15 known roost sites on the island of Anjouan, only three are not under immediate threat from agricultural activities and timber extraction. Conservation schemes for this species require a thorough understanding of the bats' remaining population and ecological needs.

In addition to annual population counts, in place since 2012, a first study in the bats' resource and habitat use has been conducted. Two individuals, one male (M) and one female (F), were equipped with GPS-loggers that collected data between January and March 2019 in the south of Anjouan, Comoros. Analysis of movement and spatial data resulted in first reports on home range sizes (minimum convex polygon: M = 14.2 km^2; F = 24.5 km^2), ranging, roost switching behavior and locations of feeding sites utilized during the wet season.

The results of this study will inform areas for participatory biodiversity monitoring and tree species to be used in reforestation campaigns. Identification of important feeding sites will allow an existing participatory conservation scheme, currently directed at local landowners around roost trees, to cover key feeding zones. These measures will increase the efficiency of in-situ conservation management of this rare fruit bat.

AO14-103

Extreme Nomadism of Fruit bats Poses Key Challenges for Management and Conservation

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Effective conservation management of highly mobile species depends upon detailed knowledge of movements of individuals across their range, yet data are rarely available at appropriate spatiotemporal scales. Fruit bats (*Chiroptera: Pteropodidae*) include the largest mammals capable of powered flight, and their capacity to move long distances makes them key seed and pollen dispersers in forest ecosystems. However, their mobility also brings them in conflict with humans and facilitates transmission of zoonotic diseases. Here we analyze the Australia-wide movements of 201 satellite-tracked individuals, providing unprecedented detail on the inter-roost movements of *Pteropus alecto* (n = 80), *P. poliocephalus* (n = 109) and *P. scapulatus* (n = 12) over up to five years. Individuals wandered thousands of kilometers among a total of 755 roosts (*Pteropus poliocephalus*: 2,268-2,564 km yr^{-1}; *P. alecto*: 1,427-1,887 km yr^{-1}; *P. scapulatus*: 3,782-6,073 km yr^{-1}), but with little uniformity among their directions of travel, suggesting a lack of common drivers to their movements. Roost site fidelity of individuals was low in all three species, resulting in extraordinarily high estimated turnover rates of fruit bat colonies locally (*P. poliocephalus*: 17.5±1.3% day^{-1}; *P. alecto*: 11.9±1.3% day^{-1}; *P. scapulatus*: 36.4±6.5% day^{-1}). Thus, fruit bat roosts form nodes of a vast continental network that sustains highly dynamic populations of extremely nomadic individuals moving at species-specific rates. We discuss the profound implications for fruit bat ecosystem services, human-wildlife conflict and zoonosis, and emphasize the importance of studies of this kind to support evidence-based conservation management of mobile species.

AO14-104

Bats and Typhoons: What Do Stronger and More Frequent Storms Mean for Large Fruit Bats?

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Over two thirds (58/86) of flying fox species live on islands that regularly experience typhoons/hurricanes. The biology, ecology, and taxonomy of these large fruit bats reflect an evolution with storms that has allowed them to persist despite such extreme weather events. However, future conservation management will depend on anticipating effects of increases in typhoon frequency and severity caused by global climate change. As a case study, I reviewed population level responses of fruit bats to typhoons in the Mariana Islands. Typhoons have resulted in immediate reductions of 16-32% of fruit bat populations. Even greater population losses (up to 70%) were attributed to post-typhoon starvation and illegal hunting by local communities. Long-distance dispersal appears to provide a refuge for bats from typhoon-affected islands. Four times in the past 30 years, fruit bat population increases have been observed on Guam after severe storms on nearby Rota. In 2015, 120+ fruit bats arrived on Guam after Typhoon Delfin. I analyzed non-invasive DNA from these immigrants and found genetic signatures matched the Rota bat population. Looking at haplotype diversity as a possible indicator of storm-directed gene flow, I analyzed fruit bat population genetics across the Mariana Islands and show occasional movement among the islands that corresponds with the frequency of strong storms. Genetic structure across the archipelago is moderate but suggests an isolation between the northern and southern islands. Conservation management should focus protection efforts on facilitating stable dynamics of fruit bat metapopulations to sustain persistence of fruit bats in their native island ecosystems.

AO14-105

Fruit bats in Singapore – what have they done for us lately?

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The ecological importance of *Cynopterus brachyotis*, especially as a seed disperser, was already well-documented in tropical forests. We were interested in its role in the urban context. Given that urbanisation alters the species composition of plant communities, we set out to study this bat's diet, thereby generating insights into how ecosystem services by tropical bats could be affected by urbanisation.

In Singapore, whose urbanisation rate is 100 %, *C. brachyotis* is the most common bat. We documented its diet to test the hypothesis that urbanisation reduces both dietary breadth and representation by native plants. We collected droppings under roosts at nine sites and used morphological and molecular methods to identify the plants they contained. We specifically asked whether species richness, proportion of native species and composition of plants in diet varied with various urbanisation metrics.

We detected 33 plant species from 25 genera and 21 families. Ten species are native, 17 are exotic, and 12 have never been reported in the diets of *C. brachyotis* anywhere. In contrast to our hypotheses, urbanisation was associated neither with reduced dietary breadth nor declining reliance on native plants.

Our results suggest urban *C. brachyotis* have adopted a generalist approach to foraging and can readily exploit exotic plants as food. Because urbanisation does not affect dietary breadth or the proportion of native species they eat, these bats can potentially provide ecosystem services by dispersing seeds of native plants even in the most urbanised sites, which could aid succession in degraded landscapes.

AO14-107

Distributional Ecology of *Pteropus lylei*: Conservation Implications for Vulnerable and Disease Reservoir Species

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Small range species can be highly vulnerable to a warming climate, highlighting the fact that assisted migration has potential as a conservation strategy for species threatened by climate change. Ecological niche modelling (ENM) represents a widely used tool in ecology, evolution and biogeography. It can be used to assess climate sensitivity and potential climate impacts, even for rare species. The Lyle's flying fox (LFF; *Pteropus lylei*) is listed as Vulnerable on the IUCN Red List due to substantial population declines and in Appendix II of CITES. Threats of LFF decline are thought to vary to some extent across geographic regions. The ecological niche for LFF was modelled using Maxent, combining presence data in Thailand, Cambodia and Vietnam with a global bioclimatic 15-variable dataset for the 2000s. The ENM estimated potential distributional area for LFF corresponded roughly with known range limits and with the occurrence data on which they were based. Results from the evaluation analyses showed good performance (the AUC = 0.974). The maximum temperature of warmest month, precipitation seasonality and minimum temperature of coldest month were the most important factors limiting habitat suitability of LFF. Our results suggest that niche modeling approaches can be used to map distributions of environmental suitability for LFF. This information can be used for conservation and land managers concerned with preserving LFF. In terms of LFF's role as the main reservoir of Nipah virus (NiV), this study could be supported by inferring potential risk areas of NiV transmission from LFF to humans in Southeast Asia.

AO14-108

Managing human/flying-fox conflict in Australia

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Ecosure Pty Ltd

Flying-foxes (*Pteropus* spp.) are nomadic pollinators and seed dispersers that are crucial for recruitment and maintenance of Australian forest systems. Over the last 200 years, expanding urban areas with year-round food supplies, loss of habitat, and other factors have brought flying-foxes and humans into closer contact. Negative outcomes to both groups include threatened flying-fox populations, cross-species transfer of virulent disease, impacts to living space and amenity.

Managing the interface between flying-foxes and humans is challenging. Community education can reduce public misconceptions about flying-foxes and eventually encourage tolerance and guardianship of these animals. Physical buffers created between flying-foxes camps and sensitive human activities may improve amenity and foster co-existence. Alternatively, relocation of animals through roost disturbance, or habitat modification may be an option. However, it is currently impossible to predict where disturbed flying-foxes will relocate; and costly, well-considered attempts at directed relocation have generally been unsuccessful. Similarly, the long-term effects of forced relocation on flying-fox population health and viability are not well understood. Finally, policy discrepancies across political jurisdictions add complexity to the conflict management challenge. There is a need for a strategic and evidence-based national flying-fox management plan aimed at reducing human-wildlife conflict and ensuring flying-fox conservation.

Long-term conflict resolution ultimately depends on suitable foraging and roosting habitat in natural areas, and governments are now investing to identify and protect these areas. Reverse engineering habitat in high conflict locations may also be required to incite animals into more traditional and low conflict areas.

How to Get an Endangered Ecological Keystone Flying Fox Species Mass-culled: the Mauritius Example

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Pteropus species typically combine important ecological roles as pollinators and seed disseminators with elevated endangerment levels making them particularly high priority for conservationists. In addition to several threats typically besetting biodiversity, Flying Foxes face mounting persecution over their consumption of commercial fruits, for which solutions are urgently required. Here we examine a particularly severe example of worsening human-wildlife conflict centered around *Pteropus niger*, the last surviving of three *Pteropus* species on Mauritius. We investigated the ecological role of the species through frugivory in native habitats and analyzed circumstances leading to the species' repeated mass-culling despite its threatened status. *Pteropus niger* appears to carry out one of the most important ecological role known of a Flying Fox by feeding on fruits and potentially disseminating seeds of a quarter of native woody plants which contribute just over half of the woody individuals and about 63% of the biomass of native forests. Its mass-culling takes support mainly from a disregard of this ecological role, combined with a specifically weakened biodiversity conservation law and a contra-evidence approach. While scientific evidence remains important to guide policy, Mauritius showed that best available evidence can easily and repeatedly be discarded in pursuit of lobbyist and political interests instead, irrespective of the outcome of mass-culling campaigns. Mauritius thus provided an excellent example of the limits of relying too heavily on evidence and reason to try swaying a government's plan away from culling a threatened species and show the importance of including broader and more impactful strategies, including litigation.

AO14-110

Bats roles in pollination networks were driven by plantation and urban landscape.

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Nectarivorous bats are essential to the functioning to both agricultural and natural ecosystems, yet these pollinator communities are declining with progressive habitat loss and direct hunting. Habitat changes leading to roosting and floral resource loss is the most important cause of bats pollination decline. This study aims to determine how the bats pollination networks in mixed-fruit orchards are affected by different land-use types. We estimated the abundance of nectarivorous and frugivorous bats using video observations to determined floral visitation rates from 18 mixed-fruit orchards in Southern Thailand. A pollination network was then created species level indices including degree, strength, and generalized degree were calculated for each bats group at each orchard. We found that nectarivorous bats showed higher value of degree, normalised degree, and strength than frugivorous bats. The degree of nectarivorous bats was positively influenced by the proportion of plantation within 2 km (proximal scale) whereas the degree of frugivorous bats was positively affected by the proportion of urban area within 30 km (broad scale). The normalised degree of frugivorous bat, but not nectarivorous bats increased with the proportion of urban area within 30 km radius. The network strength of bats was positively correlated with proportion of plantations within 2 km radius. Our results clearly show that both bats groups are strongly integrated in pollination networks where they occur and provide solid evidence that increasing the area of plantation and urban change the degree of generalization of pollinators which can significantly impact pollination success to plants.

Key words: landuse, mixed-fruit orchard, network strength, normalised degree, generalization

AO14-111

From Genes to Ecosystem: Fruit bats and their diet in a lowland forest in the Philippines

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The importance of fruit bats as primary seed disperser and pollinator has long been recognized. However, there are few studies on the ecology of these species and their interaction with the environment in the Philippines. The research program was developed as part of the International Long-term Ecological Research network and Global Earth Observatory Network. It aimed to document patterns of genetic, species diversity, community assemblage, and diet of fruit bats in various vegetation types. The research site is within the Northern Sierra Madre Natural Park, the largest protected area in the Philippines that supports 10 of the 12 forest formations known in the country. The research study employed the use of radio telemetry to study fruit bat home range and population density. Mist nets were used to determine diversity and abundance of fruit bat in various lowland vegetation types for habitat association study. Identification of fruit bat diet was made through Next-Generation Sequencing of seeds from the bat fecal samples and collection of pollen from individual bats captured. Population genetics study of fruit bats was done through DNA barcoding. The initial results of the study have been submitted for publication and currently under review. Understanding the mechanisms and processes that influence population dynamics of fruit bat in an unmodified forest is important in the conservation of the species and their habitats. Future research work will focus on food preference of fruit bats and satellite telemetry of flying fox to elucidate further the role of fruit bats in forest maintenance.

AO15-100

Neural codes for bats' natural navigation: representation of space, time, and conspecifics

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In the last 20 years, major advances have been made in elucidating the neural basis of spatial navigation; yet, several fundamental questions remain open – such as the mechanism responsible for encoding 3D space, or the impact of social environment on the brain's navigation system. The work in our lab focuses on understanding the neural basis of spatial navigation, using the Egyptian fruit bat (*Rousettus aegyptiacus*) as our animal model. Our approach relies on conducting neuroscience experiments in complex, large-scale, naturalistic settings, as well as in social settings. In my talk I will present some of our recent studies exploring how the brain represents positions and directions in 3D environments. I will describe our recent discovery of "social place-cells" in the bat hippocampus – neurons that represent the position of other bats (conspecifics). I will further describe the mechanism by which the brain represents time, related both to the bat itself and to its conspecifics. Finally, I will present ongoing work aimed at elucidating hippocampal neural codes in bats flying in realistic, kilometer-scale environments – where we discovered an unexpected multi-scale coding of space.

AO15-101

Hindlimb Steerage: Analysis of Running Gaits in the Common Vampire Bat

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The Common Vampire bat, *Desmodus rotundus*, have a bounding gait that is efficient when compared to other similarly sized mammals (Hermanson et al., 2017). We studied gait in over 30 vampire bats that ran on a motorized treadmill. Speed was variable between about 0.23 and 0.75 m/sec allowing bats to either walk or "run," the latter being a bounding gait. Bats ran for upwards of 10 minutes. This report focuses on the locomotion employed by the bats, and the consistency of their gait. Vampire bats are unique among the living bats in their expression of a terrestrial running gait. The ability of the vampires to deftly fold their wings and to run with ground contact at the carpals and extended "thumbs," allows these bats to accomplish what few others can. Compared to suspensory locomotion in bats, during which peak vertical forces are observed in hindlimbs, we observed reduced hindlimb contact with the ground during running locomotion, with a duty factor for the hindlimb of only 0.26 to 0.35. This contrasts with a duty factor of 0.49 to 0.67 for hindlimbs during slower walking gaits. Even at running speeds where hindlimb duty factor is low, forelimb duty factors remain at or above the 0.50 levels. The hindlimbs appear to coordinate (steer and stabilize) the bats at fast running speeds and contribute little to vertical force distribution or thrust production.

AO15-103

The impacts of agricultural and urban expansion on the gut microbiota and conservation of desert bats

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Understanding how human-mediated land use changes affect species is a major challenge for biodiversity conservation. We studied the effects of such changes on desert bats, focusing on the deserts of Israel, where rapid and extensive land use changes have occurred since the 20th century. Irrigation and water transportation have enabled the spread of urban areas and commercial agriculture into these deserts, providing alternative foraging habitats, prey and water sources for wildlife. However, it has also facilitated colonization by a generalist bat species not adapted to arid environments (*Pipistrellus kuhlii*), and subsequent competition for access to resources with native desert bats. Using molecular approaches (Next Generation Sequencing and DNA-metabarcoding) we quantify the impacts of agriculture and urban expansion on the nutritional ecology of three insectivorous bat species from the deserts of southern Israel, including two desert-obligate species (*Hypsugo bodenheimeri* and *Eptesicus bottae*) and one recently expanding non-desert bat (*P. kuhlii*). Faecal samples were collected from bats in a combination of natural and human-modified desert habitats to compare the composition of the gut microbiota between species and between habitats. We assess whether non-desert bats show adaptive responses to the arid environment through their gut microbiota by comparing the gut microbiota of *P. kuhlii* bats from mesic and desert ecosystems (north and south of Israel). The ability of bats to adapt rapidly to novel conditions through their gut microbiota has wider implications for their conservation and the way we view the impacts of anthropogenic environmental changes.

AP1-101

Extensive Wireless Sensor System for Proximity Detection and Sensor-based Vital Parameter Detection for BATS

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To enable biologist to gain deeper insights in the behavior of bats the BATS tracking system has been developed. It is composed out of a bat-borne light-weight (<2g) low-power tag and base stations for localization as well as data download. The main strength of the BATS system is to record encounters of up to 60 different individuals. This allows detailed investigation of interactions amongst members of entire social groups.

The BATS tracking nodes are designed in a modular way and thus were extended with a rich set of sensors to get deeper insights about the animal. For that an accelerometer, a magnetometer, a barometer as well as a self-developed ECG based heart rate sensor have been integrated. The sensor data is used to derive multiple parameters of the bats current state. This includes a simple acceleration sensor based activity detection whether a bat is currently active or resting as well as a more specific wing beat frequency using the accelerometer and barometer and a heart rate detection using the implemented ECG. The big advantage of the heart rate sensor is that it works non-invasively and thus keeps the impact on the animal low and allows easy application in the field.

The barometer and magnetometer data also provides insights in flight height and direction allowing for improved interpretation of proximity detection results to distinguish between random encounters and intended maneuvers of the animals.

We present the system design of the BATS-sensor nodes and results from tests on various bat species.

AP1-102

Bats on the Move – advancing our understanding of movement by Africa's bats

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Movement of bats within a landscape at various scales needs to be understood for conservation and public health concerns. Seven African bat species are included on Appendix II of the Convention on Migratory Species (CMS) [effective 26 January 2018]. For most species of bats, we know very little about their movement/migration patterns. Many species are too small (5-10g) to use radio or satellite tags. Here we report on the use of Radio Frequency Identification (RFID) Passive Integrated Transponder (PIT) tags. Biomark MiniHPT8 (8.4mm 134.2 kHz ISO FDX-B) tags are being implanted subcutaneously in bats representing 11 species from six families (Rhinolophidae, Hipposideridae, Nycteridae, Emballonuridae, Miniopteridae and Vespertilionidae). As of 1 February 2019, 536 individuals have been tagged, at four sites: Arnhem Cave (Namibia), Gladysvale, Mamalodi and Madimatle caves (all northern South Africa). A Biomark Cord Antenna System has been deployed at the three South African caves to passively detect tagged bats.

The cord reader system, with a deployment of 179 hrs, has the following detection rates: 7.7% (33/427) for *Miniopterus natalensis*, and 50% (1/2) for *Rhinolopus clivosus* with a survival greater than 49 days as of 16 February 2019. Preliminary results indicated movement from maternity cave by both male and female *Miniopterus natalensis* (a CMS listed species) to two hibernacula caves about 180 km from Madimatle Cave. Going forward, the 'Bats on the Move' program will incorporate assistance from citizen scientists deploying the cord across a wider geographic extent to better understand bat movement patterns in southern Africa.

AP1-103

Species or Just “Lineages”: Cryptic Diversity in Some South-East Asian Round-leaf Bats

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The problem of cryptic species is widely discussed, as is the fact that the mitochondrial data may not be enough to solve it. We try to utilize data on seven nuclear genes to explore cryptic diversity within two species complexes of the Indochinese round-leaf bats.

MRP multilocus analysis as well as some of individual genes (RAG2 and THY) support species-level separation within «*larvatus*» complex. At least *H.* cf. *poutensis* from the north-east of Vietnam is well separated from all other analyzed specimens (which supposedly should be allocated to *H. grandis*), including specimens from Kon Tum plateau. On the whole, the entire complex seems to be monophyletic.

In populations of *Hipposideros gentilis* (= *H. pomona* s.l.) from Indochina four mitochondrial lineages are present. They are separated by species-level distances, and paraphyletic with respect to other *Hipposideros* sp. However, nuclear genes support monophyly of *H. gentilis* and demonstrate distances of intra-species level (comparative to other *Hipposideros* spp).

These results better agree with morphometric analysis. Our dataset groups together this species individuals from the Central Highlands and the Dalat Plateau, as well as animals from the lowland forests of South Vietnam. Position of the form inhabiting Cat Ba Island on this tree is unresolved.

The discrepancy in tree topology and distances between different markers can be explained by the ancient hybridization between the Central Highlands population with the ancestors of *H. khaokhouayensis*.

The work is supported by RFBR grant 17-04-00689a.

Distribution and Population Status of *Myotis formosus* in Taiwan

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Formosan Golden Bat's Home, Taiwan

At least 37 bat species are known in Taiwan, a 36,000 km^2 subtropical island. However, except some common cave- or house-dwelling species, the distribution and population status of most bats, especially the foliage-roosting species, are rarely known. *Myotis formosus* is a migratory species with bright colors, distributed from Afghanistan through India, Nepal, Vietnam to Taiwan. In addition to using caves as hibernacula in winter, it generally uses foliage, and occasionally uses buildings, as summer roosts in the rural area. Between 1995 and 2018, I observed 53 colonies of *Myotis formosus*, consisting of >3 individuals, in the western Taiwan. Among them, I conducted long-term monitoring on 25 maternity colonies (22 woodlands and 3 buildings) and 3 hibernacula. The results showed that this species was experiencing a widespread and severe population decline. In total, 24 of the 25 maternity colonies and 2 of the 3 hibernacula monitored were either gradually declining or entirely disappeared. The largest known maternity colony, once 246 individuals recorded in a building in 1994, declined continuously and only 18 individuals were recorded in 2018. Another 6 maternity colonies entirely disappeared over the past 10 years. Strong associations between the colony decline and human disturbance were observed in some woodland and building roosts. Environmental degradation resulted from the pesticide contamination, water pollution, light pollution and deforestation in the surrounding areas may also relate to its population decline although further investigation is required. Besides directly protecting its roosts and habitats, public education is essential for the conservation of *Myotis formosus*.

AP1-106

Phylogenetic and morphometric variation in *Tadarida aegyptiaca* (Chiroptera: Molossidae) from southern Africa

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Tadarida aegyptiaca is a widespread Molossid bat species, yet little is understood of its taxonomy, phylogeography and ecophenotypic traits. Thus a comprehensive study of *T. aegyptiaca* from southern Africa is the focus of this research. The objectives are to assess the phylogenetic position of *T. aegyptiaca* from South Africa within the Molossidae, assess cranial size and shape variation within this species, assess their bacular morphology and determine potential environmental correlates. Phylogenetic analyses were conducted using a suite of seven nuclear and mitochondrial markers. Morphometric analyses included two techniques, traditional and geometric morphometrics, based on 12 craniometric characters, and using 16 dorsal and 17 ventral landmarks, respectively. Bacular analyses included measurements of five characteristics. Phylogenetic analyses of *T. aegyptiaca* specimens revealed a potential species level genetic distinction between representatives within the taxon. Morphometric analyses demonstrated two distinct groupings across southern Africa, an eastern operational taxonomic unit (OTU) characterised by larger, angular crania, and a central-western (C-W) OTU characterised by smaller, more rounded crania, that correspond to previously described taxa. Bacular analyses revealed the eastern OTU to have longer, narrower bacular whilst the C-W OTU were shorter and broader. Environmental correlates of cranial size and shape variation showed the eastern OTU correlated with precipitation and the C-W OTU correlated with altitude and temperature. The morphometric delineation coincided with the genetic distinction thus consistent with a possible species or sub-species level distinction, between these two taxa. Although this would require a comprehensive phylogeographic study of *T. aegyptiaca* across southern Africa.

AP1-107

May Relations Between Mainland and Island Populations in Pacific Region Highlight History of Local Bat Fauna?

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Islands, connected and disconnected with the mainland during their geological history, contain faunal elements, for various time remain isolated from their continental conspecifics or the nearest congenerics. The chain of the Japanese islands, which was repeatedly connected to Asia during glacier maxima, is inhabited by a number of bats with varying degrees of island endemism. We try to review relationships between some of Japanese species with their relatives, combining morphometric analysis with molecular genetics.

Japanese barbastelle is shown to be specifically distinct. It has closest relations with the barbastelles from Taiwan and South-East Asia, but probably not with geographically more close *B. beijingensis*. Japanese long-eared bat is currently treated as separate species, *P. sacrimontis*. Presumably is has closest relations with the Siberian *P. ognevi* from which it differs in morphometry and mtDNA; and both species probably far from Taiwanese *P. taivanus*. Long-tailed myotis, *M. longicaudatus*, is most probably specifically distinct from *M. frater*. It is represented in Japan by *M. l. kaguyae*, which subspecies status gets supports from morphometry. Japanese serotine was thought to be a separate species, *E. japonensis*. However, both morphometry and genetics justify its identity with *E. nilssonii*; meantime, island *E. nilssonii* probably deserves status of well-defined subspecies.

Even these four examples justify of at least two waves of settlement: earlier invaders came from the south, not spreading to neighboring parts of the mainland, more recent – from the nearest parts of Asia. This subject requires further study with different gene markers.

AP1-108

The First Record and Ecological Note of *Hipposideros armiger* in a Highly-urbanized Landscape in Malaysia

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The increasing urbanization usually accompanies great loss of biodiversity since highly urbanized habitats are often designed to facilitate modern life for large human population. Despite Malaysia is going through rapid urbanization today, the diversity bats in urban landscape and respond of different species the process are poorly known. The great Himalayan Leaf-nosed bat (*Hipposideros armiger*) is a large insectivorous bat with wide distribution in Southeast and East Asia. The species is by previously reported from forests, bamboo grasslands and plantations in forest-dominated landscapes, and considered sensitive to forest loss. Here we present the first record of *H. armiger* from a highly urbanized landscape in Penang Island, Malaysia. Individuals were first observed flying over a low-shaded grassland near an artificial lake and buildings in the main campus of the Universiti Sains Malaysia at dusk in April 2017. Species and feeding buzzes were further confirmed using a full spectrum bat detector. These data indicate the bats roosted and foraged in this urban area, where the nearest intact forest is c. 1.5 km apart from the site. Our findings suggest the species might be more habitat generalized than we previously known, or, at least, robust enough to trivial in degraded green patches in urban landscapes after the loss and fragmentation of its natural habitats in the last three decades.

AP1-109

Determining the Possibility of 'Long-distance Relationship' Between Distant Populations of *Rousettus amplexicaudatus* (Pteropodidae) through Microsatellite Analysis

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Population isolation in island populations tend to be greater than their mainland counterparts making them more vulnerable to local population extinction due to increased occurrence of inbreeding and reduced gene flow. One useful tool in determining correlates of population fitness such as genetic differentiation is through population genetics. This could be useful in determining management practices for the protection of ecologically important organisms such as fruit bats, which act as pollinators and seed dispersers of various plant species. In this study, we aim to determine whether geographic isolation affects the genetic differentiation of 6 *R. amplexicaudatus* (Pteropodidae) subpopulations collected from Palanan, Isabela (Forest Edge n=30; Palanan PFDP n=30; Forest Ridge n=30; High Elevation n=30; Mangrove Site n=30) and Lugait, Misamis Oriental (n=31), located in the islands of Luzon and Mindanao, respectively. From our genotype data acquired from 10 SSR primers, we determined the pairwise fixation indexes (F_{ST}), inbreeding coefficients (F), and Hardy-Weinberg (HWE) deviations of the populations using GenAlEx 6.305. Finally, we performed Principal Coordinate Analysis (PCoA) using genetic distances from each individual, and Analysis of Molecular Variance (AMOVA) to determine genetic structure of all the populations. Results show that there was no significant genetic differentiation between all populations (F_{ST}<0.15). However, loss of heterozygosity (F>0), as well as deviations from HWE in at least one SSR loci, was present in all the populations. Furthermore, absence of population-specific clustering in the PCoA analysis as well as low among population variance (2%) indicate the possibility of population admixture between all the populations.

AP1-110

Survey Design and Occupancy Modelling Combine Multiple Survey Methods for the Development of Species-habitat Relationships on a Country-wide Scale in Cambodia

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Survey design is a critical component of any scientific research effort. Here we describe a survey design for bats that combines data from multiple survey methods (mist net, harp trap, acoustic detector), incorporates imperfect detection and can be extrapolated at the country-wide level. We selected 250 stratified random sites across Cambodia. Sites were stratified according to large scale habitat type. The basic sampling interval that is the basis for occupancy modelling is the sampling occasion. We used temporal replication as a basis for our sampling occasion. We found that using multiple methods of survey at each site simultaneously, increases the probability of detection and the number of species detected. The occupancy framework can be used to estimate probability of occurrence in addition to, changes in occupancy over time when sites are surveyed repeatedly in different seasons/years. The flexibility and versatility of this analysis method is especially useful in answering many types of ecological questions and is well suited for bat surveys.

AP1-112

Thermal Imaging for Bat Research Applications

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Thermal Imaging is a cutting-edge tool which can be used for an expanding array of research applications. Thermal Imaging is now more accessible to bat researchers than ever before due to a combination of reducing hardware costs, improved user friendliness and the growing diversity of available devices. Thermal imaging is highly accurate for detecting bats in flight (even in low or zero visible light conditions) both in the laboratory and in the field. Most thermal imaging cameras provide a completely non-invasive approach to visualising bats, their flight paths and behaviours. The technique is also relatively long range in comparison with other techniques, allowing for detection distances of tens to hundreds of metres. Despite its obvious advantages for bat research applications thermal imaging is not without its limitations. Correct use of this technology for bat research applications requires appropriate knowledge, skills and equipment. Bats are easily missed when thermal imaging is used incorrectly, which can have detrimental effects on research outcomes and bat conservation efforts. Thermal imaging has been used as a key tool in bat research and survey applications. This conference poster reviews the latest research and guidance relating to thermal imaging for bat applications.

AP1-113

Polish bat guano microbiome and prey victims metabarcoding

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We present the results of the first research on microbime and the diet of Polish bats carried out using NGS sequencing. The bacterial and anthropodal DNA were isolated from the *M. myotis, N. noctula, V. murinus* and *P. auritus* fresh and frozen guano from the individuals from different habitats in Poland by the using of 16S rRNA Metagenomic Sequencing Library Preparation Protocol (Illumina, USA). The arthropods genotyping primers were designed using the barcode sequence diversity of cytochrome c oxidase subunit I (*COI*) gene. To study the diversity of bacterial species, we used a DNA fragment encoding the hypervariable V3 and V4 regions of the 16S rRNA subunit coding gene. Both barcode sequences was sequenced on MiSeq platform (Illumina, USA). The assignment of individual bacterial sequences to taxa was based on reference sequences deposited in the GreenGenes database (http://greengenes.secondgenome.com). Barcode of *COI* sequence were analysed in BOLD database (Barcode of Life Data Systems, http://www.boldsystems.org). Preliminary results showed significant variation in the microbiome between the analysed species. The presence of bacteria from pathogenic genera such as *Rickettsiella, Clostridium, Corynebacterium, Enterococcus, Sulfurospirillum* or *Vagococcus* has also been confirmed. Diet analysis showed the presence of arthropods of the family like *Noctuidae, Crambidae, Carabidae, Chrysopidae, Calliphoridae* and *Forficulidae* and others. Current study confirms the effectiveness of the NGS method used in the biodiversity analysis of bat guano microbiome and diet prey analysis. Further research will include bats from other species such as *E. serotinus, M. nattereri, M. bechsteinii* and others.

AP1-114

Skull Sexual Dimorphism in Two Sympatric Species, *Murina hilgendorfi* and *M. ussuriensis*

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Sexual dimorphism in bats has frequently been explained as the big-mother hypothesis (to get benefit in reproduction) or niche divergence hypothesis (to avoid intersexual competition). In the genus *Murina*, it is reported that extent in female-biased sexual dimorphism vary among species from little to strong and interesting group to understand the diversity of sexual dimorphism in bats. However, the relation to the above mentioned two hypotheses has not been discussed. In this study, we analyzed their patterns of sexual difference in skull by linear measurements and geometric morphometrics, using *M. hilgendorfi* and *M. ussuriensis* both widely distributed in four main-islands and several small islands of Japan, as well as in northeastern Asia. *M. hilgendorfi* is medium sized species (FA: 39-46) and *M. ussuriensis* is small (FA: 28-35), and both are forest dwelling and insectivorous species. In *M. hilgendorfi*, males and females are considered to have similar skull size and shape. In *M. ussuriensis*, females have typically larger skull than males as most characters except interorbital breadth. Moreover, total length of the skull versus forearm length exhibits considerable geographic difference only in males of *M. ussuriensis*. Our findings suggest that females might be stable in size in constrains of reproductive benefit, while males have flexibility in size to have formed complex and different patterns of sexual dimorphism among localities in *M. ussuriensis*. We also discuss sexual dimorphism strategies between sympatric *M. hilgendorfi* and *M. ussuriensis* with different body sizes in a functional context.

AP1-115

Skull Morphological Variation of *Rhinolophus ferrumequinum* in Northeast Asia

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Rhinolophus ferrumequinum is the most widely distributed species in family Rhinolophidae, and its distribution is from Europe and northwestern Africa to Northeast Asia. Many taxonomical studies about this species were done until today, but the taxonomic position of Northeast Asian population is still unclear due to lack of skull morphological studies. This study focuses on revealing features of the skull of *Rhinolophus ferrumequinum* in Northeast Asia including North Korea, South Korea, and Japan in comparison with European populations from Hungary and Croatia based on 9 skull measurements of 141 males and 132 females. As a result, there was no sexual difference on the skull in each population. There were clear cranial shape differences between European and Northeast Asian populations: the cranium was wider in Europe than Northeast Asia, but the nasal swellings and the mastoid were wider in the latter. In addition, among Northeast Asian populations, the skull length, the upper toothrow length, and the mastoid width were significantly larger in Japan than North Korea; and South Korean population showed more similarity with North Korean than Japanese as these measurements. However, Principal Component Analysis showed that Japanese population involved higher variabilities; and every South Korean and North Korean were contained within the range of Japanese. Our findings indicated that we can distinguish Northeast Asian populations from Europeans by cranial shape, and also suggested that Japanese populations might have a mixture of 2 morphological features: the one is identical with South Korea and North Korea, and the other is its own.

The Humerus Nature of Femoral Head Morphology and Its Importance in Bat Locomotion

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Similar to the adaptive nature of the humerus for flight in bats, the head of the femur shows adaptive diversity, a phenomenon likely related to a combination of phylogenetic constraints and function (e.g., hanging, use of the uropatagium, quadrupedal locomotion, and flight). The spatial and functional relationships between the fulcrum (ball of the femur or femoral head), input levers (greater and lesser trochanters), and output lever (femoral shaft) require in-depth analysis in order to understand the myriad ways the hindlimbs are used in bat locomotion. We tested the hypothesis that adaptations of the femoral head and trochanters are related to both quadrupedal and flight locomotion. We explored this first by describing the morphological diversity of femoral heads and trochanters among taxa and then used truss and principal component analyses to quantify variation in spatial relationships among the femoral components and track how these correlate with hindlimb motions during quadrupedal and flight locomotion.

AP2-101

A 3D Anatomical Study Using μCT Images for the Male Genital Organs of Greater Horseshoe Bat

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The composition of male genital organs in mammals varies considerably among species, reflecting each unique adaptive strategy. The bat has diverse reproductive patterns in accordance to their wide geographical distribution, from temperate to tropical regions. Despite their varied reproductive strategies, the anatomical diversity and patterns of the genital organs are surprisingly little understood. This study aims to describe the detailed three-dimensional morphological structure of the male genital organs in the Greater horseshoe bat, *Rhinolophus ferrumequinum,* using a micro computed tomography (μCT) system. The male accessory genital glands of this species comprised five glands. The ampullary glands possess cone-shaped bodies which are located dorsal to the urinary bladder. The vesicular glands lie distal to the ampullary glands. They are a pair, rounded and bilaterally symmetrical in shape. The prostate gland is located on dorsal and distal to the complex of ampullary-vesicular glands. This gland surrounds the urethra and continues to the urinary gland. The urethral gland is single and carrot-shaped and the bulbourethral glands are a pair oval-shaped and lying dorsolateral to the distal urinary gland. In the penis, the corpus cavernosum forms the greater part of the inside and the terminal urethra is capped by a small, bony ossicle, the os penis. In conclusion, our three-dimensional anatomical investigation characterized the male genital organs of Greater horseshoe bat, demonstrating the presence and precise location of the ampullary, vesicular, prostate, bulbourethral and urethral glands in the accessory glands and corpus cavernosum and os penis in the inside of penis.

AP2-103

FGF-23 and Klotho Patterns of Expression in the Long-Lived Big Brown Bat (*Eptesicus fuscus*) and C57BL-6 Mice

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Vespertilionid bats (Order Chiroptera) live 3-10x's longer than other mammals with an equivalent body size. *In vivo* and *in vitro* qPCR assays of our known-aged colony of big brown bats (*Eptesicus fuscus*: Vespertilionidae) showed that elderly bats maintained a youthful bone phenotype via upregulation of those genes critical for a fracture-resistant matrix (Col1A1, TGF-β). Two genes within the kidney-bone axis (FGF-23, Klotho) also showed novel expression patterns. FGF-23 inhibits bone mineralization and in a Klotho-dependent mechanism, modifies reabsorption within the kidneys. High levels of both genes contribute to vascular calcification and hypertension. Bat bones displayed 2-fold greater expression levels of FGF-23 at 10% of their lifespan and by 75% of lifespan this gap widened to 5-fold greater expression compared to mice. At 20% of lifespan, bats increased Klotho expression such that elderly bats at 75% of lifespan showed a 3-fold greater expression of Klotho compared to mice. *In vitro* assays showed that MSC-derived osteoprogenitor cells of elderly bats displayed the greatest expression levels of both genes compared to young bats and all mice. Upregulation of FGF-23, Klotho, and TGF-β are linked with endothelial calcification, hypertension, and kidney fibrosis. However, concentrations of ADMA, a biomarker for endothelial dysfunction and chronic kidney disease, showed only a moderate increase in concentration through their lifespan, similar to what is seen in healthy, non-hypertensive patients. Results suggest that bats are able to optimize the performance of the bone-kidney axis without disrupting renal or cardiac function and therefore may utilize novel mechanisms to prevent kidney disease.

AP3-103

Perceptions of Cave Management in US National Parks: A Qualitative Analysis

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White-nose syndrome (WNS) has killed more than 5.7 million bats across eastern North America and is considered one of the deadliest wildlife diseases of the modern era. The US National Park Service (NPS) manages over 4,700 caves and is tasked with balancing the conservation of natural resources with the public's recreational experiences. Despite the close connection the NPS has with the public, few studies have focused on the social consequences of rapidly changing cave management plans resulting from WNS expansion. We explored key stakeholders' knowledge, attitudes, and perceptions of bat and cave management at caves managed by the NPS through 15 semi-structured key informant interviews. WNS was identified by all of the respondents as the greatest challenge to bat and cave management, with other issues, like lack of funding, restricted cave research access, and effective communication with visitors, stemming from the impact and spread of this disease also considered important. Conversely, respondents were divided on their attitudes towards cave closures, with informants who worked with caving groups stating their disproval over national cave policies that ignored local context. Understanding the social context of how WNS has shaped cave management in national parks is crucial to effectively evaluate how these changes are perceived by various stakeholder groups and to balance park visitor experiences with bat conservation.

AP3-104

An overview of current conservation studies of two declining species of flying-foxes in New Caledonia

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Understanding the spatial and temporal dynamic of a population and its underlying factors is critical to propose efficient conservation actions. This is all the more true since conservationists are dealing with highly mobile and vulnerable animals such as flying-foxes. In New Caledonia (South Pacific), ongoing studies are conducted on spatial ecology and dynamics of harvested populations of *Pteropus ornatus* and *P. tonganus* along with the impacts of feral cats. First, spatial ecology of flying-foxes is being studied by the monitoring of individuals equipped by GPS tag with the aim to evaluate the nightly foraging areas around diurnal roosts, to compare the capacity of dispersal between roosts and to measure the distance between the most distant roosts used by flying-foxes. Second, studies are conducted on predation due to feral cats thanks to the sampling and the analysis of feral cat scats coupled with the assessment of cat density in different representative habitats (camera-trapping). This will allow us to estimate the total number of flying-foxes killed annually by feral cats and to compare this figure with the size of hunting harvest. Our ultimate goal is to be in capacity to define the most effective management scale and to make informed management choices, at the scale of the new Caledonian archipelago. The consultation of the various stakeholders is now urgently needed to fix an optimal, informed and sustainable conservation strategy for flying-foxes in New Caledonia.

AP3-106

Spatiotemporal Patterns of Bat Diversity Driven by Climate Change in Vietnam and Its Conservation Implication

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Characterizing spatial distribution of biodiversity can help to better understand ecological factors that influence biogeographical history and consequently can provide guidance for optimizing conservation planning. Vietnam sustains a diverse and abundant bat fauna of nearly 120 species. Unfortunately, most local bat assemblages are currently at risk mainly due to habitat loss or disturbance, and the species richness and phylogeographical patterns determined by historical environment changes are still poorly understood. We applied Species Distribution Modeling to hypothesize the potential taxonomy diversity patterns of Vietnamese bats under a number of climate change scenarios and consequently to identify priority areas for bat conservation. The predicted distribution maps of more than 70% of bat species in Vietnam revealed that the Northern, Central and west Central Highlands of Vietnam harbor the highest number of species. The temperature seasonality and forest cover are the most important factors influencing the bat distributions in Vietnam. We projected individual bat distributions in 2050 and 2070, and assessed the potential changes in species richness across Vietnam under different climate change scenarios. Results showed that most areas in Vietnam, especially in northeast and central Vietnam, might lose a high proportion of bat species due to climate change. Defining 9% of the total land area in Vietnam with the highest bat species richness we can delineate priority areas for bat conservation outside the current protected areas, and can provide tools for more effective conservation actions.

AP3-107

Lucky Bat: A Standard Bat Rescue Protocol in Taiwan

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In Taiwan, when people find bats, they often consult the NGO, which includes **Bat Association of Taiwan** (http://www.battw.org/), for help. People overly depend on NGO, which makes NGO be overloaded with cases. In addition, people do not raise conservation awareness after they rescue wild animals. Therefore, we designed a standard rescue protocol to make rescue more efficient, and increase the animal survival rate. It also makes it easier for people to take conservation action. We use Facebook's automatic reply system (https://www.facebook.com/battw/) to supervise people how to identify age and conditions of the bats. This teaches people how to help healthy adult and infant bats get back to their habitat, or transfer injured bats to rescue centers. Some pups or the injured bats cannot be released immediately. We provide volunteers a rescue kit developed by BAT (Endemic Species Research Institute, Bat Association of Taiwan**,** Formosan Golden Bat's Home) for rearing bats, and lecture them how to use it through a video. At the same time, we also provide online questionnaires to collect the information about the rescued bats, the location in which bats were found, and finders. In 2018, there were 167 cases in which 52% of bats were found in the building during the day. Most of the people found Japanese pipistrelle (*Pipistrellus abramus*) in those cases. 54% of the bats which people found were healthy adults, 29 % being pups, 15% being injured and 2% being dead. 46% cases were reported by females aged 18-35. These results help us to modify the rescue process, establish a collaborative platform with the government, and educate people.

Involving citizen scientists in acoustic surveys for bats: MEGA Murray Darling Microbat project

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The MEGA Murray-Darling Microbat citizen science project has expanded the geographic and scientific boundaries of a community microbat monitoring program begun in 2003. Much is still unknown about insectivorous bat species in the Murray-Darling Basin, especially the links between species diversity and habitat type and condition. This river basin is the largest and most economically important catchment system in eastern Australia. We have used a network of Natural Resource Management (NRM) groups to reach out to interested citizens throughout the South Australian part of the basin. The project has been building on historical observations of bat species occurrences and distributions using a fleet of 30 AnaBat Swift bat detectors to encourage grassroots land management effort that benefits native wildlife, inform government land management policy, and update conservation assessments. To date, we have involved 125 citizen scientists, collected data from over 400 recording sites, and developed a custom semi-automated acoustic analysis system that is suitable for use by volunteer non-specialists. The long-term goal is the ongoing monitoring of bat populations in South Australia, and providing the inspiration and wisdom for similar programs in other parts of the catchment interstate, and beyond.

AP3-112

Bats Track Mosquito Populations in Rice Paddies: Potential Impact on Human Health

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The ability of bats to suppress agricultural pests is well known and has been measured for some particular dyads of predator and prey species both in economic and food security terms. The recent emergence of new molecular techniques, such as metabarcoding, which allow for wide screenings of the bats diet, is providing a wealth of further evidence that bat consume an ample array of agricultural pest species over different regions of the planet. With few exceptions, the main focus on the regulatory services bats provide in agroecosystems has been on crop pests which cause yield loses. Rice paddies constitute a particular agronomic system with specific challenges, not only related to agronomic production but also to human health. The density of mosquitoes in such ecosystems pose a serious threat to human wellbeing, both for the direct harm and for the number of diseases mosquitoes can transmit. During 2017 and 2018 adult mosquito populations and bat activity was assessed twice a week in 15 sampling locations in the rice paddies of Alt Empordà (NE Iberia). Both mosquitoes and bats were identified to species, resulting in over 7,500 individual mosquitoes sampled and 670,000 recorded bat passes. Metabarcoding of bats feces proved the presence of mosquitoes in the diet of the bats. Furthermore, adult mosquitoes density at the sampling locations was the predictor more strongly related to bat activity according to the Generalized Linear Mixed Model run (estimate = 0.23, $p < 0.01$), suggesting that bats track and exploit the emergence of adult mosquitoes. Promoting the presence of bats next to human settlements in such agroecoystems may constitute an excellent biological control system with direct impact on both human health and crop yield.

AP3-114

Bat Taxidermy Trafficking Online: Toward a Global Survey

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Bat taxidermy is recently reported from online shops in several Southeast Asian countries and the USA. However, the global trends of bat taxidermy trading have not been fully explored. Since 2018, we have been investigating online bat taxidermy trafficking to obtain information of trading country, taxonomy, bat posture, packing, price, and potential source. To date, we found 202 records of over 20 thousand bat specimens available in 11 high-income countries. Bat specimens were sold for 8 to 340 USD per piece. Around 73% of these are marketed as dry full specimens mainly framed or bagged, and the rest are skeletons mostly without any packing. Most full specimens were displayed with their mouth open regardless of wing posture. Specimen labels were mostly referred to 26 Asian tropical taxa, except a few to African and Neotropical species. The specimens were declared imported from Australia, USA, Canada, China, three Southeast Asian and four European countries. These findings suggest that these bat specimens were potentially origin from Southeast Asia and China, and have been allocated in Europe and North America before sold. It is likely that we underestimate the spatial extent of the trading and source regions since the data were exclusively extracted from World Wide Web-based shops in a few languages. We identify an immediate need of more surveys of bat taxidermy trading with broad coverage of language and online social media to assess its impact on global bat conservation. We hope international agencies will act against this online bat trafficking.

AP3-115

Bat Conservation and Awareness Campaign: Community Participation Approach to Protect Bats of the Thar Desert, India

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Citing prevailing myths, social taboos and inadequate knowledge among locals about their ecological and economical significance Bats in Rajasthan part of the Thar Desert, India have been facing a serious threat of anthropological disturbances; not only at their day roosts but during the foraging activities as well. Reportedly, beside heavy loss in count of reported days roosts four of the total twelve species of bats reported therein through 1960's to 1970's were found missing in investigations of 1980 to 2006. Through 2007 till 2018, in attempt to eradicate the existing myths and inculcate the sense of appreciation among locals regarding bats, Bat Conservation and Awareness Campaign (BCAC) have been launched in prominent 7 of the total 12 districts in this region. Beside publishing articles in local newspapers, distributing Posters and Pamphlets, Lectures themed of species diversity, nature, ecological and economical importance of bats were delivered at over 500 schools and 2500 community cum local gatherings at various settlements and villages; apart from 14 colleges and 5 universities at towns and cities. Beside initiation of Bat Clubs at 55 schools and colleges attempts were made to prepare a network of about 25 local but trained volunteers who would not only ensure the safety of available bat roosts in their surroundings but propagate the message of bat conservation and awareness in their community and upcoming generations. The result of this BCAC is imperatively apparent to inculcate the sense of appreciation among locals about species diversity, nature, ecological and economical significance of bats.

Using Automatic Acoustic Classifiers to Identify Insectivorous Bats in Borneo

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Automated classifiers offer an efficient and standardised method for processing extensive acoustic datasets for bats, even in mega-diverse biomes. Borneo is a global hotspot for bat diversity with 99 described species, of which 80% are insectivores. However, many taxa are inadequately sampled in studies using live-capture techniques as their identification is difficult and resource intensive. In this study, we developed a regional automated classifier for the bat species of north-eastern Borneo. Release calls for 46 species were collated and pulse measurements were automatically extracted using ScanR to train a multi-stage supervised machine learning algorithm. Classifications were first made to identify call type (e.g. constant-frequency) and then refined to identify between species/groups. Five different classification models were evaluated in terms of accuracy and predictive power. Models employing the Random Forest algorithm provided the best global performance, followed by Bagging. Variable importance within the models differed between call types. As expected, curvature and peak frequency were the most important parameters to distinguish Rhinolopids and Hipposiderids. Algorithm performance varied substantially across other groups, and more reference calls are required before it can reliably distinguish between Vespertilionids. For these species we developed a specified confidence threshold at which to combine manual post-validation. Our method reduces the volume of data processing required in acoustic studies and has great potential to serve acoustic monitoring studies for bats in South-east Asia.

AP4-102

Who's calling? Acoustic identification of Brazilian bats

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Brazil is a megadiverse country with more than 180 bat species. However, most inventories have been mostly made using mist-net sampling and roost search and due to the lack of bioacoustics studies, the bat fauna is certainly sub represented and biased. The knowledge on distribution and ecology of Brazilian bats is mainly within the Phyllostomidae. Reliable data on bat echolocation calls is key to improve the knowledge on the distribution patterns and foraging ecology of the remaining eight bat families present in the country. Our work aims to: i) integrate information on echolocation calls of non-phyllostomids occurring in Brazil; ii) detect regional changes in the acoustic profile of those species; iii) identify gaps in knowledge both in terms of species and regions sampled; and iv) to point out which species are acoustically recognizable in a reliable way. Finally, we present a key to supporting the acoustic identification of non-phyllostomids in Brazil. We compiled publications on echolocation calls of Neotropical bat species occurring in Brazil and summarized qualitative and quantitative information of acoustic parameters used in call descriptions. We considered 93 non-phyllostomid bat species to occur in Brazil of which 65 have been acoustically described but for 28 we found no published information. Information on echolocation calls was retrieved from 47 publications and acquired in 17 countries. The use of bioacoustics can be a fundamental tool to expand the knowledge on Brazilian bats and improve their conservation.

AP4-103

Influences of Climate Variability on the Acoustic Diversity of Bat Communities

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Understanding how biotic and abiotic factors influence species composition and structure of ecological communities is essential for biodiversity conservation under the changing environment. Climate variability can affect trait diversity and ecological functions of a community through community assembly. According to the favorability hypothesis, high climate variability can be a strong environmental filter in the community assembly process and only allows the species which have certain traits to filter through. In addition, the climate variability hypothesis states that the species distributed in the areas with higher climate variability are adapted to have a broader climatic tolerance range and greater trait variability. Besides abiotic factors, the competitive equilibrium hypothesis states that highly variable environments could lead to an unstable competitive equilibrium and thus reduce dominance of species or traits. In this study, we used acoustic diversity of bat communities in Taiwan as a case to test the three hypotheses. We identified bat echolocation calls in the long-term ultrasonic recordings collected at ten sites across Taiwan and measured their traits in R. We then calculated three functional diversity indices to measure the trait richness, evenness and within-functional-group variation. The preliminary results showed that bat communities at high variability sites had larger within-functional-group trait variation and a more even abundance distribution than did communities at low variability sites. These results support the climate variability and competitive equilibrium hypotheses, respectively, and suggest that climate variability affects bat community assembly through both biotic and abiotic processes.

AP4-104

Mother-offspring recognition in *Kerivoula furva*

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The dark woolly bat, *Kerivoula furva*, form small groups and use furled leaves of *Musa formosana* as daily roosts. In each roost, bats were comprised primarily of one to several pairs of reproductive females and their young. The relationship between bat mothers and their offspring could last several months even after they frequently change the day roosts. Our previous selection study found the bat mother of *K. furva* could distinguish between its own pup and other's pup from the same roosting group. The purpose of this study was to test whether the bat mothers of *K. furva* use acoustics or olfactory cue to recognize their pups. We recorded calls of the pups and used playback experiments to test our prediction that the calls of the pups contain individual signature information thus can be recognized by their mothers.

AP4-105

Acoustic Survey of Bats in the Kathmandu Valley, Nepal

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Since early 19th century several bat surveys and records had been undertaken at different time intervals in the Kathmandu Valley. With an objective of developing an acoustic call library so that bats can be surveyed and monitored non-invasively, during August 2016 to April 2018 bat monitoring including acoustic survey was conducted in three phases at 19 sites. Two ECOTONE mistnets each of size 6m x 3m was administered in different classified habitats identified from Phase I habitat survey. Two Wildlife Acoustics SM4 BAT ZC detectors were operated to record echolocation of the captured bats while hand held and release and/or passing bats. Echolocation data was analyzed deploying Kaleidoscope Stand-Alone Viewer version 4.3.2. Reference calls of 18 species were documented and have been uploaded into Nepal Bat Call Library. Echolocation calls for five species of *Rhinolophus*, four species of *Myotis*, two species of *Hipposideros*, each species of *Barbastella*, *Eptesicus*, *Hypsugo*, *Megaderma*, *Miniopterus*, *Nyctalus*, *Pipistrellus*, repsectively. Two types of echolocation calls were recorded; constant frequency calls and frequency modulated calls. The mean frequency of bat calls ranges from 24 kHz to 108 kHz. These reference calls will be deployed to identify the presence and occurrence of species during the upcoming bat monitoring in the valley and within the country.

Key words: Acoustics survey, Kathmandu Valley, Nepal Bat Call Library

AP4-106

Activity of Insectivorous Bats over Rice Fields Surrounding Free-range Bat Guano Farms in Cambodia

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In many of the world's agro-production systems, insectivorous bats are voracious predators of economically-relevant pest species. However, their ecological and economic services all too often remain undocumented and under-valued, particularly in small-scale farming systems in the tropics. The practice of farming free-ranging lesser Asian house bat *Scotophilus kuhlii* for their guano is indigenous to Cambodia and a small neighbouring area of Vietnam and has potential for improving environmental conditions in agricultural landscapes and improving rice harvests and farmer livelihoods. As the role that this and other bat species may play as a biological pest control agents in such landscapes remains poorly documented in Southeast Asia, this study aimed to quantify bat species composition and activity over rice fields surrounding bat farms in Cambodia. To this end, bat activity was acoustically sampled for the entire cultivation cycle of one rice crop over a distance gradient from central clusters of bat farms in two provinces during the wet season. Bat farmers and rice farmers in both provinces were also interviewed to determine their related farming and pest-management practices. This poster reports the initial findings of our ongoing study.

AP4-108

Am I Speaking Your Language?

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Field research often requires the capture of live animals, particularly to collect morphological data or attach tracking devices. As part of a wider study on the bioacoustics of bats in Ulu Temburong National Park (Brunei) we tested the effectiveness of an acoustic lure (Apodemus BatLure) to increase catch success in harp traps, as lure effectiveness has primarily only been tested in Europe and Australia. Four harp traps were set-up at ground level before dusk, 100m apart, consecutively over 6 nights along an existing track and left for 3 hours. Each night one trap had the lure attached halfway down one side-support. Due to the unavailability of local synthesised calls, we used a collection of calls from across Europe and Asia (*Myotis, Nyctalus, Pipistrellus*). While catch success, in terms of the number of bats caught, was unaffected by the presence of the lure, the species assemblage was dominated by *Rhinolophus* in traps associated with the lure. The lack of increased catch success may be due to the lower frequency of calls played on the lure (34.53±6.95 Fc kHz) compared to the range of our recorded calls of the local community post-catch (45 – 165 Fc kHz). These results suggest that some species may not respond to unfamiliar calls as similar studies in Europe and Australia have found. Future studies utilising bat lures should incorporate bioacoustics to analyse which calls are most effective particularly when regional calls are unavailable.

AP5-100

Communication Calls of Ussurian Tube-nosed Bat *Murina ussuriensis* under Experimental Conditions

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Ussurian tube-nosed bat *Murina ussuriensis* occurs Korean Peninsula, southeastern Russian, and Japan, yet almost nothing is known about its communication calls. Adult bats were kept individually in the same room (10x6x3 m). Food and water were supplied on the floor of the cylindrical wire-meshed cage (80 [diameter] x 95 cm) every evening so that each bat could feed voluntarily. Echolocation calls were FM sweep, of short duration at around 68 kHz. Compellation calls of the solitary males were FM sweep signals with repeated calls at around, of longer duration (D: 17-37ms) and lower peak frequency (PF: 23-30 kHz), and frequency in use of the call was 1~4 per night. Male's threatening calls for other males were high intensity (PF: 45.8 kHz) and long duration (25-104 ms). Males of *M. ussuriensis* show territorial behavior in the field. After superiority or inferiority was determined between males based on the native effect, only compellation calls emitted each other. Noisy broadband calls were directed at other males when males were contiguous each other. Mating calls (PF: 22-54 kHz) were emitted to a female. Such song appeared to be intermittent during the night. The call included plural pulses, and call duration was 2-3 s, Number of its pulse increased from 3 to 8 when the distance between male and female was shorten. In any case, bats tend to use lower-frequency signals for social interactions.

AP5-101

Influence of Temperature on Energetics of Roosting Generalist and Specialist Phyllostomid Bats

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Costs of thermoregulation during roosting play an important role in the daily energy budget of bats. Roost microclimate influences and may help to minimize these costs. To assess energy expenditure associated with roost temperature (T_r), we measured resting metabolic rate (RMR) with open-flow respirometry at 21 °C, 27 °C and 32 °C, resembling the T_r range of our study species. We worked on Barro Colorado Island (Panama) with four phyllostomid species differing in roost type and degree of roost specialisation: *Artibeus jamaicensis*, *Uroderma bilobatum*, *Dermanura watsoni* and *Micronycteris hirsuta*.

We hypothesized that bats show lowest RMR at a temperature close to their T_r of 27 °C and assumed that roosting generalist species should be adapted to a broader temperature range. Our results indicate that energy expenditure of *A. jamaicensis*, *U. bilobatum*, *M. hirsuta* and *D. watsoni* decreases by 8%, 21%, 30% and 47%, respectively, with an increase of ambient temperature from 21 °C to 27 °C. We found significant differences in RMR between roosting generalist and specialist species and concluded that the roosting specialists *D. watsoni* and *M. hirsuta* are less resilient to cold temperatures than the canopy tent-roosting *U. bilobatum* and the roosting generalist *A. jamaicensis*. Our results contribute to understanding the effects of thermo-physiological adaptations on roost selection in bats, which might be crucial to predict potential effects of climate change on the distribution patterns of bats.

AP5-102

When Bats Fly During the Day

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Bats are normally nocturnal but are occasionally seen flying during the day. We surveyed *Nyctalus aviator*'s daytime emergences at a roost in Saitama Prefecture, Japan from 2012 to 2014. Daytime emergences were seen from early March to early April and from late October to late November which are just after and before hibernation. Fecal analysis and the bat's behavior during the daytime flight indicate the main purpose of daytime flight is to feed. This bat is one of the largest insectivorous bats in Japan and a swift flyer. On the other hand, daytime flight is not uncommon for flying foxes that roost in the trees. Some species of flying fox that live on isolated islands, where there are little to no diurnal avian predators, are often diurnal or crepuscular. *Pteropus dasymallus* in the southwestern part of Japan and *Pteropus mariannus* in the CNMI are active mainly at night, but after a big typhoon in 2015 and 2018, respectively, we observed daytime foraging behavior. When bats are active during the day, there are some common features: All those species are relatively large and often live on isolated islands or can fly fast, therefore the risk of predation is relatively low and there seems to be a shortage of food due to bad weather or tough seasonal conditions or tough environments.

AP5-103

Absence of natural habitats drives monoxenous bat and bat fly relationships

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Ectoparasites have evolved to use their hosts as landscapes, often at a cost of obligate inhabitancy. There is little published research on bat flies (Diptera: Nycteribiidae) in Singapore and their ecology is not well understood. Understanding the diversity of nycteribiids, their host association, sex ratio and infestation rates can provide insight into the dynamics of this host-ectoparasite relationship. Nycteribiids were collected from bats trapped in Singapore from 2011-2016 and identified using morphological keys. Host specificity, sex bias and infestation were investigated with binary logistic regression and generalised linear models. Nycteribiids were found to be monoxenously associated with their host bat species, likely due to biological factors and possible isolation between the host bat species roosts. Two of four species of nycteribiids displayed a bias towards host sex and age, likely due to biological, behavioural and environmental factors.

AP5-104

Blood-sucking Ectoparasites in *Miniopterus schreibersii fliginosus* and *Eptesicus nilsonii* in Japan

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It is known that many bat species are parasitized with blood-sucking ectoparasites such as bat flies, fleas, batbugs, and ticks. Though at least 35 species of bats live in Japan, little is known about their ectoparasites. The objective of the present study is to characterize the blood-sucking ectoparasites in two common bat species, *Miniopterus schreibersii fliginosus* (MSF) and *Eptesicus nilsonii* (EN), in Japan. In March 2013 and June and October 2016, 281 ectoparasites were collected from 114 MSF captured in Wakayama Prefecture, central Japan. In August 2017 and June and August 2018, 241 ectoparasites were also collected from 72 EN captured in Hokkaido Prefecture, northern Japan. The species of ectoparasites were first identified based on the morphology under stereomicroscopes. Phylogenetic analysis of cytochrome oxidase I sequences (*COI*) was applied for molecular identification of unidentified ectoparasites. All ectoparasites from MSF were morphologically identified as two genera of bat flies: *Penicilidia jenynsii* (n=45) and *Nycteribia* spp. (n=236). Phylogenetic analysis based on *COI* indicated that all the *Nycteribia* spp. were *N. allotopa* (n=157) and unknown *Nycteribia* species (n=79), respectively. On the other hand, the ectoparasites from EN were identified as the flea *Ischnopsyllus needhami* (n=239) and the batbug *Cimex japonicas* (n=2). No ticks were obtained from both species of the bats examined. In the present study, we showed that the ectoparasites were clearly different by the bat species or the sampling locations. Additionally, novel *Nycteribia* species was found on MSF in Japan.

AP5-105

Comparing Foraging Preference of Bat Species based on Fecal Analysis using High Throughput Sequencing (HTS)

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Habitat preference of insectivorous bats are closely related with prey resource availability. According to environmental differences of micro-habitat in forest, bats are exposed to different prey distribution. In this study, we attempted to detect foraging preference of seven insectivorous bats in South Korea by high throughput sequencing (HTS) from their fecal analysis. We captured seven different bat species using mist-net in Mt. Jumbong, South Korea. And, we collected fecal samples from captured bat species and identified foraged dietary insects from each feces by HTS. Insect composition detected from feces showed distinct differences among bat species. In case of two bat species, *Myotis petax* and *Plecotus* sp., major foraged insects were insects belonging to Lepidoptera and comprising 80% of the total foraged diets. On the other hand, preys belonging to Diptera were detected at the highest proportion (more than 95%) in another two bat species, *M. aurascens* and *Rhinolophus ferrumequimum*. There are no significant differences by sex in two bat species, *M. ikonnikovi* and *Plecotus* sp. In concept of ecological niche partitioning, bats tries to select foraging sites without overlap with other species despite living at the same place because these strategies can decrease competition with other species. Differences of foraging preference of bat species may be closely related with environmental differences of micro-habit in study sites. Although we showed only differences of diet composition between bat species and sex, we will interpret these results combine with radio tracking in aspect of ecological niche partitioning and resource partitioning.

AP5-106

The relationship between hibernating bats and environments in underground habitats in Korea

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Bats hibernating in underground habitats have a different thermal preference for each species, and bats will hibernate by selecting sites with their temperature preference. The distribution and relative abundance of hibernating bats would be closed with thermal and humidity environments and structural features of underground sites. To identify the distribution and abundance of hibernating bats, 140 underground sites including caves and abandoned mines in southern part of the Korean Peninsula were investigated for ten years (from 2005 to 2011). Total 13,288 bats of 11 species were recorded, and the most abundant species were *Miniopterus fuliginosus*, *Rhinolopus ferrumequinum* and *Myotis petax*. Clutster analysis divided the hibernacula into four groups depending the temperature environment. Bats more hibernated in sites of two groups with broad-ranged temperature zone than in sites other two groups with narrow-ranged temperature zone (cold or warm). Four species (*Myotis petax*, *Plecotus ognevi*, *Hypsugo alaschanicus*, and *Murina hilgendorfi*) hibernated mainly at sites with cold temperature, but two species (*Myotis rufoniger* and *Miniopterus fuliginosus*) hibernated at sites with warm temperature. *Rhinolopus ferrumequinum* with the broad-ranged thermal preference were distributed in most sites. Canonical correspondence analysis indicated that temperature, humidity, size of entrance and passage, and water are important factors affecting the habitat use by bat species hibernating in underground sites. In conclusion, the diversity of hibernating bats were closely related to the structural and climatic features in underground sites, and this will provide valuable information for developing suitable strategies to conserve bat populations.

The flexible energy expenditure in the hibernating bat, *Miniopterus fuliginosus*, in South Korea

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In temperature region, insectivorous bats have adapted to a generally low availability of food. It appear that hibernation is response to reduce energy loss and enhance fat storage for survival. The selection of temperature and energy strategy of hibernating bats in response to variable environment is differed between populations as well as species. Here, we tested a hypothesis that energy expenditure of hibernating bats varies among populations in a different environment. To verify the flexibility for energy expenditure, we compared the change of body condition index (BCI, mass/forearm length) and body mass and staying times in the hibernaculum among populations of *Miniopterus fuliginosus* with three different latitudes in Korea for winter of 2017/2018. The outer temperature of each region was correlated with the latitude, but ambient temperature within the hibernaculum was not correlated. BCI of *M. fuliginosus* correlated with latitude and decreased during hibernation. The body mass loss was 3.75g for Samcheok, 4.51g for Mungyeong and 4.13g for Jeju population during the hibernation period (from early December, 2017 to early March, 2018). These losses accounted for 20.7%, 25.6% and 27.6% of the early-hibernation body mass for hibernating bats, and which amounts to 0.21%, 0.28% and 0.28% per day, respectively. The hibernation period of *M. fuliginosus* was different among three populations, and was closely related to the interaction between preference temperature and external minimum temperature fluctuations. This study represented the flexibility of energy strategies in hibernating bats through difference of thermal preference and energy strategy among local populations.

AP5-108

Effects of forest disturbance on bat assemblages in Japan as revealed by acoustic monitoring

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Bats are sensitive to both natural and human-induced environmental changes, and their responses vary among species. Thus, it is considered that bats can be excellent indicator taxa and they have previously been used as ecological indicators of environmental change in forest habitats. This study aimed to assess the effects of forest disturbance on bat activity. Levels of bat activity were determined using acoustic monitoring and compared between four forest types (primary forest, selectively logged natural forest, secondary forest and conifer plantation) that have resulted from different forest management systems and typhoon disturbance in the University of Tokyo Hokkaido Forest. To identify bat species from acoustic data, we constructed an acoustic identification algorithm using deep learning. Overall bat activity was highest in the primary forest, and lowest in conifer plantation. However, the relationship between forest type and bat activity varied among species. For example, *Myotis, Vespertilio* and *Nyctalus* spp. had highest activity in primary forest, whereas activity of *Barbastella* cf. *darjelingensis* was highest in selectively logged forest. By contrast, activity of *Murina* spp. showed no difference between forest types. These results indicate guild-specific responses of bats to forest disturbance, and that bat assemblages can be used as ecological indicators of the quality of forest environment. [This research was supported by JSPS KAKENHI JP16K00568 and Asahi Glass Foundation.]

AP5-109

The Entrance Shape of Furled Leaves May Be a Cue for *Kerivoula furva* Roost Selection

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Day roost is one of important resources in bat species that is associated with their fitness. Most of studies focused on where they roost or how the social interactions affect their roost selection. However, how bats make decision during initial process of roost selection is still poorly understood. A leaf-roosting bat, *Keriovula furva*, forms a social group in furled banana plant leaves and switches roosts almost every day following foliation. To understand whether *K. furva* can find appropriate roost sites based on furled leaf structures, we hypothesize that a v-shaped opening on the top of furled leaves may be a physical cue for bats to identify roost quickly. Behavioral tests are conducted by modifying the entrance structure of v-shaped opening on furled leaves. Then, the number of bat approaching and the time of bat entering the furled leaves in different trials are examined. We attempt to realize the relationship between animal decision making and environmental cues on ephemeral resources, which may be further understanding animal cognitive abilities.

AP5-110

Are Colonies of Male Parti-coloured Bats Aggregations or Societies?

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Females in breeding colonies exhibit cooperative behaviours i.e. group foraging, communal breeding and social warming. Much less is known about affiliate social interactions of males living in colonies. It remains unknown if they form aggregations of individuals who simply share roosts or also maintain social bonds. Our aim was to describe social behaviours of male parti-coloured bats *Vespertilio murinus.* We conducted our study in the village of Białowieża and the surrounding forest in 2015–2018. We captured bats using mist-nets and harp traps, individually marked them with PIT-tags, radio-tracked individuals and recorded male behaviours next to the roost. We expected that bats live in anonymous assemblages of individuals who share common roosts. Our results show that roost scarcity is not the main factor which promotes aggregations of male parti-coloured bats. More than 50 roosts used by colony members were found in subsequent years. Roost switching occurred very often and the recapture rate was extremely low. The number of males in roosts fluctuated intensively. No distinctive subgroups were observed in the colony. However, we registered dawn swarming in the vicinity of the most utilized roost. This behaviour is known as a mechanism by which group decisions to share the roost could be made, and it can indicate that there exist some kind of social interactions between individuals. Although, most likely, no strong social bonds are formed among individuals. This work was funded by the Polish National Science Centre on the basis of decision number DEC-2013/10/E/NZ8/00725.

AP5-111

Interaction of Afrotropical Bats, Parasites, and Microbial Symbionts

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Bats are highly speciose and harbor numerous bacterial, viral, and eukaryotic symbionts. The interplay between bacterial community composition and parasitism in bats has not been well characterized, and may have important implications for studies of similar systems. In this study we identify associations between bacterial symbionts, malaria parasites, and dipteran vectors of chiropteran diseases in nearly 500 individual bats representing 9 families, 20 genera, and 31 species. Mirroring recent studies of host-microbiome co-speciation in mammals, we find a very weak correlation between bat phylogeny and bacterial communities across the skin microbiota of bats studied, suggesting that host environment is more important than shared ancestry in shaping the composition of bacterial communities in the skin of bats. Lastly, we identify significant correlations between bacterial community composition of the skin and dipteran ectoparasites across four major bat lineages, suggesting a mechanism for host selection and potential transmission of vector-borne diseases in bats.

AP5-112

Characterization of daily roost in *Myotis rufoniger*

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Forests and woodlands offer foraging and roosting habitats for wild life species. In forest management, it is important to recognize the influence of management method on bat population. Especially the *Myotis rufoniger* is rare population in Korea and is distributed locally in Northeast Asia. Usually *Myotis rufoniger* inhabits forests dwelling during the activity period whereas uses underground sites during the hibernation. Interestingly, this species has confirmed phylogenetic position of Ethiopian although it is a limited oriental region. Characteristics of preference temperature, humidity, and hibernation periods were confirmed through hibernation monitoring in Korea. *Myotis rufoniger* is legally protected in Korea. However these ecological information are insufficient to show complete activity of the *Myotis rufoniger*. The purpose of this study was to characterize the daily roost of *Myotis rufoniger* in Korea. We found 17 daily roosting location data with radio tracking and direct/indirectly search from 2007 to 2019. These were found to be foliage roosting at the edge of the forest. Land coverage of daily roosting sites consisted of forest 41.2%, agriculture area 29.4% and grass 17.6%. When examining the land cover by extending 1 km from the observation site, forest 58%, agriculture area 20.8% and grass 8.5%. Our result show that *Myotis rufoniger*'s daily roosting seems to be related to the origin of Ethiopia and is significantly different from typical forest dwelling. Therefore, this study expects that ecological information of *Myotis rufoniger*'s roosting and foraging sites as an important factor will contribute to the management of habitat.

AP5-113

GPS Tracking of the Navigation Behavior of the Birdlike Noctule during Nightly Foraging

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To understand the navigation strategy for nightly foraging behavior of echolocating bats, GPS bio-logging experiment was conducted for the birdlike noctule (*Nyctalus aviator*). We attached 13 GPS data-loggers to the bats and successfully acquired flight trajectories from 8 bats for one or two consecutive nights (totally 14 night trips). The results show that the bats left their roost just after sunset and traveled for 1- 4 hours with a flight speed of approximately 7-8 m/s on average. Maximum trip distance was approximately 45 km and one individual flew up to 14 km away from their roost per night. During the two consecutive nights, each bat didn't follow a specific route or visit a specific site. However, they flew around almost the same area for foraging in two nights. Also, almost all bats often flew along and stayed on the base of the hill. In addition, the flight routes taken to return to the roost were different from those that were taken towards foraging ground after emergence. These findings suggest that the bats conducted large-scale navigation by path integration and/or a map-based system using their surrounding topographical information as a directional cue. [This research was supported by a Grant-in-Aid for Scientific Research (A) and Scientific Research on Innovative Areas of JSPS.]

AP5-114

Investigation of navigation strategy of Japanese horseshoe bats during natural foraging using GPS and Acoustic-GPS data-Loggers

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The purpose of this research is to understand the navigation strategy of Japanese horseshoe bats (*Rhinolophus ferrumequinum Nippon*) during natural foraging. We attached 52 data-loggers to the bats at their day roost in Fukui prefecture in Japan. We successfully obtained coordinate data from 13 bats and monitored the night movement for up to 7 days. As a result, we found that they were flying toward the same spot over several days, suggesting that each bat has own preferred foraging site. Most of them were flying not only in the nearby forest but also in the agricultural field approximately 3 km from the roost. In contrast, our previous GPS bio-logging shows that the horseshoe bats in Hokkaido where forest areas prevail never flew over nearby agricultural field. This suggests that the preferred foraging site might differ among even the same bat species depending on the external environment. Furthermore, we investigated echolocation behavior during nightly movement by using custom-made acoustic-GPS data-loggers which can simultaneously log both GPS positions and pulse emission timing. [This research was supported by a Grant-in-Aid for Scientific Research (A) and Scientific Research on Innovative Areas of JSPS.]

AP5-115

Project CLIMBATS: Evaluating the Effects of Climate Change on Insectivory Provided by Bats in European Farmlands

Climbats management committee

(https://www.cost.eu/actions/CA18107/#tabs|Name:management-committee)

Climate change poses major threats to biological communities and the ecosystem services they provide. Bats are sensitive to human-driven habitat alteration, and changes in temperature and water availability induced by climate change may affect their eco-physiology, distribution and ultimately survival. Climate change is therefore likely to influence European bat populations and affect insect consumption by bats in farmland, forests and urban areas, implying serious consequences for the conservation of European biodiversity as well as economy. However, little scientific work has addressed this issue, so we lack the knowledge to devise mitigation strategies. Between years 2019 and 2023 the European Cooperation in Science and Technology (COST) organization is funding the project CLIMBATS, an international initiative gathering 47 experts (mainly ecologists, agronomists and economists) from 20 European and Mediterranean countries, with the commitment to provide a better understanding on the interaction between bats and insectivory in farmland and the primary objective to forecast climate change effects on this service. The project is divided in three main goals and actions: 1) to define, predict and quantify the effects of climate change on bats across Europe; 2) to establish strategies to develop a network to monitor and predict changes in bat distribution and inform future management and policy; and 3) to evaluate the effects of climate change on insectivory provided by bats in farmland. The project is expected to generate knowledge transferable to other regions and farmland contexts, and thus to provide relevant information to improve the mitigation strategies for this economically and ecologically crucial ecosystem service worldwide.

AP5-117

Vocal Recognition between Females and Pups in the Bat *Vespertilio sinensis*

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Maternal recognition is an important part of the animal social communication. The study on it is conducive to reveal its function and adaptive evolution capabilities to identify signals. Many birds and mammals, due to the large selection pressure and other factors, there is often a mutual recognition between mother and child. Nocturnal bats rely heavily on vocal signals to communicate, although little research has been done on whether pups can identify their mothers solely by their maternal calls. We used *Vespertilio sinensis* for the study. We first investigated whether the maternal echolocation calls and pups calls were statistically different among individuals. Then, we explored whether it is possible to use individual characteristics for two-way recognition between mother and child. The results showed that: the young bats' isolation calls were with individual acoustic characteristics significantly, all of the playbacks of isolation calls, the mother bats could recognize the young bat calls; The echolocation calls of female bats also have individual characteristics which is significantly higher than the accuracy of random classification. Playback experiments showed that at 10 days of age, the infants could not recognize the echolocation calls of the females. But, at 21 days old, the response degree of biological females was higher than that of non-biological females, and the difference was significant. These results advance our understanding of the role of acoustic signals in mother-offspring recognition and the adaptive benefits of this communication, especially in conditions where pups' recognition of their mothers is critical.

AP5-119

Foraging ranges of the Hawaiian hoary bat on Maui

Dave Johnston, Kristin A. Jonasson[*] and Brad Yuen

H.T. Harvey & Associates

The foraging ecology of the Hawaiian hoary bat (*Lasiurus cinereus semotus*) has been poorly characterized and lack of information is hampering efforts to develop effective recovery plans. Previous research has been conducted on foraging ecology in continuously wet temperate forests on Hawaiʻi, but they may not apply to the drier slopes of Haleakalā on Maui. We outfitted 16 bats with radio-transmitters to characterize their foraging ranges. Bats were tracked for 3–7 nights before transmitters were lost. Foraging ranges (95% kernel) were large, ~13,600 ha or 7% of the island and "core use areas" (50% kernel) were ~3,700 ha or 2% of the island. Ranges are likely underestimates because bats were tracked for a short timeframe and because bats routinely moved out of range (e.g., over the ridge of Haleakalā crater). Current USFWS guidelines recommend 16 ha of forested habitat to support one Hawaiian hoary bat. Our data has substantial implications for management decisions and demonstrates the need for caution when applying data from different climate zones.

Bat Borne Paramyxovirus Surveillance in Bats and Bat Harvesters

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Zoonotic pathogens constitute 58% of all human infectious diseases. Several of these recent zoonotic outbreaks result from spillover events from bats. Members in the family *Paramyxoviridae* have demonstrated the ability to infect humans, livestock and peridomestic species. The genus *Henipavirus* have primarily been detected in pteropid fruit bats from Asia, Australia and Africa and is represented by 4 species; *Nipah henipavirus, Hendra henipavirus, Cedar henipavirus*, *Ghanaian bat henipavirus*. *Henipaviruses* are shed in the saliva, urine and feces of viremic bats, and environmental exposure is a common source of exposure. Due to its geographical topology, Northeast India is geographically isolated from mainland India and thus, relatively underdeveloped compared to the rest of the country. Villages are scattered throughout the states, and traditional practices such as bushmeat hunting are still exercised. We visited two Northeast Indian villages during their annual bat harvest and collected sera from both bat harvesters and harvested bats. Sera samples were diluted and screened for antibodies against a panel of *henipavirus* glycoproteins using a multiplex microsphere immunoassay. Tissues samples were also collected from the same bats, and screened for presence of paramyxoviruses with *Paramyxoviridae* specific PCR assay. Preliminary data shows a low infection rate of 6.8% in bat tissues as well as antibodies cross reactivity towards *henipavirus* glycoproteins in bat sera. In conclusion, bats sampled during the bat harvests were PCR-positive for paramyxovirus, and had antibodies that cross-reacted to *henipaviruses.*

Investigating the Risk of Human Disease from Parasites of Bats in Cambodia

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Southeast Asia is a hotspot for emerging and re-emerging infectious diseases, many of which are of zoonotic origin and have the potential to cause severe economic, social and health consequences. Bats play a central role in the transmission of several important zoonotic agents, such as filoviruses, coronaviruses, and henipaviruses. Cambodia is a global biodiversity hotspot that provides habitats for thousands of wildlife species, including over 70 species of bats. We aim to determine circulating parasites with human pathogenic potential by sampling bat populations at 250 sites across Cambodia and screening human sera from occupationally exposed individuals. We have collected 10,673 samples from 1,310 individual bats, from approximately 62 different bat species all from a variety of different habitats including evergreen forest, dry dipterocarp forest, rice fields and agricultural plantations and karst. A standardized sampling protocol using mist nets and acoustic detectors was developed and carried out to allow us to understand ecological and environmental variables associated with host and parasite presence-absence. This will add considerably to our knowledge of bat species distribution in Cambodia and facilitate the creation of predictive ecological relationship maps and risk models to inform future disease surveillance in Southeast Asia. Developing these predictive distribution maps will also benefit ecological studies and conservation efforts in Cambodia, with the hope of utilizing them in other Southeast Asian countries.

First record of *Pseudogymnoascus destructans* on bats in Italy

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Background. The spread mycoses constitute an emerging threat to wildlife conservation. This is the case of white nose disease, caused by the fungus *Pseudogymnoascus destructans* and responsible for the death of millions of bats across the US. In Europe, the presence of *P. destructans* was confirmed through molecular analyses in 17 bat species and from 18 countries, but the fungus was never reported from Italy. Therefore, to investigate the presence of this and other mycotic diseases, a mycological survey was performed on a bat hibernaculum in NW Italy.

Methods. Sterile cotton swabs were used to take a superficial sample from the skin of wings, ears and muzzles of a representative of captured bats. Fungal isolation was performed on Sabouraud Agar (SAB) Petri dishes incubated at 4°C at dark. Strains isolated in pure culture were identified through to morphological and molecular techniques.

Results. Twenty bats, either showing or lacking visible wing lesions (holes, irregular pigmentation, necrotic edges, scars), underwent mycological analyses. Eight individuals of *Myotis emarginatus* resulted positive for the presence of *P. destructans.*

Conclusion. In Europe, the precise demographic effects of fungal infections remain to be ascertained and it is urgent to fill this gap, since the absence of mass mortality does not necessarily imply the absence of significant damages due to mycoses. Since this study confirm the presence of potentially harmful fungi, precautionary measures should be adopted to avoid the risk of man-mediated diffusion of the pathogen, paying attention to prevent their spread in large geographical areas.

Seroprevalence of Filovirus Infection in *Rousettus aegyptiacus* Bats in Zambia

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Marburgviruses and ebolaviruses belonging to the family *Filoviridae* cause severe hemorrhagic fever in humans. Epidemiological evidence has suggested that bats play important roles in the ecology of filoviruses. Especially, some populations of Egyptian fruit bats (*Rousettus aegyptiacus*) have been shown to maintain marburgviruses in endemic countries such as Uganda. To better understand the ecology of filoviruses outside the endemic areas, we carried out an epidemiological study focusing on Egyptian fruit bats in Zambia.

Cave-dwelling Egyptian fruit bats (n=290) were captured in Zambia during 2014-2017 by using harp trap and blood samples were collected to screen filovirus-specific IgG with an enzyme-linked immunosorbent assay based on the viral glycoprotein antigens. Serological data were analyzed for prevalence, virus species-specificity, seasonal patterns, and body weight range of the bats.

IgG antibodies specific to multiple filovirus species were detected in 158 of 290 serum samples (54.5%). In particular, 127 bats (43.8%) were seropositive to the marburgvirus antigen. Distinct peaks of seroprevalence were repeatedly observed in November/December. The seroprevalence was particularly high in the bats weighing less than 50 g, suggesting that pups efficiently acquired marburgvirus-specific maternal antibodies. The seroprevalence was lowest in the bats with body weights ranging 51-60 g and gradually increased as they grow. Taken together, our data suggest that marburgviruses have been maintained in the Egyptian fruit bat population in Zambia. The present study highlights the need for continued monitoring of filovirus infection in this bat species even in regions where filovirus diseases have not been reported.

AP6-105

The bacteriome of insectivorous bats from Central and Eastern Europe

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Bats are the second largest order of mammals and include about 20% of all mammal species worldwide. They live in dense colonies and can adapt to various environments, thus bats may act as a potential reservoir for different pathogens including bacteria and parasites. Most studies on bacterial pathogens in bats have been focused on species-specific PCR based detection tests, but new techniques such as NGS allow the characterization of all bacteria, the so called bacteriome. The aim of our study was to analyze the bacteriome from bat heart tissues and to validate the positive samples for the presence of two vector-borne bacteria in tissues of bats from Central and Eastern Europe. For the NGS sequencing we used the multi-primer bacterial Ion 16S™ Metagenomics Kit (including 2 sets of primers: V2-4-8 and V3-6, V7-9) and for the validation of bacterial pathogens (*Bartonella* sp. and *Rickettsia* sp.) we performed multiple PCRs targeting different genes. Targeting seven different variable regions of the 16S rRNA gene in 8 individual samples we identified that the most abundant phyla corresponded to Proteobacteria, Firmicutes and Actinobacteria, with predominance of the Gammaproteobacteria, Bacilli and Actinobacteria classes respectively. The only bat vector-borne pathogen identified was *Bartonella* spp. from the bat species *N. noctula*. Studies on the detection of *Bartonella* spp. were performed from different bat samples and it was identified one strain with a possible zoonotic potential. Our results provide a first insight into the bacterial community found in heart tissue of bats from Central and Eastern Europe.

AP6-106

Detection of haemosporidian parasites in cave-dwelling bats (Mammalia: Chiroptera) in Thailand

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Haemosporidian parasites infect diverse groups of mammals including bats. The best-known genus *Plasmodium*, a causative agent of malaria in humans, is a major public health concern in tropical countries. *Plasmodium* parasites and the other members of haemosporidians i.e. *Polychromophilus*, *Nycteria* and *Hepatocystis* were reported in African bats. To the best of our knowledge, no investigation of haemosporidian infection in bats in Thailand had been conducted until recently. Here, we explore the infection of haemosporidians in cave-dwelling bats in Saraburi, Kanchanaburi, Ratchaburi, and Songkla provinces of Thailand from 2018 to 2019. A total of 80 individual blood samples were collected from 14 different bat species. Majority of bats were *Taphozous melanopogon* (n=34) and *Hipposideros armiger* (n=10). The other bat species obtained in this study were *Kerivoula hardwickii, Megaderma spasma, Myotis siligorensis, Hipposideros* spp. and *Rhinolophus* spp. Haemosporidian parasites were detected in 17 samples of 6 different species of bats by PCR using specific primers, and 11 samples were also microscopically positive. In our preliminary result, DNA sequencing confirmed the findings of *Hepatocystis* in 3 samples of *Hipposideros armiger.* Our observation extends the current understanding of haemosporidian infection in bats in Thailand and confirms the existent of *Hepatocystis* for the first time in the country. Further investigations about the number and geographical location across Thailand are needed to understand the species diversity of both the parasites and the bats and might help the effort of bat conservation.

Key words: Bat, Detection, Haemosporidian, *Hepatocystis*, Thailand

AP6-107

Phylogenetic Analysis of *Hepatocystis* Parasites of the Four Mainland Australian Flying Fox Species

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Bats host a high diversity of malaria parasites. Old-World fruits bats (Pteropodidae) are commonly infected with the malaria parasite genus *Hepatocystis* and several recent molecular studies have investigated *Hepatocystis* parasites of African fruit bats. The knowledge of Australian *Hepatocystis* parasites is limited to morphological studies. Uncovering the evolutionary history and biology of these parasites is of interest for the study of the taxonomy and systematics of malaria parasites and will help understand biological adaptations and host switches. We investigated the occurrence and phylogenetic relationships of *Hepatocystis* parasites of the four mainland Australian flying fox species, *Pteropus alecto, Pteropus conspicillatus, Pteropus poliocephalus* and *Pteropus poliocephalus.* The multi-gene phylogeny recovered a monophyletic clade of *Hepatocystis* parasites of Asian and Australian *Pteropus* species and revealed two main parasite clades both comprising parasites of all the different host species, thus no host species specificity is apparent. Strikingly, *Hepatocystis* parasite infections in *Pteropus poliocephalus* span its entire distribution range in Australia, including tropical and temperate zones and the southern-most colony in Adelaide. The study provides evidence for a *Pteropus*-specific group of *Hepatocystis* parasites that commonly infect the four *Pteropus* species in Australia.

AP6-108

Distribution, host specificity, and variation in *Arthrorhynchus nycteribiae* and *A. eucampsipodae* (Laboulbeniomycetes), an update

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Arthrorhynchus (Ascomycota, Laboulbeniomycetes) is a genus of ectoparasitic fungi apparently restricted to Eastern Hemisphere species of nycteribiid bat flies (Diptera, Nycteribiidae). The genus has an interesting taxonomic history, first having been described (in 1857) as an acanthocephalan worm. Currently, four species are accepted in the genus, *A. acrandros*, *A. cyclopodiae*, *A. eucampsipodae*, and *A. nycteribiae*. The taxonomic status of these species is unclear, because no comparative sequence data exist. Only *A. eucampsipodae* and *A. nycteribiae* have been found since their description. During our studies, we have observed both species from the pan-European bat flies *Nycteribia schmidlii*, *Penicillidia conspicua*, and *P. dufourii*. Recent collecting efforts have expanded to Africa, and we report new country records from Rwanda (*A. eucampsipodae*), Tanzania (*A. nycteribiae*), and South Africa (both species). We also isolated DNA and generated large subunit nuclear ribosomal DNA sequences from *Arthrorhynchus eucampsipodae* on *Nycteribia schmidlii*, *N. vexata*, and *Eucampsipoda africana*, and from *A. nycteribiae* on *P. conspicua*. Molecular phylogenetic inference of the LSU dataset reveals that *A. eucampsipodae* is a species complex, segregated by host. This specificity of *A. eucampsipodae* seems to correspond to host genus-level, as one clade comprises isolates that originated from both *N. schmidlii* (Slowakia) and *N. vexata* (Bulgaria). After *Hesperomyces virescens*, this is the second species of Laboulbeniales for which phylogenetic data points to *near-cryptic*, host-associated species within a previously morphologically circumscribed taxon.

Mercury Lab – Bring the Laboratory to the Sample

Joseph A. Russell and Chris Detter

MRIGlobal – 65 West Watkins Mill Road, Gaithersburg, MD, USA 20878

The ability to extract biological information from a given environment has undergone substantial change in just the past 3 years. Some of the latest hardware designed for quantitative PCR, antibody and protein detection, and genomic sequencing can easily fit in your coat pocket. The writing on the wall illustrates a future where advanced molecular diagnostics, biosurveillance, and forensic testing no longer requires transporting a sample back to a central reference laboratory. Samples can be processed on site, at the point-of-need, alleviating processing bottlenecks and dramatically reducing the time to acquire an actionable result. However, this future has not yet been realized. Despite the footprint of the molecular hardware becoming remarkably small, the operational footprint of the work is not equally small. Ancillary equipment including (but not limited to) a stable power supply, cold-chain storage, reagent/consumables storage and transport, computational capacity, a stable workbench, biohazard waste disposal strategies, biosafety equipment, and other logistics – all necessary for the effective use of the full complement of modern, hand-held genomics hardware – are capable of growing the operational footprint of these devices to sizes that are not reasonable to deploy at the point-of-need. MRIGlobal has developed a product to address this problem. This product is a purpose-built platform that provides all the necessary operational equipment in a human-centered laboratory-workbench design such that rapid, reproducible deployment of advanced genomic technologies to field-forward locations is no longer strategically unfeasible. This mobile laboratory, *Mercury Lab*, is a first-of-its-kind product that was built to lower the barrier-to-entry of modern molecular hardware where it is needed most.

Neutralizing antibodies to pseudotyped *Scotophilus* bat coronavirus-512 in human serum

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Bats have been proved natural reservoirs of severe acute respiratory syndrome-coronavirus (SARS-CoV). Scotophilus bat CoV 512 and SARS-related CoV have been detected in 9 bat species in Taiwan. Potential zoonotic risk of bat CoV urged a survey of antibodies to bat CoV amongst bat biologists, who are at the highest risk of exposure to bat CoV due to the bites and scratches by bats and frequent contacts of bat faeces and blood. Total 58 bat biologists have given informed consent for blood samples and specific antibodies to the spike (S) protein of *Scotophilus* bat CoV-512 were detected in 18 of them (18/58, 31%) by using immunofluorescent antibody assay (IFA). To understand the neutralizing ability of the antibodies to *Scotophilus* bat CoV-512 in the human serum, lentivirus pseudotyped with the S protein of *Scotophilus* bat CoV-512 (Sco-S) was used to infect *Scotophilus* bat CoV-512 susceptible cells. Concentration-dependent infection reductions were observed after the treatment of human serum positive to S protein of *Scotophilus* bat CoV-512 by IFA to both pseudotyped *Scotophilus* bat CoV-512 carrying red fluorescent protein (Sco-S-RFP) and pseudotyped *Scotophilus* bat CoV-512 carrying luciferase (Sco-S-LUC). The results indicated the neutralizing ability of antibodies to *Scotophilus* bat CoV-512 in human serum. Therefore, *Scotophilus* bat CoV-512 can infect and induce neutralizing antibodies in human. Further studies are required for understanding the cross-transmission mechanism of *Scotophilus* bat CoV-512 and public health controls.

Host-parasite relationships between bats and bat flies of South-Eastern Europe: the importance of multi-species bat roosts

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Bat flies are strongly connected to their hosts and often they are the most abundant parasites on bats. They show a strong specialization in the parasitic lifestyle to exploit the bats with their morphological or behavioral adaptations. The European species are described as having high host specificity, often exploiting just one or a few related species as hosts. Bat flies have been confirmed to be vectors for *Bartonella* or Hemosporidia species. From epidemiological point of view, it is important to evaluate the vector potential of bat fly species. Our aim in this study was to characterize the bat fly species based on the specificity level and assess information on host-parasite relationship. We collected more than 2200 bat flies (9 species) from the Southeast European region and studied their seasonality and host specificity. A total of 2801 individual bats (13 out of 28 species carried flies, prevalence 36%) were screened. We found four fly species to be highly host specific and other four species having more than one main host. We conclude that the level of infestation shows an increasing trend from spring to autumn and the specificity level of most bat fly species is lower in autumn. In contrast, occurrences of bat flies on secondary hosts was higher in spring, due to lack of multi-species host assemblages in roosts. The level of infestation, the season and the local host species composition all influence the host specificity level of bat flies.

AP9-100

Assessing Bat Mortality at Onshore Wind Turbines in Western Taiwan

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Wind power has become the fastest-growing sector of the renewable energy industry globally. However, it is also known to be an important threat to birds and bats. In some regions, the mortality rate of bats was higher than birds, and hundreds of thousands bat fatalities were estimated. However, previous studies mainly focused on bats from Europe and North America, and the knowledge about its impacts on tropical bats is lacking where bats could remain active all the year round and the wind energy is growing fast during the past decades. Our study aims to evaluate the bat mortality caused by wind turbines in Taiwan. From November 2018, we conducted carcass searches, along with carcass detection and removal experiments, over 135 wind turbines bimonthly in the west-coast areas of Taiwan. We also analyzed the bat activity and composition around the wind turbines using bat echolocation calls recorded. The preliminary results showed that at least 6 bat species (Vespertilionidae) were found killed by wind turbines and a higher mortality rate of birds than bats was found in winter.

AP13-100

BatMap Long Island – Citizen Science Paving the Way for Bat Distribution and Landscape Ecology Research

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The distribution of bats throughout Long Island, New York are not well understood regarding which species are truly migratory, where summer roosts occur as well as landscape utilization. Of great interest is the distribution of the Northern Long-eared Bat *(Myotis septentrionalis)*, threatened both federally and in New York state as a result of the spread of white-nose syndrome. Survey 1-2-3, a mobile application associated with esri's ArcGIS Online was implemented to provide a mechanism for the general public to report incidental observations of bats in Queens, Kings, Nassau, and Suffolk Counties. The survey allows for participants to provide information on their spatial location, time and date, characterization of landscape, behavior, and number of bats observed. Participants can indicate if they would like their property further surveyed using boacoustical monitors by providing their email. Survey 1-2-3 data are collected using Apple or Android devices on or offline and upload directly to the Cloud to populate a map in real-time to show bat observations across Long Island. Seatuck Environmental Association provides trained bioacoustical technicians and equipment to assess properties indicated by Participants. The ultimate goal visualize *where* various species of bats are observed and to assess their emergence and/or feeding habitats. Where *M. septentrionalis* are recorded, the expectation is to acquire permits for capture to confirm their presence. Citizen science through the use of Survey 1-2-3 provides the means to have "many eyes on the ground" to assess *where* the bats are to more effectively research landscape gradients associated with their observed locations.

AP13-101

Establishing community-based conservation to protect flying foxes in Sulawesi, Indonesia

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Flying fox conservation is challenging as many species are not protected legally and often roost outside protected areas. However, villages in Indonesia have their own autonomy to advance innovative programs, providing opportunities to incorporate conservation projects as part of development, and increase likelihood of success and sustainability. In Central Sulawesi in 2017, we established a community-based conservation program to protect a mixed-colony of flying foxes (*Acerodon celebensis*, *Pteropus alecto*, and *Pteropus griseus*) which is threatened by hunting. We started by conducting research on flying fox ecosystem services to communicate their importance to the community. We then worked with the community based on their interests on environmental issues and vision for the village—gathering input through dialogues, key informant interviews, and focus groups. The resulting program includes monitoring of the flying fox population, hunting patrols, formulating regulations to protect the island, and establishing an ecotourism program. In order to track the impact of the new hunting ban, we monitored the flying fox population together using emergence counts. The average population in 2018 was ~3,500 individuals, which was significantly higher than the initial ~300 individuals in 2017 ($t = 6.5984$, $p < 0.05$). The results suggest that the hunting prohibition had a positive impact on the recovery of the colony, and no further hunting has been recorded since the start of the project. Currently, we are actively working with the community on greening and waste management in preparation for the ecotourism program and conservation education, and they have expressed positive attitudes toward flying foxes.

AP14-100

Reference Review and Prospect of Formosan Flying Foxes in Taiwan

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Pteropus is a genus of bats, which has about 65 species in the world, and is mainly distributed in tropics and subtropics. Their population has declined over the past several decades since natural and anthropogenic affect, such as typhoons, climate change, hunting and habitat loss. There are five subspecies belonging to *P. dasymallus*, which is listed as Vulnerable of IUCN. *P. d. dasymallus* and *P. d. daitoensis* (Daito) are Critically Endangered. *P. d. inopinatus* (Okinawa) and *P. d. yayeyamae* (Yaeyama) are Near Threatened. *P. d. formosus* (Taiwan) is on the verge of extinction. However, *P. d. formosus* is listed of Nationally Critical terrestrial mammal taxa in Taiwan. Formosan flying fox had a stable population (over 2,000 individuals) on Green Island before 1980. Overhunting and habitat destruction dramatically threatened the population during 1976-1986. It was listed as a protected endangered species by Wildlife Conservation Law in 1989. Some individuals were re-observed in eastern Taiwan, Green Island and Turtle Island from 2006-2012. Recently, we want to stop the population decline even rescue the population number. But the last wild survey of Formosan flying fox was made in 2012, therefore we have to renew the current status. First, we have restart wild survey and establish the long-term monitoring. Second, evaluate the population size by the survey data. Final, propose the action plan. We collected related references show that 62 records from 15 counties during 1990-2017. This study was using trace search, auto-camera, and visual observation in wild survey. Preliminary results found 491 ejected pellets, 21 feces, 10 auto-camera images, and 20 observations from109 sites in 2018. We will going to set up a monitoring model on main population of Taiwan and to estimate the population size. Finally, we will publish an action plan of Formosan flying fox in the future.

AP14-102

The Role of the Pteropodid Bat, *Pteropus mariannus*, As a Seed Disperser on Guam

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Since the mid-1940s, the majority of Guam's avifauna and pteropodid bat species have become extirpated due to the accidental introduction of the brown treesnake (*Boiga irregularis*); this has led to a general lack of flying seed dispersers for native flora. The Mariana fruit bat (*Pteropus mariannus*) is the last-known, native volant organism found in the wild on Guam and is likely critical to the dispersion of seeds but is itself endangered (IUCN Red List). This study sought to discern the role that *P. mariannus* play in seed dispersal and germination success. This was was assessed by measuring gut retention times and comparing the germination success rates of seeds scarified through bat handling and\or passing through its digestive tract against those that had not. The "fruit" (syconium) of native *Ficus prolixa* was chosen as the flora test species due to its dominance in the diets of *P. mariannus*, local availability and botanical significance. Initial results indicate that there is an increase in germination success rates with bat scarified seeds in addition to the dispersal services they perform adding greater importance to current efforts to conserve and enhance Guam's severely dwindled populations.

Are Eavesdropping Phyllostomid Bats Hunting in the Tropical Canopy?

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Bats from the guild of passive eavesdropping gleaners glean prey from the surfaces of substrate, using acoustic cues from their prey to detect, classify and locate them. This group has been found to passively listen to a variety of prey sounds from leaf rustling, wing beats and very commonly, sexual signals. When predators eavesdrop on the auditory sexual advertisements of prey this can lead to an evolutionary "arms race." Such prey evolve more and more cryptic signaling strategies, while predators evolve better and better detection techniques. The tropical canopy with its incredible species abundance has proven a challenging arena to study. Both gleaning bats and their sound-emitting prey use the canopy, but it is unknown to what extent if any their eavesdropping behavior contributes to selection pressure or if the canopy serves instead as a refuge for these herbivores. These results could illuminate a significant interaction in canopy ecology of the tropics. Using speakers to play back the auditory sexual advertisement signals of 8 species of katydids (Tettigoniidae) and one cicada species at four heights in the canopy, I am investigating the hunting behaviors of these eavesdropping predators in the canopy. The acoustic signals were chosen for their high detectability and have been confirmed to call at the respective heights, so we may identify if either signal or height have any effect upon prey choice. Through this study I will contribute to unravelling the role bats play in this complex and mysterious niche swaying above our heads.

AP15-102

Bat Tissues in the HNHM Collection of Genetic Resources

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The Hungarian Natural History Museum (HNHM) joined the Global Genome Biodiversity Network in 2014. Since then the Molecular Taxonomy Laboratory (MTL) of the HNHM made a significant effort to adopt GGBN standards in tissue sample storage and development of registry system. The Collection of Genetic Resources now comprises over 8000 digitally registered tissue and DNA samples belonging to more than 700 animal and plant taxa. The database follows the Darwin Core, whereas the tissues are stored in -80°C freezers, in liquid nitrogen or in silicagel at 4°C.

The importance of the HNHM samples is emphasized by the fact that the high-quality tissue samples are associated with vouchers catalogued with Unique Identifiers and identified by experts. The whole collection will soon be fully available through the GGBN search engine. In the case of vertebrates detailed additional data (habitat info, echolocation recordings, digital images, measurements) are typically also stored in the museum's archives and databases making the subsequent integrated taxonomic-systematic research possible.

The collection includes 2560 bat samples, belonging to 15 families and 84 genera, representing 353 species (including type specimens of several recently described taxa) mainly from Southeast Asia, Europe and North America (31 countries). These samples provide a solid base to a wide spectrum of phylogenetic and systematic works; hence we are open to collaborative work worldwide. The physical and virtual access is facilitated by the HNHM participation in the CETAF and DISSCo consortiums.

AP1-116

An endeavour to revise and digitise the bats of Thailand – the first step to the future of conservation

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Over 50 taxa of bats have been described or elevated to species rank from Southeast Asia during the last decade, with 12 of which are from Thailand. The increasing number of the known species suggested that we are still far from understanding the pattern of bat diversity out there. However, we cannot be simply pleased with this rich in species and ignore the threats, either habitat loss, hunting or unregulated ecotourism activities, that affect the population of bat as a whole. An integrative strategy combining scientific research, habitat management, law enforcement, as well as community conservation education, should be incorporated. Nonetheless, nothing can be geared forward at full speed without an extensive database of bats of the country. The current endeavour aims to work together with multi-institutional network to revise taxonomy, digitise distribution and specimens records, continue building capacity and modernise museum collections. It will increase the basic knowledge of bats of Thailand particularly in documenting records of all bats known in the country, which will provide information of distribution and population status for further step of conservation measures. The taxonomic study itself will aid the taxonomic issues of several Southeast Asian species complexes as Thailand is located in the centre of the distribution of most of them. At the end of road, we hope this is the first step for the sustainable future of bat conservation.

AO5-143

Ecology Outweighs Evolutionary History in Shaping the Bat Microbiome

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Recent studies of mammalian microbiomes have identified strong phylogenetic effects on bacterial community composition. Bats (Mammalia: Chiroptera) are among the most speciose mammals on the planet and the only volant mammal. We examined 1,236 16S rRNA amplicon libraries of the gut, oral, and skin microbiota from 497 Afrotropical bats (representing 9 families, 20 genera, and 31 species) to assess the extent to which host ecology and phylogeny predict microbial community similarity in bats. In contrast to recent studies of host-microbe phylosymbiosis in other mammals, we found no correlation between chiropteran phylogeny and bacterial community dissimilarity across the three anatomical sites sampled. For all anatomical sites we found host species identity and geographic locality to be strong predictors of microbial diversity and observed a positive correlation between elevation and bacterial richness. Lastly, we identified significantly different bacterial associations within the gut microbiota of insectivorous and frugivorous bats. We conclude that the gut, oral, and skin microbiota of bats are shaped predominantly by ecological factors and do not exhibit the same degree of phylosymbiosis observed in other mammals.

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