14th European Bat Research Symposium

Donostia, The Basque Country

1-5 August 2017

EBRS2017

BOOK OF ABSTRACTS

14th European Bat Research Symposium

Donostia, The Basque Country

1-5 August 2017

eman ta zabal zazu

Universidad del País Vasco

Euskal Herriko Unibertsitatea

udako euskal unibertsitatea

upna Universidad Pública de Navarra

Nafarroako Unibertsitate Publikoa

NATURAL HISTORY MUSEUM OF DENMARK
UNIVERSITY OF COPENHAGEN

14th European Bat Research Symposium - EBRS 2017
Abstract book
1-5 August 2017
Donostia, The Basque Country
ISBN: 978-84-697-4575-5

Book design: Antton Alberdi
Logo design: Tere Uribe-Etxeberria
Technical edition: Joxerra Aihartza, Antton Alberdi & Inazio Garin
Abstract edition: Anthony M Hudson & Peter HC Lina
The Organizers wish to thank the technical staff of the IM Barriola Building and the Uda Ikastaroak/Summer Courses, specially Juan Luis Cruz and Ainhoa Urbieta.
Printed in Hizki Inprimategia, Zarautz, in July 2017

Index

Organising committee

Local Commitee

Joxerra Aihartza
University of The Basque Country

Ostaizka Aizpurua
University of Copenhagen

Antton Alberdi
University of Copenhagen

Aitor Arrizabalaga
University of The Basque Country

Unai Baroja
University of The Basque Country

Ane Caro
University of The Basque Country

Amaiur Esnaola
University of The Basque Country

Inazio Garin
University of The Basque Country

Urtzi Goiti
University of The Basque Country

Lide Jimenez
University of The Basque Country

Maria Napal
University of Navarre

German Velayos
University of The Basque Country

Editorial Commitee

Anthony M Hutson

Peter HC Lina

Scientific Commitee

Joxerra Aihartza
University of The Basque Country

Stéphane Aulagnier
Université de Toulouse

Hans J. Baagøe
Natural History Museum of Denmark

Raşit Bilgin
Bogazici University

Wiesław Bogdanowicz
Museum & Institute of Zoology PAS

Dina Dechmann
Max Planck Institute for Ornithology

Jasja Dekker
Independent Consultant, The Netherlands

Carles Flaquer
Museu de Ciències Naturals de Granollers

Suren Gazaryan
UNEP/EUROBATS

Urtzi Goiti - **Coordinator**
University of The Basque Country

Marina Kipson
Charles University in Prague

Daniela Hamidović
State Institute for Nature Protection, Croatia

Ivan Horaček
Charles University in Prague

Gareth Jones
University of Bristol

Javier Juste
Estación Biologica Doñana

Thomas Lilley
University of Liverpool

Radek K. Lučan
Charles University in Prague

Sébastien Puechmaille
Greifswald University

Paul Racey
University of Exeter

Hugo Rebelo
CIBIO

Stephen Rossiter
Queen Mary University of London

Manuel Ruedi
Museum d'Histoire Naturelle, Genève

Danilo Russo
Università degli Studi di Napoli Federico II, Naples

Emma Teeling
University College Dublin

Christian Voigt
Leibniz Institute for Zoo and Wildlife Research

Supporters

Patron

eman ta zabal zazu

Universidad del País Vasco

Euskal Herriko Unibertsitatea

Sponsors

wildlife ACOUSTICS
BIOACOUSTICS MONITORING SYSTEMS

Pettersson

www.BATLOGGER.com

Other supporting companies

Avisoft Bioacoustics

TiTLEY SCIENTIFIC

DODOTRONIC

APODEMUS field equipment

HSL

PELAGIC PUBLISHING

ECOTONE

nhbs Everything for wildlife, science & environment

Wildcare Nationwide Ecology Supplies

biotope

Financial support

eman ta zabal zazu

Universidad del País Vasco

Euskal Herriko Unibertsitatea

EUSKO JAURLARITZA
GOBIERNO VASCO

Points of Interest Map


Tenis Ondarreta
Restaurant
-BANQUET-
Miramar
Palace
-WELCOME
CEREMONY-
Ondarreta
Youth Hostel
Olarain
Residence Hall
DOKA
Pub Theatre
-GASTROPARTY-
Barriola Building
-MAIN VENUE-
Manuel Agud Querol
Residence Hall
Bahía de
la Concha
Ezeiza
Hotel Avenida
De Sagastizar
Plazatxoa
Del Padre
Meagher
Plazatxoa
Eugenio Imaz
Plazatxoa
Escuela de Ingenieros
Universidad de...
Tecnun. Sede
Ibaeta. UNAV
Ibaeta Plaza
Xarma
Hotel NH San
Sebastian Donosti
1 KM (15 minutes on foot)

MONDAY, JULY 31th

17:30-20:00 Registration Desk open at Miramar Palace
19:00-20:00 **Welcome Ceremony** at Miramar Palace

TUESDAY, AUGUST 1st

8:00 Registration Desk open at Barriola
8:15-8:30 **Official opening**
8:30-9:15 Invited talk:

Emma Teeling (University College Dublin)
"Bats are special and we should care: the genomic bases of bats' extraordinary adaptations"

*Student

Morning Session 1

Subject: Population genetics, phylogenetics and taxonomy
Convenor: Gary F MacCraken

9:15	When the extant bats arose? Fossil record and molecules illuminate the history of the bat fauna in Western Palearctics. **Ivan Horacek**
9:30	Phylogeography of Daubenton's Bat *Myotis daubentonii* in Europe. **Javier Juste**
9:45	Population genetic structure of Bechstein's bats (*Myotis bechsteinii*) across Europe and Britain: has Brexit already happened? **Patrick Wright***
10:00	Complex hybridization before complete speciation: interesting mito-nuclear discordances among three *Rhinolophus* species. **Tong Liu***
10:15	Genetic structure in the mediterranean bat *Myotis capaccinii*: multiple refugia, post glacial dispersal and mito-nuclear discordance. **Elizabeth M Hemond**
10:30	General Discussion

10:45-11:15 Coffee/Tea break
(Sponsored by Pettersson Elektronik)

Morning Session 2 Tuesday, August 1st

Subject: Population genetics, phylogenetics and taxonomy
Convenor: Dina Dechmann

11:15	Contrasting phylogeography and population structure in two ecologically similar *Rhinolophus* species, *R. euryale* and *R. mehelyi*. **Sebastien J Puechmaille**
11:30	Geneflow within and among species of *Plecotus* bats in the Alpine range. **Tommy Andriollo**
11:45	The role of biotic interactions in shaping the range of cryptic bat species. **Roberto Novella***
12:00	Coexistence of two sympatric cryptic bat species of French Guiana: genetic, acoustic and ecological characterization. **Ondine Filippi-Codaccioni**
12:15	A bat out of Africa: new insights on the existence of a North African refugium for Western Palearctic bat fauna. **Francisco Amorim***
12:30	General Discussion

12:45-14:30 Lunchtime

Afternoon Session 1 Tuesday, August 1st

Subject: Population genetics, phylogenetics and taxonomy
Convenor 1A: Ostaizka Aizpurua **Convenor 1B**: Jasja Dekker

	Session 1A	Session 1B	WS
14:30	Integrating landscape genetics with connectivity analyses to prioritize regional conservation of *Plecotus auritus begognae* in the Iberian Peninsula. **Helena Santos**, presented by **Hugo Rebelo**	Rapid assessment of bats on Bougainville Island: searching for monkey-faced fruit bats and spare tires. **Frank J Bonaccorso**	Wildlife Acoustics Workshop I | 1h duration
14:45	Genetic and echolocation divergence in *Rhinolophus hipposideros*: is the population of the Maltese Islands distinct? **Clare Mifsud***	Insular bats and research efforts: a review of global patterns and priorities. **Irene Conenna**	

	Session 1A	Session 1B	WS
15:00	Species-specific impact of habitat fragmentation on the population genetic structure of Neotropical bats. **Tanja Halczok***	Bats activity in a well preserved high Alpine forest. **Dino Scaravelli**, presented by **Pamela Priori**	Wildlife Acoustics Workshop I: Hands-on Workshop with the New Echo Meter Touch 2 Handheld Bat Detector
15:15	Genetic variability of *Rhinolophus mehelyi* at the northern margin of distribution range. **Alexandra Corduneanu***	New Data on the Greater Noctule, *Nyctalus lasiopterus* (Schreber, 1780) in France. **Marie-Jo Dubourg-Savage**	
15:30	Twins or cousins: two species of "desert" big-eared bats (*Plecotus*; Vespertilionidae, Chiroptera) coexist in Mongolia. **Sergei V Kruskop**	The importance of biotic and abiotic interactions for understanding bat species distributions in an insular system. **Ana Rainho**	
15:45	Comparative phylogeography of two cryptic serotine bats in the Iberian Peninsula and gene flow consequences of being too similar. **Alejandro Centeno-Cuadros,** presented by **Javier Juste**	Distribution patterns of selected bat species in Poland – spatial modelling improved by application of fine-scale forest data. **Mateusz Ciechanowski**	
16:00	General Discussion	General Discussion	

16:15-16:45 Coffee/Tea break

Afternoon Session 2 Tuesday, August 1st

Subject: Diversity and distribution
Convenor 2A: I Ruczynski **Convenor 2B**: Julie Dahl Møller

	Session 2A	Session 2B
16:45	Determinants of spring migration onset in female common noctule bats. **Dina KN Dechmann**	A Model for the Assessment of the Favourable Conservation status of bats in a concrete planning area. **Herman JGA Limpens**

	Session 2A	Session 2B
17:00	The genetics of migration of the tequila bat (*Leptonycteris yerbabuenae*). **Angelica Menchaca Rodriguez***	Monitoring urban bat populations. **Marcel J Schillemans**
17:15	Are all mountains the same? Changes in South American bat diversity patterns along environmental gradients. **Cristina Rios-Blanco***	Changes in numbers and reproductive status of bats during swarming in Natura 2000 site PLH080003 "Nietoperek". **Justyna Blesznowska**, presented by **Tomasz Kokurewicz**
17:30	Landscape population genetics of the greater horseshoe bat (*R. ferrumequinum*) in West-Eastern France. **Orianne Tournayre***	Calculating bat trends based on car-transect monitoring data. **Thomas van der Meij**
17:45	An investigation of the social structure, species boundaries, hybridization and phylogeography of three *Miniopterus* species (Mammalia: Chiroptera). **Kanat Gürün***	Long-term bat population trends in East, Central and South-West Romania. **Georgiana Marginean**, presented by **Oana M Chachula**
18:00	Are secondary woodlands providing suitable resources for biodiversity? Bats as a case study. **Elisa Fuentes-Montemayor**	Distribution and size of summer bat colonies around a lowland wetland area – the example of 'Drużno Lake' nature reserve. **Marta Szurlej**
18:15	General Discussion	General Discussion

20:15 **European Gastro-party** at DOKA pub theatre

WEDNESDAY, AUGUST 2nd

8:00 Registration Desk open
8:15-9:00 Invited talk:

Kristine Bohmann (University of Copenhagen)
"Bat diet studies – past, present and future"

Morning Session 1

Subject: Dietary ecology
Convenor: Fabio Bontadina

9:00	Bats Aloft. **Gary McCracken**
9:15	Scrutinizing key steps for reliable metabarcoding of bat fecal samples. **Antton Alberdi**
9:30	The poop experiment: defining sampling procedures for metabarcoding dietary studies in bats. **Vanessa Mata***
9:45	Trait-based diet analysis of an insectivorous bat: novel insights into foraging ecology. **Aitor Arrizabalaga**
10:00	Diet composition and variability of the common bent-wing bat (*Miniopterus schreibersii*) in Iberia. **German Velayos-Gainza***
10:15	Regional mismatches between agricultural pest and biocontrol services by bats. An example from continental Portugal. **Javier Rodríguez-Pérez**
10:30	General Discussion

10:45-11:15 Coffee/Tea break

Morning Session 2

Subject: Dietary ecology
Convenor: Ivan Horáček

11:15	Does the gut microbiota contribute to the dietary shift of fishing bats? **Ostaizka Aizpurua**
11:30	Food availability affects energy management and reproductive tissue development in male parti-coloured bats, *Vespertilio murinus*. **Ewa Komar**, presented by **Ireneusz Ruczynski**

11:45	Sitka Spruce plantations: A potential opportunity for bat populations? **Lucinda Kirkpatrick***
12:00	Saving trees for saving bats: treed landscape elements as key foraging habitats for insectivorous bats in intensively farmed landscapes. **Sílvia Barreiro**
12:15	The importance of temporary lakes and ponds for bat conservation in Neotropical rainforests. **Laura Torrent***
12:30	General Discussion

12:45-14:30 Lunchtime

Afternoon Session 1 Wednesday, August 2nd

Subject: Behavioural ecology
Convenor 1A: SJ Puechmaille **Convenor 1B**: MJ Dubourg-Savage

	Session 1A	Session 1B	WS
14:30	Sociality as a driver of thermoregulatory and roost-switching behaviors in a forest bat. **Danilo Russo**, presented by **Leonardo Ancillotto**	Modelling roost dispersal of greater horseshoe bats using landscape connectivity models. **Domhnall Finch***	Wildlife Acoustics Workshop II: Hands-on Workshop, From the SM4BAT Recorder to Kaleidoscope Pro Analysis
14:45	New insights into the hibernation strategy of Bechstein's Bat (*Myotis bechsteinii*) in Germany. **Karl Kugelschafter**	Microhabitat density predicts roost use by a rare tree-dwelling bat. **Andrew Carr***	
15:00	Why and when do bats fly out in winter ? A field study in the north of Flanders, Belgium. **Ralf Gyselings**	Effects of forest gaps on bat communities: a case study in Valsaín. **Elena Tena***	
15:15	An influence on climatic factors on numbers of bats hibernating underground – the consequences for methodology of winter monitoring. **Tomasz Kokurewicz**	Lifetime reproductive success of fecund female greater horseshoe bats is affected by matrilineal rank and grandmother's parturition. **Roger D Ransome**	

	Session 1A	Session 1B	WS
15:30	Object characteristics, temperature regimes and hanging site selection in hibernating bats. **Luc De Bruyn**	Physiological plasticity of *Carollia perspicillata* (Seba's short-tailed bat) related to ecological and social environment. **Nicolas Fasel**	Wildlife Acoustics Workshop II | 1h duration
15:45	Behavioural and physiological responses in *Rhinolophus euryale* to hibernation. **Edita Maxinová***	Intelligent Virtual Personal Assistant for Bat Scientists. **Angel Ivanov**	
16:00	General discussion	General discussion	

16:15-16:45 Coffee/Tea break

17:00-19:00 **Poster Session**

THURSDAY, AUGUST 3rd

8:30-17:00 Field trip to Aizkorri-Aratz Natural Park and Sanctuary of Arantzazu

The Franciscan Sanctuary of Arantzazu was built in the 1950s and provides access to the meadows of Urbia and the Aizkorri-Aratz mountain range. Photo: Wikimedia Commons.

Aizkorri peak (1511m) and the meadows of Urbia (1100m) are one of the most visited mountain destinations in the Basque Country. Photo: Wikimedia Commons.

FRIDAY, AUGUST 4th

8:15-9:00 Invited talk:

Danilo Russo (University of Naples)
"How to be a successful bat in the Anthropocene: coping with urbanisation, climate change and livestock grazing"

Morning Session 1

Subject: Conservation ecology
Convenor: Eeva-Maria Kyheröinen

9:00	The impact of climate on trends in common bat species. **Niamh Roche**
9:15	Activity patterns of bats at the top of wind turbines has implications for efficient mitigation. **Stefan Pettersson**, presented by **Jens Rydell**
9:30	Effectiveness of bat mitigation on roads - a review. **Morten Elmeros**
9:45	Long-term effects of flood-lights on brown long-eared bats in churches. **Sonia Sánchez-Navarro**
10:00	Why bat boxes are not effective as compensation for the loss of roost trees. **Andreas Zahn**
10:15	Using landscape genetics to understand bat responses to climate change. **Orly Razgour**
10:30	General discussion

10:45-11:15 Coffee/Tea break

Morning Session 2

Subject: Conservation ecology
Convenor: Hugo Rebelo

11:15	Should we use *Myotis daubentonii* as an ecological indicator to evaluate riparian ecosystems health? **Adrià López-Baucells***
11:30	A national-scale assessment of the effects of wind energy installations on bats: what have we learnt, and how useful are current approaches to minimising risk? **Fiona Mathews**

11:45	Influence of local landscape features on road collision risks. **Charlotte Roemer***
12:00	Quantifying the impact of light pollution at the city scale: urban-dweller bats are negatively affected by artificial light. **Julie Pauwels***
12:15	Population genetic structure of *Pseudogymnoascus destructans* in the Western Palearctic: where did it all start? **Sebastien J Puechmaille**
12:30	General Discussion

12:45-14:30 Lunchtime

Afternoon Session 1 Friday, August 4th

Subject: Conservation ecology
Convenor 1A: Tomasz Kokurewicz **Convenor 1B**: Fiona Mathews

	Session 1A	Session 1B	WS
14:30	Bats and windfarms monitoring and mitigation measures implementation across Western Palearctic and what can be done? **Daniela Hamidovic**	Investigating the role of environmental reservoirs in the persistence and transmission of *Pseudogymnoascus destructans*, the causative agent of White-Nose Disease. **Nicola M Fischer***	Apodemus Workshop "Test your bat detector" | 1h duration
14:45	Predicting commuting corridors of bats. **Thomas Ravessoud**, presented by **Martin K Obrist**	Do the bats obey Rensch's rule? **Zuzanna Wikar***	
15:00	Re-assessing the potential benefits of hedgerows on bats - a multi-scale approach. **Jérémy SP Froidevaux***	Less common synchronized rewarming in WNS tolerant bats as hibernation strategy. **Tomáš Bartonička**	
15:15	Movements of barbastelle bats in a wind farm. **Grzegorz Apoznánski***	Validation of a field-portable, hand-held qPCR system for detecting *Pseudogymnoascus destructans*, the causative agent of White-nose Syndrome in Bats. **Sybill K Amelon**	

	Session 1A	Session 1B	WS
15:30	The effects of LED street lighting on bat activity. **Elizabeth G Rowse***	Importance of host ecology for the presence of Bartonella spp. in the ectoparasites of insectivorous bats in Central and SE Europe. **Attila D Sándor**	Apodemus Workshop "Test your bat detector" | 1h duration
15:45	Bat boxes and climate change: The impact of changing environmental temperatures on the thermic response in the Mediterranean region and its consequences as a tool for conservation. **Garazi Martin***	Differences in whole-transcriptome gene expression control susceptibility to white-nose syndrome in *Myotis lucifugus* and *Eptesicus fuscus*. **Thomas M Lilley**	
16:00	General discussion	General discussion	

16:15-16:45 Coffee/Tea break

Afternoon Session 2 Friday, August 4th

Subject 2A: Conservation
Convenor 2A: Ana Rainho

Subject 2B: Developmental biology
Convenor 2B: Kirsty Park

	Session 2A	Session 2B	
16:45	Status of Romanian bat populations: the 2010-2017 review of research and conservation. **Szilárd-Lehel Bücs**	Development of a body condition scoring system validated by DEXA and deuterium oxide in big brown bats (*Eptesicus fuscus*). **Sarah E Hooper***	Titley Scientific Workshop "What's new from Titley Scientific" | 1h duration
17:00	Reproduction and post-natal growth of *Rhinolophus hipposideros* roosting in illuminated buildings. **Jasmina Kotnik**	Bat skull in three dimensions: photogrammetry as portable and reliable scanning solution. **Giada Giacomini***	
17:15	Call activity and species diversity of bats at nacelle height in wind parks of Austrian montane forests. **Senta Huemer**	Are aggressive vocalizations the honest signals of body size and quality in female Asian particolored bat (*Vespertilio sinensis*)? **Xin Zhao***	

	Session 2A	Session 2B	
17:30	Testing the performance of bats as indicators of habitat quality in riparian ecosystems. **Carmelina De Conno***	Use of body condition index to describe phenology of french bats populations from mist-netting data. **Julie Marmet**	Titley Scientific Workshop "What's new from Titley Scientific" | 1h duration
17:45	Why are rocket boxes favored by a maternity colony of social bark-roosting bats? **Julia PS Hoeh***	Differential effects of climate change on the body condition of bats. **Xavier Puig-Montserrat**	
18:00	Roads and bats: are overpasses attractive for bats? **Fabien Claireau***	Using DNA techniques to improve national population estimates of a threatened Irish bat species, the lesser horseshoe bat. **Andrew P Harrington***	
18:15	General Discussion	General Discussion	

20:30 **Banquet** at Tenis Ondarreta Restaurant

SATURDAY, AUGUST 5th

8:15-9:00 Invited talk:

Gloriana Chaverri (University of Costa Rica)
"Social communication in bats: so far and the way forward"

Morning Session 1

Subject: Acoustic ecology and taxonomic identification
Convenor: Frank Bonaccorso

9:00	From bat calls in the field to validated species records – the approach of the Swiss Bat Bioacoustics Group SBBG. **Elias Bader**
9:15	Detection distances for bats in southern African savannas. **Ara Monadjem**
9:30	Do we need to include the aerosphere in our conservation efforts? **Christian Voigt**
9:45	Identification of Rhinolophid bat nursery roosts from recordings of adult ultrasound social calls and ultrasound development calls made by infants. **Margaret M Andrews**
10:00	Optimization of automatic bat identification tools for long term acoustic monitoring schemes. **Bruno Silva**
10:15	Articulating citizen science, semi-automatic identification and free web services for long-term acoustic monitoring: examples from France and UK. **Yves Bas**
10:30	General Discussion

10:45-11:15 Coffee/Tea break

11:15-12:15 **Closing Ceremony**

Bats are special and we should care: the genomic bases of bats' extraordinary adaptations

Tuesday, August 1st - 08:30

Emma C Teeling
University College Dublin

Living mammals (~5,400 species) originated approximately 217-238 Million Years Ago, inhabit every biome on Earth, and are arguably one of the most phenotypically diverse group of vertebrates. From the largest, 170 ton blue whale, to the smallest, 2 g flying, echolocating bumblebee bat, the huge diversity and extraordinary adaptive radiations in mammalian form and function have fascinated evolutionary biologists for centuries. Increasingly, this environmental niche specialization is reflected in animal genomes and studying the molecular mechanisms that are responsible for this vast diversity has allowed some of the greatest insights into the functioning and evolution of our own genome. Exploration and harnessing of this vast diversity is now possible due to the development of state-of-the-art NGST which enable the 'parallel' sequencing of up to one billion base pairs per day at a comparably low cost. Bats represent one fifth of all mammalian diversity and arguably show some of the most spectacular of all mammalian adaptations (e.g. flight, echolocation). Phylogenomic studies have revolutionized our understanding of the evolutionary history of this order and bats' position within the mammal tree of life. The underlying genomic bases for bats' unique adaptations such as echolocation, flight, viral tolerance and extraordinary longevity are now being uncovered. The genomic revolution has provided great insight into the evolution of bats and the molecular bases of their unique adaptations, this will be discussed.

Biosketch

Professor Emma Teeling established the Laboratory of Molecular Evolution and Mammalian Phylogenetics in 2005 and is the Founding Director of the Centre for Irish Bat Research at University College Dublin (UCD), Ireland. She has been awarded a prestigious European Research Council Starting Grant (2012) and a Science Foundation Ireland, President of Ireland Young Researcher Award (2006). Prof. Teeling's integrative research in the fields of zoology, phylogenetics and genomics uncovers the genetic signatures of survival that enables species to adapt to an ever-changing

environment. Her main study group are the bats. The two main goals of her research are: (1) study unique model species to enable a better understanding of the structure and function of the human genome to inform medicine and molecular biology; (2) understand and therefore conserve, natural populations and environments to promote ecosystem well-being and functioning. Her record of leadership and research excellence is demonstrated by her publication record of >80 internationally peer-reviewed papers, 5 book chapters, 4 invited subject reviews. A number of these publications have over-turned conventional paradigms in mammalian biology and therefore have been published in high profile journals such as Nature (n=1), Science (n=4), Proceedings of the National Academy of Sciences (n=3), and Nature Communications (n=1), Nature Ecology and Evolution. Her high standing in the international community is highlighted by a total citation record of 5670; prestigious international keynote lectures; invited high profile collaborations such as Genome 10K; leadership of Bat1K; and, high profile invited public presentations (e.g. TEDx talk; ~ 453,769 views; BBC's Science Club with Dara O'Briain), election to academic institutes (e.g. Royal Irish Academy).

Bat diet studies – past, present and future

Tuesday, August 2nd - 08:15

Kristine Bohmann
Natural History Museum of Denmark
University of Copenhagen

The over 1200 living bat species inhabit nearly all the corners of the world and feed on a huge range of things: nectar, fruit, insects, fish, frogs, reptiles, birds, and even blood, to mention a few. Through time, considerable effort and creativity has gone into deconstructing their diets. For instance, bat diet studies have been carried out by observing bats feeding in the wild, observing what captured bats will eat, morphological identification of prey fragments that have survived the passage through the bat's digestive system, isotope analyses of both bat faecal and hair samples, and in the case of vampire bats, observing which domestic animals have bite wounds. Then there are the DNA-based diet assessment methods - of which the currently most popular and (arguably) most effective approach used today is PCR-based metabarcoding using next generation sequencing platforms such as the Illumina MiSeq.

The number of metabarcoding bat diet studies and the questions addressed highlight the importance of ensuring that results are reliable. But despite a seemingly straightforward process, metabarcoding has its challenges. For instance, even slight differences in the metabarcoding laboratory and bioinformatics set-up can result in different numbers of bat prey taxa in the final results. Another challenge is the need to translate the obtained prey DNA sequences to taxa through comparisons against appropriate DNA reference databases. However the completeness of such databases varies with geographic region and taxonomic group under study - both in terms of numbers of species and the amount of DNA reference data per species.

To overcome DNA reference database limitations and as sequencing costs have decreased, a few regional DNA reference database projects have emerged, which generate comprehensive DNA reference data for each species. One such project is the newly started DNAmark project. In this project, we establish a comprehensive national DNA reference database for Danish animal, plant and fungi species with reference data consisting of whole mitochondrial or chloroplast genomes. Such comprehensive DNA reference databases are not only useful when using the metabarcoding approach to assess bat diet. It is also useful in the so-called shotgun sequencing approach, which might be the future method of choice in bat

diet studies. Here, higher DNA sequencing efforts are used to sequence the total DNA in bat faecal samples as opposed to the metabarcoding approach in which only certain markers in certain taxa are sequenced. Thereby, the shotgun approach does not only generate sequences for diet taxa, but also for the bat itself and its microbiome, which will allow future studies that couple information on the individual bats, their diet, and microbiota.

Biosketch

Kristine Bohmann is an assistant professor at the Natural History Museum of Denmark, University of Copenhagen and a Sapere Aude fellow at the University of East Anglia. She both founded and is the scientific leader of the DNAmark DNA reference database project at the Natural History Museum of Denmark. Kristine's research exploits environmental DNA analyses for diet and biodiversity assessments, with a particular emphasis on bat diet. Her particular focus is on development, optimisation and validation of environmental DNA techniques, with emphasis on DNA metabarcoding. Despite being an early career researcher, she is influential in the field, for example having published the first metabarcoding bat diet study on a next generation sequencing platform, and several key methodological papers. Furthermore, she teaches on international environmental DNA courses and is involved in several international collaborations.

Kristine received her PhD in 2015, which was awarded the PhD prize at the Science Faculty at University of Copenhagen. Since then, she has received the Individual Postdoctoral Grant and the prestigious Sapere Aude Research Talent Award from the Danish Council for Independent Research. She recently received a grant from the Aage V. Jensen Nature Fund to establish a DNA reference database for Danish species, DNAmark, at the Natural History Museum of Denmark. Kristine has published in journals such as Trends in Ecology and Evolution, Molecular Ecology, Molecular Ecology Resources, Methods in Ecology and Evolution and Nature Ecology & Evolution.

How to be a successful bat in the Anthropocene: coping with urbanisation, climate change and livestock grazing

Friday, August 4th - 08:15

Danilo Russo
Università degli Studi di Napoli Federico II

The term 'Anthropocene' refers to the current time period in which humans influence the planet and its dynamics as much as, or more than natural processes. Changes in land use and climate, spread of alien species, overharvesting and pollution are profoundly affecting biodiversity. Bats are long-lived, slowly reproducing habitat specialists highly sensitive to human impact, so they represent interesting study subjects to analyse the complex relationships between wildlife and humans. Here I refer to some of my recent work to explore the ecological and evolutionary effects of human action on bats, looking at processes such as light pollution, climate change and livestock grazing. While many bat species are experiencing population declines in response to human activities, a few ones tolerate or even thrive in human-modified landscapes. The latter species offer an excellent model to understand what separates the "winners" from the "losers", so I will concentrate on them. Urbanisation has detrimental effects on many bat species, but a common bat, *Pipistrellus kuhlii*, selects roosts surrounded by areas subject to urban development. Colonies in cities and suburbs advance parturition time and produce more pups than those in rural areas. Permanent water sources and artificial lights in the surrounding habitats also favour this species, often exploiting streetlamps for foraging. According to correlative evidence, streetlamp foraging may have selected for larger skulls that perform best in catching tympanate moths, whose antipredatory reactions are impaired by artificial illumination. The effects of light pollution on *P. kuhlii* at drinking sites are different and more complex, and I will provide examples from experiments carried out in forests and deserts. Despite the importance of urbanisation for *P. kuhlii* at least on a small scale, large-scale modelling points at climate change, rather than urbanisation, as the main driver of the species' impressive (> 400%) range increase recorded in Europe. Climate change threatens many bat species, but might also be favouring another house-dwelling bat, *Hypsugo savii*. Ongoing thermal telemetry work shows that the species tolerates bursts in ambient temperature and hyperthermia, likely an important property to cope with a warming climate. Another powerful driver of species decline is given by the

large-scale exploitation of rangeland by livestock, or deforestation aimed at creating new grazing areas. However, we found that a few bat species, and especially opportunists such as *P. kuhlii* and *H. savii*, forage over cattle, and that their activity increases with herd size following a "type II" predatory response. Overall, population expansion of Anthropocene "winners" may have major ecological consequences, from increases in ecosystem services (pest suppression) to competition with other bat species, so understanding them constitutes a research priority for 21st century bat specialists.

Biosketch

Danilo Russo obtained a PhD at Bristol University in 2002 where he worked on the foraging ecology of Mediterranean bat assemblages. He is currently an assistant professor of Ecology at University of Naples Federico II where he teaches conservation biology and wildlife ecology and management. His research work lies at the interfaces between ecology, behaviour and evolutionary biology and often addresses questions of practical conservation relevance, such as managing forests sustainably for the conservation of bats and beetles, or exploring the role of bats as livestock pest suppressors. Danilo also employs species distribution models and niche analysis to investigate current and future patterns of biological invasions, spanning from bacteria and fungi to alien squirrels, and to inform surveillance and management. Danilo has worked in many regions of the world, from the tropical forests of W Africa to the deserts of Israel, from Mediterranean countries to oceanic islands. He has authored over 90 international peer-reviewed articles and several book chapters. He has also published a conservation biology textbook, a monograph on the effects of land abandonment on vertebrates upon invitation by the European Commission and two popular science books.

Danilo is vice-chair of EUROBATS Advisory Committee, a position which offers a unique perspective on current trends in international bat conservation. The multifaceted world of science communication and scientific publishing is one of his main passions: Danilo is the Editor in Chief of the top-ranking journal Mammal Review and associate or academic editor for several other journals (Mammalian Biology, Frontiers in Ecology and Evolution, Hystrix – Italian Journal of Mammalogy, PLoS ONE, and Journal of Ecoacoustics). He has served as invited guest editor for two successful special issues of Mammalian Biology and Hystrix, respectively on the role of bats as bioindicators and the application of species distribution models to mammal studies.

Social communication in bats: so far and the way forward

Saturday, August 5th - 08:15

Gloriana Chaverri
University of Costa Rica

The study of social communication in bats has made significant advances over the last 15 years, yet the topic still lags behind our understanding of communication in other taxa. Bats represent a fascinating taxon to further our knowledge of social communication given their highly variable gregarious behaviour, their perceptual capabilities in a diversity of sensory modalities, their use of diverse roosting and feeding resources, and their highly variable life histories.

Here I provide an overview of social communication in bats, from the reasons why they communicate to the diversity and application of different signal modalities exhibited by this large and diverse group of mammals. I also suggest some potentially interesting and novel topics of research for future studies. Acoustic communication is the most widely studied signal modality in bats. There are two types of sounds that have a communicative role in bats, namely echolocation and social calls. Echolocation is known to mainly provide information regarding activities performed by vocalizing bats, such as acquisition of food, or specific information about individuals, such as sex or age. These signals are not ideally suited for communication because they cannot encode a large amount of information, yet are not costly to produce. Social calls are better suited for communication as their complex spectral characteristics allow these signals to encode a large number of cues of individual identity. Bats are known to use social calls in different contexts, such as during aggression, distress, isolation, to maintain contact with group members, recruitment to roost sites, and during mate attraction. Olfaction is also a well-studied signalling mode in bats; its functions include discrimination of conspecifics vs. heterospecifics and colony vs. non-colony members, territory marking, and recognition of potential sexual partners. The functions of vision so far established or suggested for bats are mostly limited to sensory ecology, including obstacle avoidance, food location, navigation and escape, whereas its involvement in intraspecific communication is almost anecdotal. The most common form of tactile communication in mammals in general, and bats in particular, is social grooming, and this may allow individuals to strengthen their social ties and facilitate future cooperative behaviours. Potentially rewarding venues for further research on the topic of social

communication in bats include the costs of producing social signals, the role of olfactory communication for sexual selection, the capacity of bats to adaptively adjust their signals to specific habitats and contexts, and many others.

Biosketch

Gloriana Chaverri has been a professor at the University of Costa Rica since 2011, where she has worked since completing her doctoral and post-doctoral studies at Boston University, under the guidance of Tom Kunz. Her doctoral work was aimed at understanding how the environment influences social aggregations in bats. More recently, Gloriana's research has focused on bat acoustic communication, mainly its role in maintaining cohesive groups, but also how habitat and environmental conditions influence sound transmission, and the strategies employed by organisms to exploit the acoustic properties of their surroundings. Gloriana teaches at a small campus in rural Costa Rica, which has allowed her to actively pursue field-based research at some of the best preserved and biodiverse ecosystems in Central America.

[O] = Oral presentation
[P] = Poster presentation
[*] = Student presentation
** = Corresponding author

A RETROSPECTIVE EVALUATION OF THE CAUSES THAT MAY HAVE CONTRIBUTED TO THE DECLINE OF BAT POPULATIONS IN EASTERN FRANCE [P]

EVE AFONSO[1]**, DAMIEN RIUS[1], CHRISTOPHE MAVON[1], ANNE-CLAUDE GOYDADIN[1], ISABELLE JOUFFROY-BAPICOT[1], LANDRY CHIARELLO[1], FLORENT BILLARD[2], LOÏC ROBERT[3], RENAUD SCHEIFLER[1], **eve.afonso@univ-fcomte.fr
[1]Chrono-Environnement UMR 6249 CNRS, Université Bourgogne Franche-Comté, Place Leclerc, F-25030 Besançon, France;
[2]Commission de Protection des Eaux, du Patrimoine, de l'Environnement, du Sous-sol et des Chiroptères (CPEPESC) Franche-Comté, 3 rue Beauregard, F-25000 Besançon, France;
[3]Société d'Histoire Naturelle et des amis du Muséum d'Autun, Maison du Parc, F-58230 Saint-Brisson, France.

The populations of many European bat species experienced a dramatic decline in the latter half of the twentieth century, and most of them are currently considered to be vulnerable or endangered species. The causes of this decline have not formally been identified but bat experts attributed it to a combination of various factors, such as the extensive spread of chemical pollutants, habitat destruction, changes in landscape structure, disturbance and destruction of roost sites (through deforestation and/or urban expansion), climate change, declines in insect prey, genetic inbreeding, and/or diseases. In ecology and conversation biology the persistence of these environmental stresses are challenging our ability to understand the mechanisms of biodiversity erosion and the relative importance of threats to species and their habitats. In some bat roosts, guano can accumulate to a considerable depth (up to 1 to 2 meters) and constitute a valuable and underused historical archive. We developed an original approach based on coring and dating guano accumulations and quantifying several bat-decline related descriptors such as pesticides and trace metal concentrations, bat species richness, bat genetic diversity, and diet. The potential power of this approach is to enable the reconstitution of changes in both bat communities and their stress factors over the last 150yrs, i.e. back to pre-industrial conditions. Here we present the analysis of guano accumulations collected in eastern France and measuring from 13 to 65cm. These cores represent historical archives of the presence of bat populations, stretching back several decades. They can constitute the basis of scenarios to explain bat decline, conservation measures to face current threats, and predictions to anticipate future population disturbances.

DOES THE GUT MICROBIOTA CONTRIBUTE TO THE DIETARY SHIFT OF FISHING BATS? [O]

OSTAIZKA AIZPURUA[1]**, ANTTON ALBERDI[1], M. THOMAS P. GILBERT[1,2,3],
**ostaizk@gmail.com
[1]*EvoGenomics, Natural History Museum of Denmark, University of Copenhagen, Øster Voldgade 5-7, 1350 Copenhagen, Denmark;*
[2]*Trace and Environmental DNA Laboratory, Department of Environment and Agriculture, Curtin University, Perth, Western Australia 6102, Australia;*
[3]*NTNU University Museum, N-7491 Trondheim, Norway*.

Gut microorganisms provide animals with enhanced nutritional capabilities by degrading many compounds the host's enzymatic toolbox is unable to process. Thus, we hypothesized that the gut microbiota could play a central role in dietary niche expansion processes such as that experienced by the primarily insectivorous long-fingered bats, *Myotis capaccinii*, that incorporated fish into their diet. *M. capaccinii* was thought to be a strictly insectivorous bat until regular fish consumption was discovered in a small colony in Eastern Iberia. Aiming to understand the role of gut microorganisms in this dietary shift, we studied the diet and gut microorganism composition of bats from different populations using metabarcoding and shotgun sequencing approaches. Specifically, we compared the diet and gut microbiota of six bats from the fishing population with, i) four *M. capaccinii* from elsewhere in Europe, ii) three phylogenetically and ecologically similar *Myotis daubentonii* bats and iii) three fisherman bats, *Noctilio leporinus*. Fish traces were only detected in three *M. capaccinii* from the fishing colony and all analyzed *Noctilio leporinus*. We observed that *M. capaccinii* from the fishing colony, irrespective of the detection of fish traces in their faeces, exhibited slightly different microbial profiles compared to conspecifics from other colonies. This might suggest that although fish traces were not detected in some of the bats from the fishing colonies, they actually fish regularly throughout the year. The microbiota composition of *Myotis daubentonii* and *Noctilio leporinus* were different, suggesting that both phylogenetic and ecological factors shape the gut microbiota of fishing long-fingered bats.

BEYOND MOTHS AND MOSQUITOS: THE EXCEPTIONAL DIETARY DIVERSITY AND DISPARITY OF THE LONG-FINGERED BAT, *MYOTIS CAPACCINII* [P]

OSTAIZKA AIZPURUA[1], AITOR ARRIZABALAGA[2], PANAGIOTIS GEORGIAKAKIS[3], CARLOS IBÁÑEZ[4], LIDE JIMENEZ[2], HUGO REBELO[5], EÑAUT IZAGIRRE[6], M. THOMAS P. GILBERT[1,7,8], ANTTON ALBERDI[1]**, **anttonalberdi@gmail.com
[1]*EvoGenomics, Natural History Museum of Denmark, University of Copenhagen, Øster Voldgade 5-7, 1350 Copenhagen, Denmark;*
[2]*Department of Zoology and Animal Cell Biology, University of the Basque Country, Sarriena z/g, 48940 Leioa, Bizkaia, The Basque Country;*
[3]*Department of Biology School of Sciences and Engineering, University of Crete, Rethymno, Crete, Greece;*
[4]*Evolutionary Ecology Dpt., Estacion Biologica de Donana (CSIC), Avda Américo Vespuccio 26, 41092 Seville, Spain;*
[5]*CIBIO-InBIO, Centro de Investigação em Biodiversidade Recursos e Genéticos, Universidade do Porto, Vairão, Portugal;*
[6]*Dirección de Programas Antárticos y Subantárticos, Universidad de Magallanes, Punta Arenas, Chile;*
[7]*Trace and Environmental DNA Laboratory, Department of Environment and Agriculture, Curtin University, Perth, Western Australia 6102, Australia;*
[8]*NTNU University Museum, N-7491 Trondheim, Norway.*

The long-fingered bat, *Myotis capaccinii*, is a small trawling chiropteran with a pan-Mediterranean distribution and a threatened conservation status. Its dietary ecology has been studied using visual methods in many areas of its wide geographical distribution. Although these analyses showed that dipterans and lepidopterans dominate its diet, the dietary ecology of *M. capaccinii* has not been studied at species-level resolution. This, however, can be achieved using current molecular methods, which coupled with extensive sampling can provide a fine characterization of the dietary ecology of the species. Following that objective, we analysed faecal samples from 54 long-fingered bats captured in 9 caves distributed all around Europe (6 countries) using a metabarcoding approach. The diet of each individual was characterized using two primer sets targeting arthropod COI and 16S mitochondrial regions and three PCR replicates per primer set. PCR replicates were processed using a restrictive strategy whereby only sequences appearing in more than one PCR replicate were considered for further analysis. Our results confirmed that *M. capaccinii* mainly preys on lepidopterans and dipterans throughout its distribution, although 14 other insect orders were detected. In total, we identified 156 arthropod species, including species with a low preference towards water environments, such as praying mantis and crickets. We observed high levels of alpha (individual), beta (colony) and gamma (whole distribution) diversity, and low structuration of dietary patterns. Our results show that even individuals from the same colony can show rather different dietary patterns, suggesting diverse foraging habits, and also indicate that the diet of *M. capaccinii* incorporates prey with barely any connection to aquatic environments.

SCRUTINIZING KEY STEPS FOR RELIABLE METABARCODING OF BAT FAECAL SAMPLES [O]

ANTTON ALBERDI[1]**, OSTAIZKA AIZPURUA[1], M. THOMAS P. GILBERT[1,2,3], KRISTINE BOHMANN[1,4], **antton.alberdi@snm.ku.dk
[1]*EvoGenomics, Natural History Museum of Denmark, University of Copenhagen, Øster Voldgade 5-7, 1350 Copenhagen, Denmark;*
[2]*Trace and Environmental DNA Laboratory, Department of Environment and Agriculture, Curtin University, Perth, Western Australia 6102, Australia;*
[3]*NTNU University Museum, N-7491 Trondheim, Norway;*
[4]*School of Biological Sciences, University of East Anglia, Norwich Research Park, Norwich, Norfolk NR4 7UG, U.K.*

Metabarcoding of faecal samples has many challenges and limitations that require a good laboratory set-up and careful analysis to obtain reliable results. Using faecal samples from 54 insect-eating bats, we evaluated the performance of four primer sets targeting mitochondrial COI and 16S regions, and investigated how metabarcoding results are affected by a number of parameters: i) number of PCR replicates per sample, ii) sequencing depth, iii) additive and restrictive (using only sequences appearing in multiple replicates) PCR replicate processing strategies, iv) minimum copy number for sequences to be retained, v) chimera removal, and vi) similarity thresholds for OTU clustering. We also analysed how those parameters change the dissimilarity between PCR replicates, and we used a shotgun approach to measure the relative amount of target DNA (arthropod COI and 16S regions) in the analysed extracts. Finally, we measured within and between-taxa dissimilarities at different taxonomic levels using reference database data to decide the most appropriate thresholds for OTU clustering and taxonomy assignment. We observed that the use of multiple primers targeting the same taxonomic group minimised the effect of biases of individual primer sets and increased taxonomic coverage. The yielded taxonomic profiles were mainly altered by the number of PCR replicates employed and their filtering approach, the copy number threshold and the OTU clustering similarity threshold. Our results also revealed high levels of PCR stochasticity, which is probably related to the relatively low amount of target DNA (0.01% of the total DNA belonged to arthropod COI and 16S regions). In addition, sequencing depth increased the dissimilarity between PCR replicates unless the bioinformatic strategies to remove allegedly arteficial sequences were adjusted according to the number of analysed sequences. Finally, we observed that the appropriate identity thresholds for OTU clustering and taxonomy assignment differ between target markers.

CONTINENTAL-LEVEL METABARCODING OF THE BAT *MINIOPTERUS SCHREIBERSII* REVEALS WIDESPREAD CONSUMPTION OF PEST INSECTS [P]

ANTTON ALBERDI[1]**, IVANA BUDINSKI[2], VANESSA MATA[3], FARKAS SZODORAY-PARÁDI[4], DANILO RUSSO[5], VIOLETA ZHELYAZKOVA[6], VIDA ZRNCIC[7], M. THOMAS P. GILBERT[1,8,9], OSTAIZKA AIZPURUA[1], **anttonalberdi@gmail.com

[1]EvoGenomics, Natural History Museum of Denmark, University of Copenhagen, Øster Voldgade 5-7, 1350 Copenhagen, Denmark;
[2]Department of Genetic Research, Institute for Biological Research "Siniša Stanković", University of Belgrade, Bulevar despota Stefana 142, 11060 Belgrade, Serbia;
[3]CIBIO-InBIO, Centro de Investigação em Biodiversidade Recursos e Genéticos, Universidade do Porto, Vairão, Portugal;
[4]Romanian Bat Protection Association, Satu-Mare, Romania;
[5]Wildlife Research Unit, Dipartimento di Agraria, Università degli Studi di Napoli Federico II, Portici, Italy;
[6]National Museum of Natural History, Sofia, Bulgaria;
[7]Geonatura d.o.o., Fallerovo šetalište 22, 10000 Zagreb, Croatia;
[8]Trace and Environmental DNA Laboratory, Department of Environment and Agriculture, Curtin University, Perth, Western Australia 6102, Australia;
[9]NTNU University Museum, N-7491 Trondheim, Norway.

Biological control of agricultural pest insects is one of the most important ecosystem services bats provide based on estimated economical impact. *Miniopterus schreibersii* is one of the European bat species with the most promising biological features to potentially act as a natural pest controller, as it can form aggregations comprised of thousands of individuals, and its home range exceeds 20 kms. As a first step to assess the actual potential of *M. schreibersii* as a pest controller, however, it is essential to measure the incidence of major pest species in its diet. In this study we present the molecular analysis of faecal samples directly collected from 80 *M. schreibersii* bats captured in 16 caves surrounded by different agricultural production areas distributed across 8 southern European countries. With over 200 arthropod species identified, we detected the highest prey species richness so far reported in an insectivorous bat. Further, locality rarefaction curves indicated that our study identified only a fraction of the actual species-level diversity of the dietary niche of *M. schreibersii*. All identified prey belonged to 13 arthropod orders, although lepidopterans overwhelmingly dominated over the other taxonomic groups. Lepidopterans were detected in all but three individuals, and they were the main group in all but five analysed bats. Among the detected lepidopterans, 40 are known to cause damage in crops and gardens, and 23 of them are considered as major agriculture pests; e.g., *Noctua pronuba* and *Prays citri*. Since pest species were detected in all analysed localities and most of the analysed individuals, our results suggest *M. schreibersii* might be playing an essential role as pest controller in crops throughout its distribution. However, localized studies with longitudinal design and large number of individuals will be necessary to quantify the biological and economic impact of *M. schreibersii* on pest insects and their associated crops.

NEW DATA ON THE PRESENCE OF NATHUSIUS'S PIPISTRELLE IN THE CANTABRIAN COAST: A MIGRANT OR RESIDENT SPECIES? [P]

JUAN T. ALCALDE[1]**, MIKEL ETXANIZ[2], ESTELA RUIZ DE AZÚA[2], NEREA AZPEITIA[2], ALBERTO LUENGO[2], IÑAKI MARTÍNEZ[1], **jtalcalde@gmail.com
[1]*Spanish Association for the Study and Conservation of Bats, SECEMU, Spain;* [2]*Ekoetxea Txingudi - Plaiaundiko Parke Ekologikoa. Irun, Gipuzkoa, Spain*.

Nathusius's pipistrelle is a long distance migrant species, although sedentary populations are also known. In the Iberian Peninsula it is a very rare species: most of the data come from isolated individuals found in autumn or winter and are attributed to migrant specimens, but so far, their movement patterns are unknown. However, on the Mediterranean coast (NE of the Iberian Peninsula) there is a small resident population, which in summer only hosts males. In the last two years observations of this species have been collected in two bat boxes located in the Bay of Txingudi (Cantabrian coast). Both males and females have been identified, and their presence has been verified for 8 consecutive months, from the end of August to the beginning of May. Only in the warmer months does it seem to be absent from the site.

PRELIMINARY DATA ON TROPHIC NICHE PARTITIONING AMONG RHINOLOPHIDS IN THE BASQUE COUNTRY [P*]

MIREN ALDASORO[1]**, AITOR ARRIZABALAGA-ESCUDERO[1], INAZIO GARIN[1], URTZI GOITI[1], JOXERRA AIHARTZA[1], **maldasoro005@ikasle.ehu.eus
[1]*Department of Zoology and Animal Cell Biology, University of the Basque Country UPV/EHU, Sarriena z.g., Leioa, The Basque Country.*

Resource partitioning is thought to be one of the main mechanisms facilitating the coexistence of ecologically similar bat species. Studies on diet composition of insectivorous bats have been hampered due to methodological limitations, but the advent of new molecular tools has allowed advances in prey identification. In this study we analyze the dietary niche overlap between the sympatric and ecologically similar bat species *Rhinolophus hipposideros*, *R. euryale* and *R. ferrumequinum*, through identification of consumed prey by massive sequencing and metabarcoding of DNA from bat faeces. These three horseshoe bats differ in size, wing-load, manoeuvrability and in their echolocation frequencies, so that we expected to detect dietary differences associated with these echomorphological characteristics. We determined the consumed prey species of 35 faecal samples of *R. hipposideros*, 20 of *R. euryale* and 40 of *R. ferrumequinum*. From all identified MOTUs, 52, 164 and 56 respectively, we assigned nine to species level for *R. hipposideros*, 61 for *R. euryale* and 21 for *R. ferrumequinum*. They were mostly lepidopterans, although a third of the identified prey occurrences in *R. hipposideros* faeces corresponded to dipterans. Each bat species pair only shared 2 or 3 prey species, and only a single prey species was shared by all three of them. Prey variables related to the predators' hunting ability, such as wing-load and mass, were different between bat species.

EMERGENCE, RETURN AND ACTIVITY PATTERNS OF *MINIOPTERUS SCHREIBERSII* AND *RHINOLOPHUS* SPP. AT CADAVAL BAT ROOST (PORTUGAL) [P*]

PEDRO ALVES[1]**, BRUNO SILVA[2,3], SÍLVIA BARREIRO[2,3], **pjalves@plecotus.com
[1]*PLECOTUS – Estudos Ambientais, Unipessoal, Lda, Portugal;*
[2]*UBC – Conservation Biology Lab, Department of Biology, University of Évora, Portugal;*
[3]*CIBIO/InBIO-UE – Research Centre in Biodiversity and Genetic Resources. Pole of Évora, Portugal.*

Cadaval is a cave classified as an Important National Bat Roost, located in the Serra de Montejunto Natura 2000 site (PTCON0048), an area also classified as Protected Landscape (Paisagem Protegida da Serra de Montejunto). This roost holds a colony with a few thousand *Miniopterus schreibersii* during winter, and several hundred in spring and autumn. Historical data also refers to the presence of a few hundred non-breeding males and females during summer. *Rhinolophus* spp and *Myotis* spp are also present in relative small numbers throughout the year. In the scope of a wind farm environmental impact assessment, and taking into account the roost importance to *M. schreibersii* with the fatality risk at wind farms, we aimed to study the emergence and return patterns of these species, and their activity levels at the roost entrance. Bat movements were monitored using a night-shot video-camera, IR projectors and a heterodyne bat detector. A total of 250 hours of recordings (22 nights) were obtained from November 2009 to November 2010, during fortnightly surveys (no surveys were made between 15 December and 15 February, the hibernation period of *M. schreibersii*). Our results show that on average, about 550 *M. schreibersii* and 60 *Rhinolophus* spp were present during spring and autumn, while in summer both numbers decrease to about 300 and 20 bats respectively. Both emerged earlier, returned later and had broader overnight activity levels near the roost when larger number of bats occupied the roost. Further analysis will be made to understand the influence of other variables and see if *M. schreibersii* and *Rhinolophus* spp are also affected by factors already known to influence time and duration of emergence on other species.

VALIDATION OF A FIELD-PORTABLE, HAND-HELD QPCR SYSTEM FOR DETECTING *PSEUDOGYMNOASCUS DESTRUCTANS*, THE CAUSATIVE AGENT OF WHITE-NOSE SYNDROME IN BATS [O]

SYBILL K. AMELON[1]**, TRACY DRAZENOVICH[2], MARIA CHACON-HESZELE[3], KATIE HAMAN[4], GREG TURNER[5], JESSE VANWESTRIENEN[3], MAX PERELMAN[3], SARAH HOOPER[6], KEVIN KEEL[2], **batworldozarks@gmail.com

[1]Northern Research Station, US Forest Service, US Department of Agriculture, 202 ABNR Bldg, University of Missouri, Columbia, Missouri 65211, USA;
[2]Department of Veterinary Medicine, Pathology, Microbiology, Immunology, School of Veterinary Medicine, University of California, Davis, CA 95616, USA;
[3]Biomeme, 1015 Chestnut Street Suite 1401, Philadelphia, PA 19107, USA;
[4]Wildlife Program, Washington Department of Fish and Wildlife, 1111 Washington Street SE, Olympia, WA 98501, USA;
[5]Bureau of Wildlife Management, Pennsylvania Game Commission, 2001 Elmerton Ave,
Harrisburg, PA 17710, USA;
[6]Department of Veterinary Pathobiology, College of Veterinary Medicine, University of Missouri, Columbia, MO 65211, USA.

White-nose syndrome (WNS), caused by the cold-loving fungus *Pseudogymnoascus destructans* (Pd), has decimated bat populations across North America (N.A.). In some species and hibernacula mortality rates are 95-100%. Since the discovery of Pd in North American bats in 2006/07, WNS/Pd surveillance has focused primarily on screening hibernating bats using a series of diagnostic tools. However, the recent discovery of WNS/Pd in Washington highlights the need for a modified approach to allow for early detection of Pd in new areas. Such an approach must address differences in bat habits/habitats and the distinct lack of large aggregations of hibernating bats in the American Pacific Northwest. The ability to rapidly diagnose Pd in bats would improve our ability to respond to and manage Pd. Due to lack of information regarding distribution of Pd and western bat species that may be impacted by this fungus, reliable, rapid on-site detection is critical. We thus evaluated the feasibility of using a hand-held field portable quantitative PCR (qPCR) system (Biomeme two3) for detection of Pd. We compare the results from a bench-top molecular approach used by labs conducting WNS/Pd surveillance to the Biomeme qPCR (two3) platform in a lab setting and in ongoing field trials. Results of this comparative study will be presented. The establishment and validation of a rapid, field assessable detection platform for Pd will significantly improve not only surveillance capacity, but also on-the-ground management and response efforts. This will further strengthen the conservation responses to protect bats across North America from the devastating impacts of WNS/Pd.

A BAT OUT OF AFRICA: NEW INSIGHTS ON THE EXISTENCE OF A NORTH AFRICAN REFUGIUM FOR WESTERN PALAEARCTIC BAT FAUNA (O*)

FRANCISCO AMORIM[1,2]**, RAQUEL GODINHO[1], JAVIER JUSTE[3], CARLOS IBAÑEZ[3], STEPHEN ROSSITER[4], PEDRO BEJA[1,2], HUGO REBELO[1,2,5], **fnlamorim@gmail.com

[1]CIBIO/InBio, Centro de Investigação em Biodiversidade e Recursos Genéticos da Universidade do Porto, Vairão, Portugal;
[2]CEABN-InBIO, Centre for Applied Ecology "Prof. Baeta Neves", Institute of Agronomy, University of Lisbon, Lisbon, Portugal;
[3]Estación Biológica de Doñana (CSIC), Sevilla, Spain;
[4]School of Biological and Chemical Sciences, Queen Mary University of London, U.K.;
[5]School of Biological Sciences, University of Bristol, U.K.

In the last decades, phylogeography studies have been paramount to understanding how geography and historical processes shape current species' genetic patterns. For Europe, regions such as the Balkans, Italy and the Iberian Peninsula have been widely recognized as refugia for a number of European bat species during the Last Glacial Maximum. However, one of the most surprising results is the lack of evidence of colonization routes between Southern Europe and North Africa, with the latter seldom addressed as a possible refugium. *Tadarida teniotis* is a fast-flying species that is able to cover long distances. It is also the only European representative of the widespread family Molossidae, whose greatest diversity is concentrated in the tropics. These features render this species particularly suitable to address the hypothesis of a refugium that includes both Southern Europe and North Africa. Using a standard phylogeography approach, we combined results from the analysis of four mtDNA fragments (N=122) and 14 microsatellites (N=134), with ecological modelling tools. We have identified three main haplogroups, one of which is restricted to the eastern Mediterranean while the remaining two are widespread across the Iberian Peninsula and Morocco. Phylogenetic reconstruction further supports the hypothesis that the Iberian Peninsula and Morocco were a single refugium for *T. teniotis*. Regarding nuclear data, we have identified three clusters, with Canary Islands showing the lowest signs of gene flow with the continental populations. Gene flow between the remaining clusters shows a typical Isolation-by-distance pattern, decreasing from west to east. Interestingly, gene flow between Morocco and central Mediterranean is higher than that between the Iberian Peninsula and central Mediterranean. This study highlights the importance of North Africa in the population history of this bat, and unveils a refugium relatively neglected in the European phylogeography research.

CLOUDEDBATS.ORG - FREE SOFTWARE FOR OPEN DATA [P]

ARNOLD ANDREASSON[1]**, **arnold@mellifica.se
[1]*Arnold Andreasson Konsult AB, Sweden.*

We need more data about bats from all regions where they occur, and it needs to be collected soon if we wish to document the current situation before things start to change more rapidly. One way to do this is to record and store sound in full spectrum or time expanded formats for future analysis when better tools and reference libraries of bat sounds are available. But there are some problems that must be fixed. Recording units for high quality recordings are expensive, it is time-consuming to analyse recorded sound from clusters of detectors, sharing and publishing data is complicated and it is hard to find reference recordings to be used for automatic or semi-automatic analysis. CloudedBats.org is a project where I am trying to use my skills in software development to address these problems. The software is developed as free and open source software and the project home page can be found here: http://cloudedbats.org/. Last year, 2016, I developed software for a less expensive recording unit based on a high quality microphone (Pettersson M500-384) and affordable standard hardware. This year I am working on a web server software used to collect near real time data from a cluster of recording units. It will also contain functionality for computer assisted species identification and tools for publishing survey data in the DarwinCore format. The latest test version of the web page can be found here: http://test.cloudedbats.org/. Future work will include cloud storage and computation of huge amounts of data. Great technical possibilities are available and I am looking forward to digging deeper into that area. Open data facilitates data sharing and is becoming the standard alternative for biological monitoring data. The Creative Commons (https://creativecommons.org/) licence alternatives CC0 and CC-BY are recommended by international actors like GBIF (http://www.gbif.org/species/734). The poster presents software and hardware for bat recordings and data management.

IDENTIFICATION OF RHINOLOPHID BAT NURSERY ROOSTS FROM RECORDINGS OF ADULT ULTRASOUND SOCIAL CALLS AND ULTRASOUND DEVELOPMENT CALLS MADE BY INFANTS [O]

MARGARET M. ANDREWS[1]**, AMELIA M. HODNETT[2], PETER T. ANDREWS[3],
**mmandrews37@gmail.com
[1]*Liverpool John Moores University, Liverpool L3 3 AF, U.K.;*
[2]*Gavia Environment, Perth, PH 1 3FX, U.K.;*
[3]*Department of Physics, University of Liverpool, Liverpool L69 3 BX, U.K.; deceased*.

Ultrasound calls of infant greater horseshoe bats (*Rhinolophus ferrumequinum*) and lesser horseshoe bats (*Rhinolophus hipposideros*) were recorded from birth to 27 days of age in two separate roosts in Wales in June and July using a time expansion bat detector modified for 24 hour recording periods. The ultrasound social calls of adult greater and lesser horseshoe bats were also recorded in the two nursery roosts and were classified according to the frequency of the fundamental, the number and duration of the harmonics and the number of syllables in a phrase. The constant frequency (CF) or frequency modulated (FM) calls were compared with adult social calls identified previously. Although the echolocation frequencies of the greater horseshoe bats were typically 83-84 kHz and the lesser horseshoe bats 110-114 kHz the infant calls were similar. Ultrasound calls with fundamental frequencies between 15-42 kHz were identified as 7 categories of infant development calls and 15 categories of adult ultrasound calls. There were five distinct stages in the development of infant ultrasound calls recorded with the age of the infant bats, determined by forearm length. Stages 1-3 developed from polyharmonic isolation calls uttered through the mouth to attempts at echolocation and corresponded with Type A-C adult ultrasound social calls. Stages 4-5 infant calls were nasal attempts at echolocation that corresponded with Type E adult modified echolocation calls. There were no comparable infant calls to the Type D adult advertisement calls. A survey of ten lesser horseshoe roosts in Wales showed that infant ultrasound calls provide a means of identifying not only the presence of a nursery roost but the dates at which births started and infants began flying, The ideal time for static preset extended periods of monitoring would be from 20.00 - 08.00 h GMT in June and July. This ultrasound monitoring provides a simple non-invasive method of identifying nursery roosts.

GENEFLOW WITHIN AND AMONG SPECIES OF *PLECOTUS* BATS IN THE ALPINE RANGE [O*]

TOMMY ANDRIOLLO[1,2]**, MARZIA MATTEI-ROESLI[3], RAPHAËL ARLETTAZ[4], MANUEL RUEDI[1], **tommy.andriollo@gmail.com
[1]*Department of Mammalogy and Ornithologie, Natural History Museum of Geneva, Geneva (GE), Switzerland;*
[2]*Section of Biology, University of Geneva, Geneva (GE), Switzerland;*
[3]*Centro protezione chirotteri Ticino, Semione (TI), Switzerland;*
[4]*Division Conservation Biology, University of Bern, Bern (BE), Switzerland.*

European species of long-eared bats (genus *Plecotus*) have similar morphologies, karyotypes and echolocation calls, but molecular studies revealed the existence of several cryptic lineages, rendering reliable species identification in the field even more problematic. The presence of morphologically intermediate individuals observed in the Alps poses further challenges to species recognition, and raises the possibility of interspecific hybridization. To address this important question, we used biopsy samples of over 400 individuals living in areas of sympatry and analysed them with both mitochondrial and nuclear DNA markers (23 microsatellite loci). This combination of genetic markers allowed us (1) to estimate rates of current interspecific gene flow, (2) to detect possible events of historical introgression and (3) to test the usefulness of various morphological characters to recognise species. The hypervariable nuclear markers also provided new insights into the genetic diversity and population structure of these bats across the potential barrier represented by the Alpine range.

MOVEMENTS OF BARBASTELLE BATS AT A WIND FARM [O*]

GRZEGORZ APOZNÁNSKI[3]**, TOMASZ KOKUREWICZ[3], STEFAN PETTERSSON[2], SONIA SÁNCHEZ-NAVARRO[4], JENS RYDELL[1], **apoznanski.grzegorz@gmail.com
[1]Biology Department, Lund University, SE-223 62 Lund, Sweden;
[2]EnviroPlanning AB, SE-411 04 Göteborg, Sweden;
[3]Wroclaw University of Environmental and Life Sciences, Institute of Biology, Department of Vertebrate Ecology and Paleontology, Kożuchowska 5b, 51-631 Wrocław, Poland;
[4]Department of Evolutionary Ecology, Estación Biológica de Doñana-CSIC, Américo Vespucio s.n., Sevilla 41092, Spain.

We investigated the relationship between barbastelle bats, *Barbastella barbastellus*, and wind turbines in a small wind park (10 turbines) in southern Sweden. Two methods were combined for three seasons from 2014: acoustic monitoring and carcass search. Also in 2016, in order to get a more detailed picture of the flight paths near the wind turbines, we radio-tracked 8 females and 2 males. Detectors were mounted at 30m and 100 m above ground on the turbines, placed on gravel access areas around the turbines, as well as at the adjacent forest edge ca. 30 m from the turbine. Barbastelles were frequently recorded at forest edges (on average 4 flight passes per night), occasionally (0.25 passes per night) over the open gravel access areas around the turbines, but never at the turbine towers. Carcass searches were carried out near the turbines at one week intervals but did not reveal any dead barbastelles. Radio tracking revealed that despite some of the turbines being located between the bats' roost and their foraging areas they were apparently actively avoided by the commuting bats. We conclude that wind farms are not necessarily incompatible with effective conservation of barbastelle bats in Sweden, even though they still may pose a threat to some other bat species.

DO BATS HIBERNATE IN COASTAL AREAS IN SOUTHERN EUROPE? [P]

FRANCISCO ARCOS[1,2]**, RAFAEL SALVADORES[1], **farcos@arcea.net
[1]*Arcea Xestión de Recursos Naturais S.L., Velázquez Moreno 9, planta 3, oficina 305, 36201 Vigo, Spain;*
[2]*Departamento de Zoología, Genética y Antroplogía Física, Facultad de Biología, Universidad de Santiago de Compostela, Lope Gómez de Marzoa s.n., 15782 Santiago de Compostela, Spain.*

Climate change, associated with an increase in extreme weather events, will probably become one of the main risk factors affecting global biodiversity, and in particular bats. In temperate zones, during winter, the combined decline of food resources and ambient temperature (Ta) make it difficult for bats to maintain a high body temperature; seemingly, they enter a period of prolonged and deep, although variable, torpor. There is a notable lack of knowledge about the effects of climate change on the hibernation of bats. Different spatial responses are expected, conditioned by the existence of different local microclimates. For this reason different geographic scenarios must be studied. During 2015-2016 winter, we measured nocturnal bat activity (*Pipistrellus pipistrellus*, *Plecotus austriacus*) inside a hibernation refuge located on Cíes Islands (NW Iberian Peninsula), at the entrance of Ría de Vigo. We modeled (GLM) cumulative 5-seconds recordings with bats per night (Pettersson D500X bat detector). The independent variables selected were the external minimum Ta, daily hours with a Ta ≤ 7ºC, external Ta 60 minutes before sunrise, and external Ta, relative humidity (%) and corrected barometric pressure (hPa) 30 minutes after sunset. Nocturnal activity was mostly continuous, having recordings on all but 7 of 56 nights. Outside activity was visually registered (during sunset) on a minimum of 25 nights (44.6%, n=56). Ta and humidity 30 minutes after sunset explained 44% of the observed variability - bat activity increased with these variables. Feeding opportunities for bats on Cíes Islands (nocturnal Ta ≥ 10ºC) during winter seem frequent. High activity levels suggest a stronger link with the acquisition of fat reserves than with hydration, and the absence of hibernation.

TRAIT-BASED DIET ANALYSIS OF AN INSECTIVOROUS BAT: NOVEL INSIGHTS INTO FORAGING ECOLOGY [O]

AITOR ARRIZABALAGA-ESCUDERO[1]**, INAZIO GARIN[1], URTZI GOITI[1], THOMAS MERCKX[2], N. WAHLBERG[3], JOXERRA AIHARTZA[1],
**arrizabalaga.aitor@gmail.com
[1]*Department of Zoology and Animal Cell Biology, University of the Basque Country UPV/EHU, Sarriena z.g., 48940 Leioa, The Basque Country;*
[2]*Behavioural Ecology and Conservation Group, Biodiversity Research Centre, Earth and Life Institute, Croix du Sud 2, 1348, Universite Catholique de Louvain (UCL), Louvain-La-Neuve, Belgium;*
[3]*Department of Biology, Lund University, Solvegatan 35, SE-223 62 Lund, Sweden.*

Understanding the degree of prey-specialization and adaptive flexibility of insectivorous bats is pivotal to assessing their ability to adapt to varying environments. However, challenges often stem from methodological difficulties to identify predator-prey interactions and interpret the functional meaning of the vast diversity of consumed prey in wild populations. In this study we introduce an innovative approach to analyze and interpret the foraging ecology of insectivorous bats. We aimed to analyze the trophic flexibility of a moth specialist horseshoe bat (*Rhinolophus euryale*) by linking prey's functional traits (e.g. mass, wing-loading) and bats' intraspecific variables (i.e. sex, size and ontogeny) through diet and across space and time. Diet was analyzed using DNA metabarcoding in combination with RLQ and the fourth-corner analyses. Our trait-based approach showed that prey's traits related to energy content (i.e. mass) and flight performance (i.e. wing loading and manoeuvrability) changed significantly across seasons and bats' ontogenetic stage. These results showed that a moth-specialist bat is trophically flexible enough to take advantage of seasonally varied moth types. Moreover, we identified functional dietary differences between juveniles and adults hardly possible to identify by taxonomy-based approaches, as both consumed moths. Our results showed that trait-based approaches open new insights to understanding the foraging ecology, evolutionary relationships and conservation of insectivorous bats.

THE IRISH BAT MONITORING PROGRAMME: RECRUITING AND RETAINING BAT VOLUNTEERS [P]

TINA AUGHNEY[1]**, NIAMH ROCHE[1], FERDIA MARNELL[2],
**info@batconservationireland.org
[1]Bat Conservation Ireland, Virginia, Ireland;
[2]National Parks and Wildlife Service, Dublin, Ireland.

Bat Conservation Ireland coordinates the monitoring of six of Ireland's nine bat species. A combination of methods are used, including walked transects, vehicle driven transects and roost counts, depending on the target species. Most of the survey work is carried out by trained volunteers. From the data collected we have been able to produce robust population trends for all six bat species. While using volunteers to conduct ecological surveys is not a new enterprise in Ireland, standardised bat surveys conducted by citizen scientists is a relatively new field. Some of the first citizen science bats monitoring schemes were promoted in the UK by the Bat Conservation Trust in the mid-1990s. Encouraged by the BCT's success, bat monitoring with the help of citizen scientists was introduced to Ireland in 2003. By the end of 2016, more than 1000 trained volunteers had participated in bat surveys in Ireland in the last 14 years. In this poster we examine the process of engaging and training volunteers, as well as some of the more challenging aspects, for example retaining volunteers. We also discuss potential changes to our own recruitment, training and feedback strategies that may help improve the volunteer experience of bat survey work and help us to retain experienced individuals, year on year. This poster is intended to generate discussion on how to continue to mobilise public participation and optimise the use of citizen science-collected bat data into the future.

BATS IN SPANISH PHILATELY: THE LEGACY OF JAMES I [P]

STÉPHANE AULAGNIER[1]**, **stephane.aulagnier@inra.fr
[1]*Comportement & Ecologie de la Faune Sauvage, Université de Toulouse, I.N.R.A., CS 52627, 31326 Castanet Tolosan cedex, France.*

The only bat species depicted on a Spanish stamp was issued in 2015. However bats appeared on bat stamps as early as 1962-1963 in the set of coats of arms including the cities of Albacete and Valencia. The later coat of arms was also included in three other stamps including a special issue to raise funds after the tragic flooding of October 1957. This bat is the symbol of the reconquest of Aragonese troops over the Moors by James I the Conqueror, the most renowned of the medieval kings (1213-1276). There are several legends dealing with the role of one bat when he laid siege to Valencia in 1238, including a bat that had flown into King James' tent before he conquered the city. Another Spanish (fantasy) hero, Don Quixote of La Mancha was depicted in the Montesinos cave on a 1998 stamp. In addition, several postal stationeries including Valencia's coat of arms have been issued. There is also plenty of other philatelic material from the Valencian Community, but also from Catalonia (Barcelona). We recorded 31 temporary cancellations since 1962: 5 mechanical frankings and 14 meter cancels, most of them depicting the batty coat of arm. The first ones were mainly issued to announce or celebrate philatelic exhibitions and some football competitions and teams, but also for a variety of events: metal art exhibition, congresses of bombers and pharmacists, international week of orange, anniversary of the theatre... The meter cancels were used by one bank, the Chamber of commerce and industry and the city hall of Valencia, one mutual company of insurances and several feasts.

OFFSHORE BAT MIGRATION IN THE GERMAN NORTH AND BALTIC SEA IN AUTUMN 2016 [P]

LOTHAR BACH[1]**, PETRA BACH[1], HENRIK POMMERANZ[2], REINHOLD HILL[3], CHRISTIAN C. VOIGT[4], MATTHIAS GÖTTSCHE[5], MICHAEL GÖTTSCHE[6], HINRICH MATTHES[6], ANTJE SEEBENS-HOYER[7],
**lotharbach@bach-freilandforschung.de
[1]Bach Freilandforschung, Hamfhofsweg 125b, 28357 Bremen, Germany;
[2]Büro Nachtschwärmer, Augustenstraße 77, 18055 Rostock, Germany;
[3]Avitec Research GbR, Sachsenring 11, 27711 Osterholz-Scharmbeck, Germany;
[4]Leibniz Institute for Zoo and Wildlife Research, Alfred-Kowalke-Straße 17, 10315 Berlin, Germany;
[5]Sodwiese 1, 24326 Stocksee, Germany;
[6]Faunistica, Jaguarring 4, 23795 Bad Segeberg, Germany;
[7]NABU Mecklenburg-Western Pomerania, Wismarsche Straße 146, 19053 Schwerin, Germany.

In 2016 a research project "BATMOVE – Effects of offshore windfarms on bat migration over the Sea" (FKZ 3515 82 1900) was initiated by NABU Mecklenburg-Western Pomerania with the aim of improving the knowledge about the spatial and temporal occurrence of migrating bats over the North Sea and Baltic Sea and about their connectivity. The results of the project will serve as a basis for the development of methods to prevent collision with offshore wind turbines of migrating bats crossing seas. Here, we present the first results, which have been conducted in preparation for a follow-up 2-year-study. Automated bat detector systems were installed at FINO 1 and on Heligoland (both North Sea) and at a buoy E/69 between Gedser and Warnemünde (Baltic Sea). Bat activity was recorded at all three locations with the lowest activity occuring at FINO 1, followed by Heligoland. Astonishingly high activity was found at the buoy E/69. At the North Sea only three species were recorded: *Pipistrellus nathusii* as the main species, also *Nyctalus noctula* and *N. leisleri*. At buoy E/69 additionally *Pipistrellus pygmaeus* and *Eptesicus nilssonii* were found. The project is supported by the Federal Agency for Nature Conservation (BfN) with funds of the Federal Ministry for the Environment, Nature Conservation, Building and Nuclear Safety (BMUB).

FROM BAT CALLS IN THE FIELD TO VALIDATED SPECIES RECORDS – THE APPROACH OF THE SWISS BAT BIOACOUSTICS GROUP (SBBG) [O]

ELIAS BADER[1]**, FABIO BONTADINA[1], ANNIE FREY-EHRENBOLD[1], CYRIL SCHÖNBÄCHLER[1], PETER E. ZINGG[1], MARTIN K. OBRIST[1],
**elias.bader@zoo.ch
[1]*Swiss Bat Bioacoustics Group SBBG, Swiss Federal Institute for Forest, Snow and Landscape Research, WSL, Biodiversity and Conservation Biology, Zürcherstrasse 111, CH-8903 Birmensdorf, Switzerland.*

Acoustic recording of bat calls has proven to be a powerful technique for assessing distribution, behaviour and threat status of these inconspicuous and widely threatened species. With its commercial potential being increasingly recognized, systems for semi-automated ultrasound recording have conquered the market, followed by automated bat species identification software. As a consequence, nowadays, many people with different backgrounds work on bat bioacoustics in Switzerland. However, the accuracy as well as the comparability of results of such systems still need further improvement to strengthen bat bioacoustics as tool for ecological assessments. To close the gap the Swiss Bat Bioacoustics Group (SBBG) was formed with the aim to develop an independent alternative for validation of species identifications. This procedure holds criteria elaborated in conjunction with the Swiss center of faunistic cartography CSCF and Swiss Bat Conservation (KOF/CCO). To confirm records and make them valid for the national fauna database and further use, the SBBG relies on 1) national distribution data of bat species from CSCF and regional experts, 2) the level of species specific difficulty of identification, agreed on in literature and among experts alike, and 3) region specific quantity of recordings of the species. These factors are combined to a response matrix, which is supposed to guide executive authorities in their requests for proof of species occurrences. The matrix assigns each species by region to one of three categories, ranging from plausible records for species that are common and easy to identify, to records that need verifiation by an independent expert for species that are uncommon to a region and/or hard to identify. The presentation introduces the SBBG and its hands-on approach to alleviate the challenge of acoustic species verification.

RESPONSE OF BAT ACTIVITY TO CHANGES IN A VINEYARD MOTH PEST: PRELIMINARY RESULTS [P*]

UNAI BAROJA[1]**, JOXERRA AIHARTZA[1], INAZIO GARIN[1], URTZI GOITI[1],
**ubaroja001@gmail.com
[1]*Zoology and Animal Cell Biology Department, UPV/EHU, Sarriena z/g, 48940 Leioa, The Basque Country.*

Insect pests cause an annual loss of 470 billion dollars in agriculture worldwide. Only recently has the role of bats as potential biocontrol agents been emphasized, and studies on that topic have increased. However, according to current literature, none has studied the case of the grape vine moth (*Lobesia botrana*) in vineyards from southern Europe. We compared the moth phenology and the foraging activity of bat species during the study period. In addition, to assess the effects of intensification on bats, we analyzed the bat-specific diversity, activity and moth abundance in two different agricultural management plots (one organic and one intensive) located in the Atlantic part of the Basque Country. To obtain data on male moth flights, one delta trap equipped with a synthetic pheromone attracting *L. botrana* was used in each station and an automatic ultrasound detector system (Song Meter SM3BAT) for bat monitoring. Generalized Linear Mixed Models were used to assess the effects of the moth abundance on bat activity. The most active bat species were widely distributed, common and generalist species. Bat activity and diversity, as well as moth abundance were greater in the organic plot. We did not observe any significant relation between moth abundance and bat activity, except for *Nyctalus leisleri*, whose activity was negatively related to moth abundance. Nevertheless, the maximum activity of *Pipistrellus kuhlii* coincided in time with the peak of the moth numbers, precisely in the lactation period. Based on our results, we conclude that intensification could affect bat activity and diversity. In addition, *L. botrana* may possibly be an important food resource for *P. kuhlii* during the lactation period. Due to the limitations of this methodology and in order to determine the trophic interaction between bats and the grape vine moth more precisely, further studies combining faecal molecular analyses techniques are required.

SAVING TREES FOR SAVING BATS: TREEDS IN LANDSCAPE ELEMENTS AS KEY FORAGING HABITATS FOR INSECTIVOROUS BATS IN INTENSIVELY FARMED LANDSCAPES [O]

SÍLVIA BARREIRO[1,2]**, JOÃO TIAGO MARQUES[1,2], BRUNO SILVA[1,2], JOSÉ MANUEL HERRERA[1,2], **silviapereirabarreiro@gmail.com
[1]*UBC- Conservation Biology Lab, Department of Biology, University of Évora, Évora, Portugal;*
[2]*CIBIO/InBIO-UE – Research Center in Biodiversity and Genetic Resources, Pole of Évora, Évora, Portugal*.

Landscape homogenization caused by agricultural intensification has detrimental effects on several insectivorous bat species that provide valuable agricultural pest control services. To understand the mechanisms that promote bat persistence in intensively farmed landscapes, we investigated the patterns of species richness, flight and feeding activities, for individual species and for three foraging guilds (open, edge and closed-space bats), across structural features of increasing complexity (open fields, single trees, tree lines and woodlands). Bats were surveyed during the summer of 2014, in an intensive agricultural landscape, by acoustic methods, and arthropods were sampled with light traps. We tested for differences between structural features with GLMMs considering also the landscape context, prey availability and weather variables. We recorded a total of 16,099 bat passes, of which 79.4% belonged to edge, 19.9% to open-space and 0.7% to closed-space bats. The most frequentlyrecorded species were *Pipistrellus pipistrellus* (40.5%), *P. pygmaeus* (20.0%), *P. kuhlii* (10.1%), *Eptesicus serotinus/isabellinus* (8.6%) and *Nyctalus leisleri* (7.7%). Species richness and bat activity were significantly lower in open fields where the closed-space *Myotis* spp were not recorded. Feeding activity of edge bats was significantly higher at tree lines. Bats showed species-specific responses to structural features; most species were more active on tree lines and woodlands. However, *Myotis myotis/blythii* and *Plecotus auritus/austriacus* activity was higher at single trees, whereas *N. leisleri*, *E. serotinus/isabellinus* and *Tadarida teniotis* were more active over woodlands. Therefore, different structural tree elements probably provide distinct commuting and feeding opportunities. These species-specific responses to the trees of structural elements should be included in the management of agricultural landscapes to promote the provisioning of biodiversity ecosystem services.

EFFECT OF QUARRY REHABILITATION PLANS ON BAT FLIGHT ACTIVITY AND SPECIES COMPOSITION AT OPERATING QUARRIES [P]

SÍLVIA BARREIRO[1,2]**, DÉNIS MEDINAS[1,2], SOFIA EUFRÁZIO[1,2], CARMO SILVA[1,2], VÂNIA SALGUEIRO[1,2], PEDRO SALGUEIRO[1,2], ALEXANDRA SILVA[3], ANTÓNIO MIRA[1,2], **silviapereirabarreiro@gmail.com
[1]UBC – Conservation Biology Lab, Department of Biology, University of Évora, Évora, Portugal;
[2]CIBIO/InBio-UE – Research Centre in Biodiversity and Genetic Resources, Pole of Évora, Évora, Portugal;
[3]Centro Técnico Corporativo CTEC – CTBQ, SECIL – Companhia de Cal e Cimento, S.A.,Outão, Portugal.

Quarries are often considered as ecologically degraded sites with negative impacts on biodiversity as a consequence of extraction operations. The increasing awareness of the importance of the ecosystem services provided by biodiversity led to the execution of several Quarry Rehabilitation Plans (QRP) and Biodiversity Management Plans (BMP) in such areas. We evaluate the effects of a QRP, being implemented since 1982 at the actively operating SECIL-Outão limestone and marl quarries (Arrábida Natural Park, Setúbal, Portugal) on species composition and flight activity of three bat guilds (short-, mid-, long-range echolocators). We surveyed 20 sites by acoustic methods in June, July, August and September of 2010, 2013 and 2016. Bat passes were identified to species or species complexes. Generalized Linear Mixed Models and Canonical Correspondence Analysis were used to analyse the influence of rehabilitation time, rehabilitation type, soil type and dominant vegetation cover on bat activity and species composition. We recorded a total of 1127 bat passes of which 47% belong to long-range, 35% to mid-range and 1.1% to short-range echolocating bats. The most recorded species and species complexes were *Pipistrellus pipistrellus* (18%), *Nyctalus leisleri/Eptesicus serotinus/isabellinus* (19%) and *E. serotinus/isabellinus* (12%). Rehabilitation type and cover influenced bat activity and species composition positively and significantly. Mid-range echolocating bat activity was higher at natural and orographic rehabilitated areas; the activity of long-range echolocating bats *N. leisleri* and *E. serotinus/isabellinus* was higher at slope-rehabilitated and tree covered areas, while *Tadarida teniotis* and *Nyctalus lasiopterus/noctula* were more active at steppe rehabilitated areas. We suggest that different types of rehabilitation enhance the diversity of bat communities in quarries. These results will contribute to species specific management measures for quarry rehabilitation.

LESS COMMON SYNCHRONIZED REWARMING IN WNS TOLERANT BATS AS HIBERNATION STRATEGY [O]

TOMÁŠ BARTONIČKA[1]**, JÁN BLAŽEK[1], HANA BANDOUCHOVA[2], HANA BERKOVÁ[3], JIRI PIKULA[2], ZDENĚK ŘEHÁK[1], NATÁLIA MARTÍNKOVÁ[3,4], JAN ZUKAL[4], **bartonic@sci.muni.cz

[1]*Department of Botany and Zoology, Masaryk University, Brno, Czech Republic;*
[2]*Department of Ecology and Diseases of Game, Fish and Bees; University of Veterinary and Pharmaceutical Sciences, Brno, Czech Republic;*
[3]*Institute of Vertebrate Biology, Czech Academy of Sciences, Brno, Czech Republic;*
[4]*Institute of Biostatistics and Analyses, Masaryk University, Brno, Czech Republic.*

Torpor bouts and arousals in hibernating bats need to be optimized according to the hibernaculum temperature and bat fat reserves. Clustering is a behavioural phenomenon that has significant physiological and ecological benefits promoting consequences for the successful hibernation of individuals. Aggregated bats probably maintain optimal temperature at lower costs than solitary hibernating bats, which allows them to reduce energy consumption. However, clustering could also be risky when aroused bats interfere with hibernating bats, which in turn initiate energy-demanding awakening. Our study was conducted over two winters in two different hibernacula in the Czech Republic, where bats were previously diagnosed with WNS. The thermal behaviour of four hibernating clusters of greater mouse-eared bats (*Myotis myotis*) was recorded using thermographic cameras. Normothermic events (Tfnorm, 119 in total) were not more frequent at the end of the winter, as occurs in North American bats that are affected by WNS. Most of the normothermic events (60%) did not exceed 1.5 hours. We were not able to find any relationship between Tfnorm timing and sunset. Characteristics of Tfnorm significantly differ between winters and sites. Synchronized rewarmings were found in 17 (14%) of Tfnorms. During the winter there was a constant number of cascades, but their percentage was the highest in mid-March. Our results show differences in the hibernation of bats with WNS between the Czech Republic and North America, and at the same time highlight the specific role of climate and sites that fundamentally affect hibernation strategies.

ARTICULATING CITIZEN SCIENCE, SEMI-AUTOMATIC IDENTIFICATION AND FREE WEB SERVICES FOR LONG-TERM ACOUSTIC MONITORING: EXAMPLES FROM FRANCE AND UK [O]

YVES BAS[1,2]**, STUART NEWSON[3], JEAN-FRANÇOIS JULIEN[1], CHRISTIAN KERBIRIOU[1], **yves.bas@mnhn.fr
[1]*CESCO, National Museum of Natural History, 43, rue Buffon, 75005 Paris – France;*
[2]*CEFE-CNRS, 1919, route de Mende, 34000 Montpellier – France;*
[3]*British Trust for Ornithology, BTO, The Nunnery, Thetford, Norfolk IP24 2PU, U.K.*

Bats often have high conservation prioritisation but identification issues and surveying challenges mean that large-scale monitoring is less developed than for some other taxa. Static detectors deployed to record bats throughout whole nights have been recommended for standardised acoustic monitoring but until recently cost and lack of software to support analyses has prohibited wide uptake. To overcome this issue, we developed several open tools: (1) the Tadarida software toolbox detecting and classifying sound events, and (2) an open web portal (www.vigiechiro.herokuapp.com) to allow participants to manage and upload their data, then being processed through Tadarida to get a quick feedback on taxa present. These allowed us to manage standardized monitoring schemes in both UK and France, collecting millions of bat records together with interesting data on non-targeted taxa such as bush-crickets. We demonstrate how such data can accurately describe pronounced ecological patterns for numerous species at different scales: spatial variation in activity as a proxy for relative abundance, habitat selection and phenology of seasonal and nocturnal activity. Maintained in the long term, such schemes will also improve estimates of species temporal trends and hence the assessment of conservation priorities. The feedback produced by these two monitoring schemes provide useful insights for the sustainability of long-term acoustic monitoring of bats. We indeed recommend an adaptive management of sound data so that they could be re-analysed every time identification softwares make significant progress. Moreover, there are real benefits of developing long-term acoustic monitoring within a collaborative framework, specifically (1) for collaboration among bat scientists for the collection of reference sound data, and (2) for work on bats to consider the wider acoustic monitoring of other species groups by working with other zoologists to share resources and costs.

HIBERNATION STRATEGY CHANGE IN DAUBENTON'S BAT, *MYOTIS DAUBENTONII*, IN "NIETOPEREK" BAT RESERVE (WESTERN POLAND) [P*]

ANNA BATOR[1]**, JAN CICHOCKI[1], AGNIESZKA WAŻNA[1], **mystacinaa@gmail.com
[1]*Department of Zoology, Faculty of Biological Sciences, University of Zielona Góra, Szafrana 1,65-516 Zielona Góra, Poland.*

Daubenton's bats, *Myotis daubentonii*, hibernate under varying temperature conditions. In Central Europe, they hibernate mainly in underground sites. In "Nietoperek" reserve, which is the largest bat hibernaculum in Central Europe, an explicit decline in the number of hibernating Daubenton's bats has been recorded. Our research was aimed at investigating whether in the past 30 years, aside from the change in number, also a change in the hibernation strategy has occurred. We counted the hibernating bats in a 1700 m long section of the reserve every two weeks during two seasons: 2015/2016 and 2016/2017. We recorded whether bats hibernate alone or in clusters. We compared our data with those collected in the same section in the 1980s. Our results point to a change in hibernation strategy of Daubenton's bats. Observations from the last two seasons compared with those from the 1980s show the disappearance of clustering behaviour in this bat species. The number of Daubenton's bats hibernating in one cluster used to reach up to 140 specimens, whereas now, it reaches up to four, and solitary specimens outnumber the clustering ones. We also noticed the decline in population size of Daubenton's bats hibernating in "Nietoperek" from 11,842 to 4,549 in 2015. Shorter and warmer winters are probably one of the main reasons why Daubenton's bats changed their hibernation strategy. The decline in the population size might have been caused by cold springs during the seasons of the study. However, it is also possible that the decline in the number of Daubenton's bats hibernating in underground sites is due to their choice of alternative overground roosts. Also, a general population trend cannot be excluded.

TREATMENT OF SOME BACTERIAL INFECTIONS IN FIVE EUROPEAN BAT SPECIES [P*]

ANNA BATOR[1]**, BARBARA GÓRECKA[2], KATARZYNA PTAK[3], KATARZYNA SIEDLECKA-KOWALCZEWSKA[4], KATARZYNA SULIMA,
**mystacinaa@gmail.com
[1]*Department of Zoology, Faculty of Biological Sciences, University of Zielona Góra, Szafrana 1, 65-516 Zielona Góra, Poland;*
[2]*BAT MOM Barbara Górecka, Poland;*
[3]*Animal Care Vet Clinic in Klodzko, Poland;*
[4]*Andi Vet Clinic in Kielce, Poland.*

We describe bacterial infections first diagnosed in two European bat species (common noctule bat, *Nyctalus noctula* – two specimens; and greater mouse-eared bat, *Myotis myotis* – one specimen). All animals had the same unspecific symptoms: weight loss, skin redness, skin pigmentation loss, baldness, swollen joints, weakening of the skin structure, necrosis of distal parts of tail and phalanges. All bats were diagnosed using antimicrobial susceptibility testing of swab samples. Three different antibiotics were prescribed for three different bacteria: *Pseudomonas aeruginosa* – marbofloxacin (two common noctule bats and one greater mouse-eared bat), *Staphylococcus intermedius* – enrofloxacin (one common noctule bat). Treatment was long and exhausting. Bats suffered from weakness and spot skin necrosis (marbofloksacin). We used convalescence support instant diet for cats and dogs, betaglucane, Duphalyte and probiotics. The same treatment was successfully applied to other bats with the same symptoms but without laboratory diagnostics (nine common noctule bats, five parti-coloured bats (*Vespertilio murinus*), three serotine bats (*Eptesicus serotinus*) and one Nathusius's pipistrelle (*Pipistrellus nathusii*). Bats during rehabilitation or living in captivity suffer from immunodeficiency, probably caused by previous malnutrition, mono diet, lack of milk antibodies (infants), stress or a combination of these. There is a clear need to include the laboratory diagnostics in the treatment and rehabilitation of bats.

THE MITOCHONDRIAL PHYLOGEOGRAPHY OF THE LONG-FINGERED BAT, *MYOTIS CAPACCINII*, AROUND THE MEDITERRANEAN BASIN [P]

RAŞIT BILGIN[1]**, KANAT GÜRÜN[1], KÜBRA KARAMAN[1], JAVIER JUSTE[2], PETR BENDA[3, 4], ANDREA VIGLINO[5], EMRAH ÇORAMAN[1], AHMET KARATAŞ[6], ANDRZEJ FURMAN[1], **rasit.bilgin@boun.edu.tr

[1]*Institute of Environmental Sciences, Boğaziçi University, 34342 Bebek, İstanbul, Turkey;*

[2]*Doñana Biological Station (CSIC), Avda. Américo Vespucio s/n, Isla de la Cartuja, Seville 41092, Spain;*

[3]*Department of Zoology, Faculty of Science, Charles University in Prague, Viničná 7, CZ–128 44 Praha 2, Czech Republic;*

[4]*Department of Forest Protection and Wildlife Management, Faculty of Forestry and Wood Sciences, Czech University of Life Sciences, Kamýcká 1176, CZ–165 21 Praha 6, Czech Republic;*

[5]*Conservation Genetics Laboratory, National Institute for Environmental Protection and Research (ISPRA), Via Cà Fornacetta 9, 40064 Ozzano dell'Emilia (BO), Italy;*

[6]*Department of Biology, Niğde University, Niğde, 51100, Turkey.*

The long-fingered bat, *Myotis capaccinii*, is a widely distributed species in the western Palearctic, spanning the Mediterranean basin, extending into North Africa, and as far east as Iran. The species is considered to be polytypic, with a taxonomic break considered to occur around former Yugoslavia. More recent genetic studies indicated that the break might actually take place in southeastern Europe. In this study, using a partial fragment of the cytochrome-b gene, we investigated the mitochondrial DNA phylogeography of the long-fingered bat around the Mediterranean coasts of Europe, as well aswith samples from North Africa, Anatolia and Iran. The results indicate two genetic breaks, a deeper split in southeastern Europe, as recorded previously, and a more recent one in the Alps. Both of the splits date to the Pleistocene, indicating the importance of the ice ages in causing genetic differentiation in Europe. Environmental niche modelling analyses indicate potential refugial areas for the three mitochondrial entities.

CHANGES IN NUMBERS AND REPRODUCTIVE STATUS OF BATS DURING SWARMING IN NATURA 2000 SITE PLH080003 "NIETOPEREK", POLAND [O]

JUSTYNA BŁESZNOWSKA[1], EWA KWASIBORSKA[2], TOMASZ MARSZAŁEK[3], TOMASZ KOKUREWICZ[4]**, ANITA GLOVER[5], JOHN HADDOW[6], GRZEGORZ APOZNAŃSKI[4], **tkokur@gmail.com

[1]Walecznych 112, 57-300 Kłodzko, Poland;
[2]Rynek 52/4, 56-400, Oleśnica, Poland;
[3]Ansee Consulting, Św. Antoniego 2/4, 50-073 Wrocław, Poland;
[4]Wrocław University of Environmental and Life Sciences, Institute of Biology, Department of Vertebrate Ecology and Paleontology, Kożuchowska 5b, 51-631 Wrocław, Poland;
[5]The Vincent Wildlife Trust, 3 & 4 Bronsil Courtyard, Eastnor, Ledbury, Herefordshire HR8 1EP, U.K.;
[6]Auritus Wildlife Consultancy Ltd, 27 Balmoral Court, FK15 9HQ, Dunblane, U.K.

A study of swarming activity at Nietoperek, Poland, was carried out from 6 August to 30 September 2014 and 13 August to 9 October 2015. Altogether 32 nights of mist netting (4 session per year x 4 nights each) was performed for both swarming seasons. To minimise the impact of disturbance on the results the netting was carried out on alternate nights near two entrances to the underground system. The netting period in the second season was changed by a week to ensure the whole swarming period was covered. In total 3265 bats from 13 species were caught, marked by fur clipping, sexed, aged, weighed, forearm length measured, and reproductive status recorded. The number and species composition differed significantly between both netting sites located only 4 km apart. In both netting sites no re-trapped individuals were recorded, indicating near-nightly changes of population at the swarming sites. On average 144 Bechstein's bats, *Myotis bechsteinii*, were caught per swarming season, while the largest number recorded hibernating underground has been only 48 individuals. This suggests that either "Nietoperek" is a stopover during migration, or there is a significant underestimation of wintering population of the species. Based on the largest number of caught individuals, the highest activity for *B. barbastellus* and *M. bechsteinii* was recorded in the first half of September, while for *M. nattereri* and *P. auritus* it was later in that month. In Daubenton's bat and mouse-eared bat two separate activity peaks were observed, which could indicate the presence of local and migratory populations swarming at different times. In Daubenton's bat there was significant positive correlation between the number of sexually active males and the average daily temperature, while in Natterer's bat negative correlation was found ($r_s=0.42$ and $r_s=-0.46$, $n=32$, $P<0.05$ respectively). Sexually active males aged 2–4 months were found in Daubenton's bat (n=58), Natterer's bat (n=7), Bechstein's bat (n=3), mouse-eared bat (n=29), barbastelle (n=3) and brown long-eared bat (n=1).

RAPID ASSESSMENT OF BATS ON BOUGAINVILLE ISLAND: SEARCHING FOR MONKEY-FACED FRUIT BATS AND SPARE TIRES [O]

FRANK J. BONACCORSO[1]**, DAVID WALDIEN[2], CHRISTOPHER M. TODD[3], JUNIUS REPIRIRI[4], PEDRO URAVUTU[4], **fbonaccorso@usgs.gov
[1]U.S. Geological Survey, Kilauea Field Station, Hawaii National Park, Hawaii, USA;
[2]Bat Conservation International, Austin, Texas, USA;
[3]University of West Sydney, Richmond, Australia;
[4]Rotokas Ecotourism, Wakunai, Bougainville Autonomous Government.

We conducted a two week field assessment of bats across the central region (Wakunai-Mt. Balbi-Torokina) of Bougainville Island from 22 February through to 5 March 2017 as part of a conservation initiative jointly hosted by Rotokas Ecotourism (RET) and Bat Conservation International (BCI). Bougainville and neighboring Buka are the two principal islands forming the North Solomons Province of Papua New Guinea, although currently local government is under the authority of the Autonomous Bougainville Government, which will conduct a plebiscite in 2019 leading to a decision on independence. Our biological assessment was conducted using mist-nets, a bat trap, acoustic recordings, cave and vegetation roost observations, and interviews with local people. We collected wing tissue biopsies, photographic records, and hand release echolocation calls to verify species identifications based on field characters of morphology and echolocation recordings of free-flying bats. We report on the numbers and species of bats surveyed, which notably include the first records of *Miniopterus medius* on Bougainville. We report behavioural observations of the IUCN designated Endangered Species, *Pteralopex anceps* (Bougainville monkey-faced fruit bat). Our species accounts communicate information on body size and morphology, echolocation call characteristics, food habits, roost selection, and conservation status. Finally, we present a summary of conservation outreach and education efforts conducted by RET and BCI at levels of "grassroots" communities (schools, women's groups, and councils of chiefs) through local and national government that importantly promise to facilitate bat conservation on Bougainville into the future.

DEVELOPING A MONITORING METHOD FOR WHISKERED AND NATTERER'S BATS IN IRELAND [P]

EMMA S.M. BOSTON[1]**, NIAMH ROCHE[1], TINA AUGHNEY[1], FERDIA MARNELL[2],
**esmboston@hotmail.com
[1]*Bat Conservation Ireland, Ulex House, Drumheel, Lisduff, Virginia, Co. Cavan, Ireland;*
[2]*National Parks and Wildlife Service, 7 Ely Place, Dublin 2, Ireland.*

This Pilot Woodland Bat Survey aims to devise a method for monitoring populations of whiskered and Natterer's bats in Ireland. Previous efforts to monitor these rarer *Myotis* species have met with little success given the scarcity of known roosts of these species and the difficulty of catching them in the field. In addition, until now, it had been difficult to distinguish between the *Myotis* species based on echolocation calls. In 2014, a project conducted in the UK applied newly developed automated species identification software to this problem with great success. This study aims to determine the feasibility of collecting data using full spectrum bat detectors during walked woodland transects and analysing the bat call data using automated software. The initial step is to determine the probability of detection of each species and then to calculate through power analysis how many woodland sites would need to be surveyed annually across Ireland to make this a statistically robust monitoring scheme based on woodland occupancy. Here we present initial results from the 2016 field season, including the development of a bespoke automated species identification software for monitoring these bats in Ireland.

AUTOMATED BAT SOUND IDENTIFICATION: RELIABLE OR NOT? COMPARING THE RESULTS OF FOUR WIDELY USED AUTOMATED BAT IDENTIFICATION SOFTWARE PROGRAMS [P]

ROBIN BRABANT[1], BOB JONGE POERINK[2]**, YVES LAURENT[1], UMIT DOLAP[2],
**bob@fieldworkcompany.nl
[1]*Royal Belgian Institute of Natural Sciences (RBINS), Operational Directorate Natural Environment, Vautierstraat 29, 1000 Brussel, Belgium;*
[2]*The Fieldwork Company, Van Schendelstraat 1, 9721 GV Groningen, The Netherlands*.

Recently a few papers were published addressing the prudency needed when using automated identification software programmes to analyse recordings of bat echolocation sounds. We want to contribute to that discussion by analysing a reference dataset of bat recordings with four widely used and commercially available software programs (BatIdent, BatExplorer, Kaleidoscope and Sonochiro). The reference data were all recorded in western Europe with a batcorder. For most of the recordings there was a visual confirmation of the recorded species. In a few other cases certainty was obtained because the specimens were captured and released or because the recordings were made in certain areas which were outside of the range of other species (e.g. at high altitude to separate *Eptesicus serotinus* and *Eptesicus nilssonii*). After running the different programs on the reference data, we compared the outputted results. Overall, identification of the recordings to species level in this test was best with Batident (81% correct identifications), followed by Kaleidoscope (71%), Sonochiro (63%) and BatExplorer (53%). We can conclude that each of the tested programmes has its own strengths and weaknesses, but none of them should be used unsupervised. Outputted results need to be checked by a trained expert. In this way, our test confirms the conclusions of previous tests in Northern Europe and the USA.

STATUS OF ROMANIAN BAT POPULATIONS: THE 2010-2017 REVIEW OF RESEARCH AND CONSERVATION [O]

SZILÁRD-LEHEL BÜCS[1,2]**, ISTVÁN CSŐSZ[2], DANIELA COCIUBA (BORDA)[3], IOAN COROIU[4], DRAGOȘ ȘTEFAN MĂNTOIU[5], IRINA POCORA[6], TEODORA SINCULEȚ[7], DRAGOȘ BĂLĂȘOIU[8], CSABA JÉRE[2], **contact@lilieci.ro
[1]*Nature of Transylvania Association, Cluj-Napoca, Romania;*
[2]*Romanian Bat Protection Association, Satu-Mare, Romania;*
[3]*Institute of Speleology Emil Racoviță, Cluj-Napoca, Romania;*
[4]*Faculty of Biology-Geology, Babeș-Bolyai University, Cluj-Napoca, Romania;*
[5]*Wilderness Research and Conservation Association, Bucharest, Romania;*
[6]*SistemIS Association, Iași, Romania;*
[7]*Semenic-Cheile Carașului National Park, Reșița, Romania;*
[8]*Dobrogea Research Group, Constanța, Romania.*

With 32 bat species and some of Europe's largest colonies, Romanian bat populations need effective and long-term conservation actions. We present a synthesis of the 2010-2017 bat research, the situation of the bat fauna in Romanian Natura 2000 sites, but also examples of real conservation vs. ineffective conservation. Based on recent discoveries of large colonies (ex. 7.400+ medium-sized *Rhinolophus* in the Topolnița cave), we can state that EUROBATS's lists of internationally important roosts in Romania have the potential to expand to hundreds. Several key caves in NW Romania received bat-friendly closings in the 2012-2013 period, but others continue to be threatened or even intentionally degraded, despite legislation and advice from bat expert groups. Threats include mass-tourism, specialized speleo-tourism, religious activities, as well as the unwillingness of decision makers to recognize the importance of these caves. A series of overground sites had bat-friendly measures installed in the 2014-2016 period, aiming to protect both colonies and buildings, but the relationship between bats and building owners remains fragile. On the positive side, bat rehabilitation works intensely, and the inclusion of volunteers experiences a boom. The threat coming from the uninformed public is receding. There is an increasingly positive perception about bats, with media channels starting to recognize the value of bats and the need of protection. However, there is still little to no conservation planning in case of road infrastructure projects. Wind farms are rarely operated with post construction monitoring, and bat fatality reduction measures are scarcely implemented (with a few exceptions). In order to be truly effective in protecting Romania's bat fauna in the long-term, conservation efforts must be well planned, targeted and monitored, and the support of official bodies must be secured. The current review aims also to assist in the elaboration of the national report for the upcoming 2018 EUROBATS MoP.

RUINS OR MORE: THE BAT FAUNA OF THE FORTIFIED CAROL LINE, NORTH-WESTERN ROMANIA [P]

SZILÁRD-LEHEL BÜCS[1,2]**, CSABA JÉRE[2], ISTVÁN CSŐSZ[2], LEVENTE BARTI[2], DÉNES DOBROSI[3], **contact@lilieci.ro
[1]*Nature of Transylvania Association, Cluj-Napoca, Romania;*
[2]*Romanian Bat Protection Association, Satu-Mare, Romania;*
[3]*Governmental Office of Jász-Nagykun-Szolnok County, Hungary.*

The 'Carol' line is a former WW2 defence line, build between 1937 and 1940, but almost completely dismantled as early as 1940. It consisted of 320 bunkers, stretching along a 200 km transect between Maramureș and Bihor counties, in north-western Romania. Between May 2016 and April 2017, a EUROBATS EPI project entitled "The Carol line: assessing the importance of 150+ deserted bunkers for the conservation of the Romanian-Hungarian cross-border bat fauna" surveyed for the first time these bunkers, to establish their importance for the local and trans-border bat fauna. The project included field work in all major seasons (summer, autumn, winter, spring), using standard methods of bat research (visual observations, mist nettings and ultrasound recordings). Of the 320 former bunkers only 17 proved to be potentially useful for bats; the rest of the fortified line is in an advanced state of degradation. We identified a total of 12 bat species (more than one third of the Romanian bat fauna) using these ruins, or their surroundings, with good quality habitats (deciduous forests and wetlands). Identified species include strictly protected species, such as *R. ferrumequinum*, *M. myotis*, *B. barbastella* and *M. schreibersii*, but also long distance migrants such as *P. nathusii* or *N. noctula*. Bats are present along the Carol line and adjacent habitats all-year round, but most notably in the spring period, when we observed the greatest diversity in a single site during the project (3 species), and the largest number of bats. A transitory group of *M. schreibersii* (34 bats) was observed in the subterranean level of a semi-intact bunker around Nojorid (Bihor county) in April 2017, pointing to the potential importance of these roosts as migration stopovers. The distance to the closest potential roost in Hungary is 70 km, with the two regions also being directly linked by the Crișul Repede river valley. Trans-border movements must be further investigated to clearly establish this link.

AN UPDATE ON THE BAT FAUNA OF THE DOBROGEA REGION, SOUTH-EASTERN ROMANIA [P]

SZILÁRD-LEHEL BÜCS[1,2]**, CSABA JÉRE[2], ISTVÁN CSŐSZ[2], ALEXANDRA TELEA[3], DRAGOȘ BĂLĂȘOIU[4], FARKAS SZODORAY-PARÁDI[2], OANA MIRELA CHACHULA[5], LEVENTE BARTI[2], **contact@lilieci.ro
[1]*Nature of Transylvania Association, Cluj-Napoca, Romania;*
[2]*Romanian Bat Protection Association, Satu-Mare, Romania;*
[3]*Ovidius University, Constanța, Romania;*
[4]*Dobrogea Research Group, Constanța, Romania;*
[5]*National History Museum of Romania, Bucharest, Romania*.

The Dobrogea region, between the Black Sea, the Danube and the Danube Delta was historically home to large Rhinolophus mehelyi colonies (3.000-5000 bats). From the 1960s agricultural activities intensified in the region and caves begun to be exploited for religious and touristic reasons, leading to significant declines of bat populations, including those of *R. mehelyi*. Currently, besides ongoing agriculture, there are extensive wind farms operating, including the largest on-shore wind farm of Europe, in the Fântânele-Cogealac area. In the period of 2009-2015 we surveyed the bat fauna of Dobrogea, in a total of 16 sites, including known key roosts and also new locations. A total of 11 species were identified, with the most frequent being R. ferrumequinum (0.52), Miniopterus schreibersii (0.41), large Myotis spp (0.36 combined for both species), and *M. daubentonii* (0.27). *R. mehelyi* was discovered in a new location, expanding slightly northward the regional distribution of the species, but is not reported since 2004 from a former key site, the Gura Dobrogei cave. Several abandoned mines offer good roosting conditions, especially for *R. ferrumequinum*. A small nursery colony of *R. hipposideros* (17 bats) was discovered in the Canaraua Fetii cave No 1, but is threatened by religious activities of the area. The maximum size of the *R. mehelyi* colony from Limanu cave was 157 bats in January 2015, however the colony is able to retreat to inaccessible parts of the cave, making colony counts impossible. The greatest bat aggregations of the region are still represented by mixed colonies of *M. schreibersii* and large *Myotis* spp in the Gura Dobrogei cave (350-400 bats), however they are only a fraction of their historical size, and continue to be threatened by human activities and are also exposed to the largest on-shore wind farm of Europe. Uncontrolled tourism in all Dobrogean caves continues to threaten the known bat colonies of the area.

THE BAT FAUNA OF THE F□GET FOREST, ROMANIA: RESEARCH AND CONSERVATION NEXT TO A BUZZING CITY [P]

SZILÁRD-LEHEL BÜCS[1,2]**, FRANCISKA-LILLA PÁL[3], HORAŢIU POPA[4], CRISTIAN ZAHA[4], MIHAI CONSTANTINESCU[1,5], **contact@lilieci.ro
[1]*Nature of Transylvania Association, Cluj-Napoca, Romania;*
[2]*Romanian Bat Protection Association, Satu-Mare, Romania;*
[3]*Faculty of Biology-Geology, Babeş-Bolyai University, Cluj-Napoca, Romania;*
[4]*Ecouri Verzi Association, Cluj-Napoca, Romania;*
[5]*Technical University of Cluj-Napoca, Cluj-Napoca, Romania.*

The Natura 2000 site ROSCI0074 Făgetul Clujului - Valea Morii, located in Transylvania, north-western Romania, is a protected area with a remarkable biodiversity. Covering just over 16 km^2, it is a small protected area, but characterized by extensive deciduous forests, small streams and also marshes. At the same time it is also one of the most important recreational areas of Cluj-Napoca, a city with over 400,000 inhabitants. Faced with such anthropic presence, the Natura 2000 site is threatened by the development of new residential buildings, pollution, deforestation, habitat fragmentation and uncontrolled tourist activities. With several strictly protected species and habitat types in the site's standard form (including Lepidoptera species), bats were missing from the description of the area. In the period of 2014-2016 we undertook basic surveys in order (1) to identify bat species present and key feeding areas, (2) to contribute to the elaboration of the area's management plan with adequate bat conservation measures, and (3) to start concrete bat conservation activities. We identified four bat species in the area (*E. serotinus*, *N. noctula*, *P. pipistrellus*, *P. pygmaeus*), but the area's potential is higher, given that in the city itself we are aware of the presence of other additional species, such as *P. austriacus*. Also, the forests present conditions adequate for forest-dwelling species such as *B. barbastellus*. In September 2016, after identifying the most suitable areas (mostly wetlands surrounded by forests, and flooded forest patches), we sited 12 bat boxes to help local bat populations cope with forest loss, and to offer alternative roosting possibilities. In 2017 bat conservation activities continued with mapping the exact location of old-growth hollow trees, to mark them and protect them from felling. At the same time, awareness activities are also undertaken, in order to familiarize city inhabitants with bats and the necessity for bat conservation.

UNITING THE EFFORTS OF ROMANIAN BAT CONSERVATION: A PROJECT AIMED AT BAT RESEARCHERS [P]

SZILÁRD-LEHEL BÜCS[1,2]**, ANA STAMATESCU[3], FERENC KÖLCSEI[4], TOMASZ POSTAWA[5], CSABA JÉRE[2], **contact@lilieci.ro
[1]*Nature of Transylvania Association, Cluj-Napoca, Romania;*
[2]*Romanian Bat Protection Association, Satu-Mare, Romania;*
[3]*Avenul Braşov Speleological Club, Braşov, Romania;*
[4]*Freelance programmer, Satu-Mare, Romania;*
[5]*Institute of Systematics and Evolution of Animals, Polish Academy of Sciences, Krakow, Poland.*

In recent years, the Romanian bat research community experienced a diversification in terms of new organizations and new approaches, but well-known challenges continue to threaten the bat fauna (habitat fragmentation, roost degradation, sub-optimal legislation). It is essential to acknowledge that these challenges cannot be addressed in a systemic manner without a united bat research community. The current project was implemented during the 2015-2017 Klaus Toepfer Fellowship Programme, with some activities continuing to this date. Our objectives were (1) to revitalize professional discussions inside the community, and (2) to increase public visibility of bat research and conservation. Funds for implementation were obtained through crowdfunding and direct sponsorships, with a total amount of 2,500+ EUR. Finished by January 2017, the project had several positive outcomes. In October 2016, the 2nd National Bat Research Conference was organized after a ten year break. Modern communication channels were created and are currently being used. With the input from several community members, ethical guidelines for Romanian bat research, and bat protection recommendations for the outdoor-oriented public were created. The Romanian bat portal (www.lilieci.ro) was launched in December 2016, representing by far the most complex and diverse online resource about Romanian bats and bat research. The portal is available in three languages (Romanian, Hungarian, English) and reaches a very wide audience. The project was successful in restarting communication inside our community. The bat portal will continue its activity, representing a significant link between the bat research community and the public, as well as being important for the research community per se. Future challenges remain (such as standardization of the national bat monitoring system and of ringing activities), but these can be gradually addressed through the contribution of a diverse bat research community.

POPULATION GENETIC STRUCTURE OF THE MEDITERRANEAN HORSESHOE BAT, *RHINOLOPHUS EURYALE*, IN SERBIA [P*]

IVANA BUDINSKI[1]**, JELENA BLAGOJEVIĆ[1], VLADIMIR JOVANOVIĆ [1], BRANKA PEJIĆ[1], MARIJA RAJIČIĆ[1], MILAN PAUNOVIĆ[2], MLADEN VUJOŠEVIĆ[1], **ivana.budinski@ibiss.bg.ac.rs

[1]*Department of Genetic Research, Institute for Biological Research "Siniša Stanković", University of Belgrade, Bulevar despota Stefana 142, 11060 Belgrade, Serbia;*

[2]*Biological Department, Natural History Museum, Njegoševa 51, 11000 Belgrade, Serbia.*

Mediterranean horseshoe bat (Rhinolophus euryale) is considered to be a sedentary species, with seasonal movements usually shorter than 50 km. Known roosts of R. euryale in Serbia are restricted to karstic areas in western and eastern parts of the country. Due to a distance greater than 150 km between caves in western and eastern Serbia, we expected genetic differentiation of populations (isolation by distance pattern). We studied population structure of 11 populations using 8 nuclear microsatellite loci, and examined population structuring within and among these geographic regions. Genetic diferentiation among populations (Fst) was very small, ranging from 0.007-0.075. AMOVA did not support the geographical structuring of the populations, showing among groups a variation of only c. 1%. Mantel test revealed no statistically significant correlation between geographic and genetic distances. The results obtained suggest possible gene flow between two karstic areas and existence of colonies in Central Serbia (non-karstic region). These findings have an important role in the future conservation management of Mediterranean horseshoe bat populations.

ROOST SELECTION BY A RARE TREE-DWELLING BAT AT DIFFERENT SPATIAL SCALES [O*]

ANDREW CARR[1]**, MATT ZEALE[1], ANDREW WEATHERALL[2], GARETH JONES[1],
**andrew.carr@bristol.ac.uk
[1]*University of Bristol, U.K.;*
[2]*University of Cumbria, U.K.*

We investigated roost selection by *Barbastella barbastellus* in upland oak forests in southern England. Twenty-nine bats were radio tracked to 44 roosts between 2007 and 2015. Twenty-four different characteristics of trees and forest stands were measured by field observations and by use of open source airborne light detection and ranging (LiDAR) datasets. Roost characteristics were compared with random tree and forest stand characteristics. We also measured the number of potential roosts in commercially managed (continuous cover silviculture) and minimum intervention managed (including abandonment) forest stands (n = 54). Bats selected trees in semi-natural broadleaved forests. Standing dead oak, while scarce, was positively selected over mature live oak and other tree types, and supported significantly more suitable microhabitat (preferred roost features). Roost selection depended on the number of cavities present on trees, and on canopy openness around roosts. Distance to water and reproductive status of females also appear to influence selection. Minimum intervention forest stands had a greater frequency of roosts than their commercially managed equivalents. Semi-natural broadleaved woodland is critically important for roosting *B. barbastellus* and should be conserved. LiDAR technology identified forest stand features important to roosting bats, and its application can reduce the need for labour-intensive field surveys. At least five cavities per tree and a canopy openness of 65-80% is optimal for encouraging roost use. Minimum intervention forestry, including abandonment, provides more roosts per tree than commercial forestry, but not the equivalent frequency found in semi-natural forests. Standing deadwood is a driver of roost formation, but evidence from research and policy guidelines that encourage the retention of standing deadwood has yet to provide a suitable amount of roosting opportunity for *B. barbastellus* in commercially managed forests in the UK.

COMPARATIVE PHYLOGEOGRAPHY OF TWO CRYPTIC SEROTINE BATS IN THE IBERIAN PENINSULA AND GENE FLOW CONSEQUENCES OF BEING TOO SIMILAR [O]

ALEJANDRO CENTENO-CUADROS[1], ORLY RAZGOUR[2], CARLOS IBÁÑEZ[1], OSCAR DE PAZ[3], GONZÁLO PÉREZ-SUÁREZ[3], SUSANA MARTÍNEZ-ALÓS[3], JUAN L GARCÍA-MUDARRA[1], ADRIÁN REDOND[1], JAVIER JUSTE[1,4]**, **juste@ebd.csic.es

[1]*Estación Biológica de Doñana (CSIC), Seville, Spain;*
[2]*Biological Sciences, University of Southampton, Southampton, U.K.;*
[3]*Depto. Ciencias de la Vida, Universidad de Alcalá, Madrid, Spain;*
[4]*CIBER of Epidemiology and Public Health (CIBERESP), Madrid, Spain.*

We investigated the genetic diversity and structure within two sibling serotine bats (*Eptesicus serotinus* and *E. isabellinus*) in Iberia, both in their contact zone and in allopatric areas of their respective distributions and combining the information of a fast evolving mtDNA Hyper Variable (HVII) fragment and 10 microsatellites. A multi-marker approach combining the information of the microsatellites with mtDNA sequences through Approximate Bayesian Computation (ABC) was used to test different phylogeographic patterns, and clustering algorithms based on codominant markers were used to identify possible gene flow and the presence of hybrids between the two species. Sampling included a total of 107 *E. serotinus* bats from 6 maternity colonies (two of them located in the contact zone between the two species), and 231 *E. isabellinus* from 13 maternity colonies (five within the area of sympatry). mtDNA diversity was slightly higher and showed deeper geographic structure for *E. isabellinus*. Haplotypes relationships showed no mitochondrial introgression or capture between the two species. Microsatellites showed two main groupings corresponding to the two species with similar diversity values between them and null within species structure, as expected in a male mediated gene flow system. ABC inference placed both species' populations split times as post-LGM and in continuous expansion. The central sympatric populations were colonised from the allopatric populations at approximately 6250 years ago for *E. isabellinus* and 2600 years ago for *E. serotinus*. The combined model indicates that contact between the sympatric central populations has resulted in gene flow from *E. isabellinus* to *E. serotinus*. Specific assignment tests confirmed the existence of hybrids in both species and which were found only in the contact zone. Hybridization proved to be highly asymmetrical, and as predicted by the ABC, most of the cases were found within the two sympatric colonies of *E. serotinus*,

ROMANIA – A MOMENT OF GRACE IN THE RESTORATION OF HISTORIC MONUMENTS THAT HOST BAT COLONIES [P]

OANA MIRELA CHACHULA[1]**, IOAN COROIU[2], GEORGIANA MĂRGINEAN[3], REGINA KLÜPPEL[4], **oana_chachula@yahoo.com
[1]*National Museum of Romanian History, Calea Victoriei street 12, Bucharest, Romania;*
[2]*Faculty of Biology and Geology, Babes-Bolyai University, Clinicilor street 5-7, Cluj-Napoca, Romania;*
[3]*Department of Biology, Bucharest University, Splaiul Independenţei street 95-97, Bucharest, Romania;*
[4]*Büro für angewandte Ökologie und Landschaftsplanung, Osnabrück, Germany.*

Since 2008, our team has been investigating a number of cases where restoration work has been conducted on churches, some of which are listed in the UNESCO World Heritage List. It is a legal requirement that specialist bat workers need to be engaged in the initial phase of the work, so early intervention can take place in order to save a colony. For this reason it is believed that the number of certified conservation biologists should increased in the future, as at the moment there are only five such specialists certified by the Ministry of Culture in the country. Some of the historic monuments where research was conducted are: the Orthodox Church in Prundu Bârgăului (Bistriţa-Năsăud County) with a nursery colony of up to 1600 *Myotis myotis/blythii* , the Humor Monastery, the Catholic Curch from Iacobeni and Dragomirna Monastery (Suceava County), Rogozu Monastery (eastern Romania) with a nursery colony of 15 *Eptesicus serotinus*; the Orthodox Church in Ciocadia (Gorj County) with up to 100 *Rhinolophus ferrumequinum* ; the Orthodox Church in Lisa (Braşov County) with a nursery of 40 *Plecotus austriacus* , the Orthodox Church in Suşeni (Gorj County) with a nursery of 12 *E. serotinus* and the Orthodox Church in Balota (Vâlcea County) with a nursing colony of 2300 *M. myotis/blythii* (southern Romania); the Greek-Catholic and the Unitarian Church (Roşia Montană, in western Romania). One of the major problems that we are confronting is the lack of awareness, knowledge, understanding and education of the beneficiaries, some of which have ended with attempts to eliminate the bats. Our efforts not only address the protection of historic monuments through a correct rehabilitation, but also the conservation of bat colonies in danger, by raising awareness and informing the restorers, conservationists, architects, ministry representatives and church personnel.

DISTRIBUTION PATTERNS OF SELECTED BAT SPECIES IN POLAND – SPATIAL MODELLING IMPROVED BY APPLICATION OF FINE-SCALE FOREST DATA [O]

MATEUSZ CIECHANOWSKI[1]**, MARTYNA JANKOWSKA-JAREK[1], KONRAD BIDZIŃSKI[1], **matciech@kki.net.pl
[1]*Department of Vertebrate Ecology and Zoology, Faculty of Biology, University of Gdańsk, ul. Wita Stwosza 59, 80-308 Gdańsk, Poland.*

Range limits of animal species are considered as lines, beyond which populations fail to adapt to conditions exceeding their ecological tolerance, while inside the range, many species reveal patchiness in their distribution, related to factors acting on a local scale. Recently, spatial modelling become an increasingly popular tool not only to predict species' occurrence outside surveyed areas but also to test for factors that affect the range topology. We examined distribution patterns for five species that reveal geographic range limits in Poland or strongly heterogeneous distribution within the country. Among them, *Myotis myotis* and *Myotis bechsteinii* reach the NE limit of their distribution, *Plecotus austriacus* – the northern limit, records of *Eptesicus nilssonii* are aggregated in mountains and in NE Poland, while *Myotis dasycneme* occurs sparsely all over the country, with a concentration of records in North Poland. Probability maps were prepared with presence-only data spatial modelling, using maximum entropy models in MaxEnt software, based on the GIS layers of mean air temperature and mean precipitation for each month and land cover, supported by a database of State Forests, consisting of detailed information about species composition and age of tree stands. The results confirm the important role of land cover for the occurrence of species, at least in the local scale: for *P. austriacus* it is the urban area, for *M. dasycneme* distance to water, while for *M. bechsteinii* deciduous woodlands and their low fragmentation, expressed as distance to the edge of the forest. Occurrence of oak, ash, hornbeam and sycamore, especially in the understory, appeared to be an important predictor for presence of the latter species. The effect of climate was secondary, probably acting mainly in a broad, geographical scale and the response appeared species-specific. A notable case is the association between *M. bechsteinii* and April temperature, i.e. the period when breeding females may face significant food shortage.

FACTORS AFFECTING DISTRIBUTION OF MATING SITES OF THREE *PIPISTRELLUS* SPECIES IN A SMALL COASTAL CITY [P]

MATEUSZ CIECHANOWSKI[1]**, ANNA KREFT[1], KATARZYNA LESZCZYŃSKA[1],
**matciech@kki.net.pl
[1]*Department of Vertebrate Ecology and Zoology, Faculty of Biology, University of Gdańsk, ul. Wita Stwosza 59, 80-308 Gdańsk, Poland.*

Recently much attention has been given to determinants of bat distribution and abundance in urban environments, where several, more plastic species, successfully thrive, usually benefiting from a overabundance of roosts, but suffering from low availability of foraging habitats. The majority of habitat studies on bats, including those conducted in cities, are based on recordings of foraging and commuting individuals and focus on the nursing period, when energy demands of breeding females are the highest. Studies that analyse habitat preferences of displaying bat males during mating period are extremely scarce, although the phenomenon of establishing territories and emission of advertisement calls is widespread among European bat species, including the genus *Pipistrellus*, one of the most successful vespertilionid taxa in human-affected landscapes. To fill that gap, we analysed distribution of mating sites of three *Pipistrellus* species in Sopot, a small resort city in northern Poland, located on the coast of the Baltic Sea. Locations where bats emitted their species-specific advertisement calls were mapped, using broadband ultrasound detectors and GPS. Among 228 locations, 158 were occupied by *P. pipistrellus*, 47 by *P. pygmaeus* and 23 by *P. nathusii*. *P. pipistrellus* strongly selected low- and high-density built-up areas with high trees, while avoided forests, woodlands and built-up areas without trees. The remaining two species did not reveal any significant selection or avoidance, probably due to low sample size. However, *P. pygmaeus* was found significantly closer to forests and woodlands than *P. pipistrellus*, *P. nathusii* and random points, while *P. pipistrellus* occurred significantly closer to built-up areas. The results reveal new aspects of fine-scale niche partitioning between sympatric, morphologically similar species of the genus *Pipistrellus*.

ROADS AND BATS: ARE OVERPASSES ATTRACTIVE FOR BATS? [O*]

FABIEN CLAIREAU[1,2,3]**, YVES BAS[1], SÉBASTIEN J. PUECHMAILLE[2], BENJAMIN ALLEGRINI[3], NATHALIE MACHON[1], CHRISTIAN KERBIRIOU[1],
**fabien.claireau@mnhn.fr
[1]*National Museum of Natural History of Paris, 55 rue Buffon, Center for Ecology and Conservation Sciences, UMR 7204 MNHN-CNRS-UPMC, 75 005 Paris, France;*
[2]*Greifswald University, Zoology Institute and Museum, Johann Sebastian Bach-Str. 11/12, D – 17 487 Greifswald, Germany;*
[3]*Naturalia Environnement, 20 rue Lawrence Durrell, BP 31 285, 84 911 Avignon, France.*

In addition to animal mortality, roads have an important impact on habitat loss and fragmentation. In the case of bats, fragmentation could lead to loss of connectivity between colonies (i.e. potential decrease in gene flow) or between roosts and foraging areas (i.e. potential impact on breeding success). However, highways are strong economic drivers, new ones are created and others are modernized. Therefore, it is necessary for stakeholders to be able to reconcile economic development and biodiversity conservation. Several studies suggest that underground passages may restore ecological connectivity for some bats. But in some situations, technical constraints only allow the installation of crossings over the highway. Depending on the characteristics of these sites, it is sometimes possible to adapt the designs of overpasses (e.g. the material) to increase their use by bats. In France, only 5 overpasses have been specifically designed for bats; three of them were monitored in 2016. Their designs are different: U-shaped metal structure or rope with polystyrene balls. With the aim of assessing their efficiency and to define the landscape characteristics that favour bat road crossings, we placed 12 paired acoustic recorders per overpass during 4 nights on both sides of the highway. To quantify bat road crossings we built bat trajectories from acoustic recorders data. We recorded a total of 102,432 bat passes involving 17 species, and we detected, for 7 of them, 284 bat trajectories suggesting road crossings. Overpasses represented 25-56% of the total of bat road crossings. These first results suggested that overpasses could be attractive for bat road crossings, when sited at ecological continuities. We assume that bats are able to detect the structures which help them to cross the road safely. Thus, overpasses could be a solution against fragmentation but their efficiency seems species-dependent and strongly influenced by their location in the landscape, and on their design.

INSECTIVOROUS BATS IN AGROECOSYSTEMS: FROM ECOSYSTEM SERVICES TO AN INTEGRATED PEST MANAGEMENT APPROACH [P*]

YUVAL COHEN[1]**, SHIRLI BAR-DAVID[1], CARMI KORINE[1], **uvicohen@gmail.com
[1]*The Mitrani Department of Desert Ecology, The Jacob Blaustein Institutes for Desert Research, Ben-Gurion University of the Negev, Sede Boqer Campus, Israel.*

Arthropod pests are responsible for substantial yield-loss in various agricultural industries; consumption by natural enemies can provide a means to suppress pest populations and their damage. Predation of pests by natural enemies can be quantified in measurable economic terms, often referred to as ecosystem services. Bats are repeatedly cited to provide ecosystem service of this nature; in recent times, the scope of their contribution is finally beginning to be unraveled. Few studies have succeeded in taking this potential a step further by actively enhancing the contribution of bats to pest suppression or integrating them into pest management schemes (IPM). Here we propose a theoretical workflow to guide the integration of bats in pest management through the following steps: (1) we start from identifying trophic interactions between bat-pest species, by measuring temporal and spatial activity patterns of bats and pests to determine if synchronous patterns occur, (2) we check for indirect and direct evidence of predation, and (3) we estimate the contribution of bats to reduce damage to yields; (4) we attempt to enhance these contributions via adjustments in agricultural management practices or in the agroecosystem (i.e., installing artificial roosts or providing a drinking source), and finally (5) we evaluate whether such adjustments enhance ecosystem services and how they affect biodiversity in the agroecosystem. We discuss the importance of guidance and funding to farmers, as their commitment to an IPM approach is crucial. We advocate continuous monitoring with a long-term adaptive management approach to maximize the project success and to avoid harmful ecological consequences. We believe that an effective IPM project can support conservation efforts to protect bats, while increasing the benefits farmers obtain from pest suppression.

INSULAR BATS AND RESEARCH EFFORTS: A REVIEW OF GLOBAL PATTERNS AND PRIORITIES [O]

IRENE CONENNA[1]**, RICHARDO ROCHA[1,2,3], DANILO RUSSO[4 5], MAR CABEZA[1],
**irene.conenna@gmail.com
[1]*Metapopulation Research Centre, Faculty of Biosciences, University of Helsinki, Helsinki, Finland;*
[2]*Centre for Ecology, Evolution and Environmental Changes, Faculty of Sciences, University of Lisbon, Lisbon, Portugal;*
[3]*Faculty of Life Sciences, University of Madeira, Funchal, Portugal;*
[4]*Wildlife Research Unit, Laboratorio di Ecologia Applicata, Dipartimento di Agraria, Università degli Studi di Napoli Federico II, Napoli, Italy;*
[5]*School of Biological Sciences, University of Bristol, Bristol, U.K.*

Evidence-based knowledge is critical for the delineation and success of conservation interventions. However, despite limited research resources, research efforts frequently fail to target conservation priorities. Island endemic bats (IEBs) are a poorly studied group inhabiting some of the world's most vulnerable habitats, and for which no review of research allocation has ever been conducted. We conducted a bibliometric review to evaluate the global research patterns for IEBs with respect to individual species, geographical distribution and IUCN Red List categories. We also studied the relationship between research effort and changes in Red List category, and identified species-based and area-based priorities for future research. IEBs are significantly more threatened than non-IEBs. However, research focusing on IEBs is scarce, centred on species of lesser conservation concern, and spatially asymmetric. Conservation-oriented research seems to target species facing high extinction risk, but is extremely thinly and unevenly distributed. Although we found a positive association between research effort and improvement in Red List category, an increase in extinction risk did not trigger more attention. Prioritisation highlighted, as the top five islands for species richness in the least-studied and highest conservation concern IEBs: Sulawesi, Timor, New Guinea, Java and Borneo. The ten species of highest research priority include threatened and Data Deficient species from Southeast Asian and Pacific islands. Conservation-oriented research seems to be too scarce to satisfy conservation needs. The observed mismatch between research allocation and conservation priorities may indicate that highly endangered species are unattractive targets for fund-raising, due to species crypticity and high risk of project failure. Our findings support the importance of research for the conservation of IEBs, and we advocate that more attention is directed towards the least-known species.

GENETIC VARIABILITY OF *RHINOLOPHUS MEHELYI* AT THE NORTHERN LIMIT OF ITS DISTRIBUTION RANGE [O*]

ALEXANDRA CORDUNEANU[1]**, CHRISTIAN DIETZ[2], LEVENTE BARTI[3], SZILÁRD-LEHEL BÜCS[4, 5], ISTVÁN CSŐSZ[5], ENDRE JAKAB[6, 7], RÉKA JAKAB[6], CSABA JÉRE[5], BEA KELEMEN[8], **alexandra.corduneanu@usamvcluj.ro
[1]*Department of Parasitology and Parasitic Diseases, University of Agricultural Sciences and Veterinary Medicine of Cluj-Napoca, Romania;*
[2]*Biologische Gutachten Dietz, Balinger Straße 15, D-72401 Haigerloch, Germany;*
[3]*Romanian Bat Protection Association- Central Branch, Odorheiu Secuiesc, Romania;*
[4]*Nature of Transylvania Association, Cluj-Napoca, Romania;*
Romanian Bat Protection Association, Satu-Mare, Romania;
[6]*Molecular Biology Center, Institute of Interdisciplinary Research in Bio-Nano-Sciences, Babeș-Bolyai University, Cluj-Napoca, Romania;*
[7]*Hungarian Department of Biology and Ecology, Faculty of Biology and Geology, Babeș-Bolyai University, Cluj-Napoca, Romania.;*
[8]*Faculty of Biology and Geology, Babeș-Bolyai University, Cluj-Napoca, Romania.*

Rhinolophus mehelyi is a medium-sized horseshoe bat, with a primarily Mediterranean distribution and vulnerable status all over Europe. The species has a highly fragmented range in Europe, with large declines noted in the 20th Century. In Romania the species was known to occur in SE Romania, Central Dobrogea (Gura Dobrogei and Limanu caves), but local populations, being affected by agriculture and intense habitat modifications, currently number around 150 bats in the Limanu cave. However, in the period of 2014-2016 the constant presence of *R. mehelyi* was demonstrated also in the Banat region, SW Romania, extending the northern distribution of the species in Europe. In order to assess the genetic diversity, we collected 20 skin biopsy punches from each of three populations lying at gradually increasing (55, 83, 188 km) distances from the core population. Two mitochondrial markers, the second hyper variable (HVII) domain of the mitochondrial D-loop region and the 12S region, as well as the nuclear recombination activating gene II (RAG2) are amplified by PCR. We calculate haplotype diversity (h), nucleotide diversity (π) for all samples, as well as the number of polymorphic sites (S), and average number of pairwise differences (k). Our intention is to evaluate the genetic variability of known Romanian *R. mehelyi* populations, and to compare it to a large core population from Bulgaria (Muselievo, Tscherven). Our intention is to test whether these two populations constitute remnants of a former more widely distributed (but unknown) population, or these are new colonisation events of an expanding population. Our main hypothesis is that populations which are the results of a recent colonisation event will have overlapping, but greatly reduced haplotype spectra, while old remnants should retain similar haplotype diversity in comparison to individuals belonging to the core population.

TOWARDS THE CLARIFICATION OF THE PHYLOGENY, TAXONOMY AND DISTRIBUTION OF SOUTH-EAST ASIAN *HYPSUGO* [P]

GÁBOR CSORBA[1]**, VUONG TAN TU[2], NEIL M. FUREY[3], SERGEI V. KRUSKOP[4], LEE-SIM LEE[5], TÁMAS GÖRFÖL[1], **csorba.gabor@nhmus.hu
[1]*Department of Zoology, Hungarian Natural History Museum, Budapest, Hungary;*
[2]*Institute of Ecology and Biological Resources, Vietnam Academy of Science and Technology, Hanoi, Vietnam;*
[3]*Fauna & Flora International, Cambodia Programme, Phnom Penh, Cambodia;*
[4]*Zoological Museum, Moscow State University, Moscow, Russia;*
[5]*School of Distance Education, University Sains Malaysia, Penang, Malaysia.*

Although species of *Hypsugo* were often included in *Pipistrellus* by many authors in the past, external, dental and bacular investigations as well as phylogenetic reconstructions proved that they form separate genera. The majority of the 10 South-east Asian species of *Hypsugo* are rare bats, known only from a handful of specimens and their evolutionary relationships, distribution, ecology and conservation status are largely unknown. In 2014, a new species was described by our research group based on specimens from Lao PDR and Vietnam. After careful re-examination of museum holdings and recently collected material, the species is now confirmed from further SE Asian countries. The new data revealed that it may be a cave-dweller, which sheds light on the importance of these underground habitats. *Hypsugo macrotis*, a species from the Sundaland Biogeographical Region was known only from a few specimens. In consequence, nearly nothing was known on its roosting habits and phylogenetic relationships. A house-dwelling colony was found in Peninsular Malaysia in 2013, which confirmed the importance of anthropogenic habitats for bats. The newly obtained barcoding gene sequence can help the identification of further specimens and also suggests that the species belongs to the "cadornae-group". Recent morphological investigations proved that specimens from the Indian Subcontinent identified previously as *Philetor brachypterus*, in fact belong to *Hypsugo joffrei*, which was originally described in the genus *Nyctalus*. In a Vietnamese expedition carried out in 2016, several individuals of the species were caught and a few voucher specimens were taken for further analysis. The new morphological and genetic data suggest that *H. joffrei* has close evolutionary relationship with *Philetor* and *Tylonycteris*.

SEASONAL ACTIVITY OF MOUSE-TAILED BATS (GENUS *RHINOPOMA*) IN THE NORTH-WESTERN EDGE OF SAHARA [P]

RIDHA DALHOUMI[1], HIBAT-ELLAH LOUMASSINE[2], BENJAMIN ALLEGRINI[3], FARID BOUNACEUR [2], STÉPHANE AULAGNIER[4]**, **stephane.aulagnier@inra.fr
[1]*Laboratoire de Biosurveillance de l'Environnement, Faculté des sciences de Bizerte, 7021 Zarzouna, Tunisia;*
[2]*d'Agro-Biotechnologie et Nutrition en Zones Semi-Arides, Université Ibn Khaldoun, Tiaret, Algeria;*
[3]*Naturalia, Green Park, Bâtiment C. 149 avenue du Golf. 34670 Baillargues, France;*
[4]*Comportement & Ecologie de la Faune Sauvage, Université de Toulouse, I.N.R.A., CS 52627, 31326 Castanet Tolosan cedex, France.*

Of the 12 bat species ranging within the Saharan desert boundaries, mouse-tailed bats may aceept harsh conditions of temperature (very hot on summer days, cold on winter nights), low hygrometry inducing water evaporation loss, reduced water and food availability. They roost in caves, mines, boulders, rock crevices, underground irrigation tunnels, wells, and sometimes inhabited or ruined buildings. The lesser mouse-tailed bat (*Rhinopoma cystops*) is widely distributed over the Sahara and its edges, and the greater mouse-tailed bat (*R. microphyllum*) has only been recorded in Morocco and western Algeria. While *R. cystops* was active throughout the year on the southern side of the Atlas Mountains at 32°N, it was not recorded in winter in an arid area of Tunisia at 34°N, where an acoustic study was completed in several habitats. Though ranging over the desert, the species was mainly recorded at water bodies, even when water was scarce. In Algeria, *R. microphyllum* was also found in sympatry close to water bodies, the seasonal activity being under study together with small-scale habitat use. Diet of these two species should be investigated further in the area, and conservation undertaken to protect their main roosts.

STRUCTURE CHARACTERISTICS, TEMPERATURE REGIMES AND ROOST SITE SELECTION IN HIBERNATING BATS [O]

LUC DE BRUYN[1,2]**, RALF GYSELINGS[1], LIES TEUNEN[2], MARK HEUS[2],
**luc.debruyn@inbo.be
[1]*Research Institute for Nature and Forest (INBO), Brussels, Belgium;*
[2]*Evolutionary Ecology, Department of Biology, University of Antwerp, Antwerp, Belgium.*

Temperature is an important factor determining the suitability of a structure to serve as a hibernation site for bats in temperate regions. In western Europe many bats hibernate in artificial structures. Conservation managers try to adapt such structures to optimise the wintering conditions for bats. The intended goals, however, are not always reached. In Flanders, Belgium, a large part of the bat population hibernates in the fortresses around Antwerp. In these forts, several actions, such as the closure of rooms in the fort or the addition of extra artificial roost features were carried out. In the present study we assessed how room structure, localization of the room within the fortress, and management actions influence the temperature regimes and how this influences roost site selection of the bat species. We deployed temperature loggers, active for several winter months, to analyse how room characteristics influence temperature fluctuations. In addition, we assessed how different types of artificial roost sites might further improve hibernation conditions. The exposure of a room to the outside (e.g. open wall, window, sealed window) largely determines the temperature regimes. Temperature is more buffered in less exposed rooms. The most abundant species in the forts were *Myotis daubentonii*, *M. mystacinus/brandtii*, *M. emarginatus* and *M. nattereri*. Cold-sensitive species (e.g. *M. emarginatus*) were only found in the best temperature-buffered rooms. Species that hibernate in crevices were found over a much broader range of (room) temperatures. For the latter, the suitability of a chamber is significantly determined by the number of possible roost sites.

DETERMINANTS OF SPRING MIGRATION ONSET IN FEMALE NOCTULE BATS [O]

DINA K.N. DECHMANN[1,2]**, MARTIN WIKELSKI[1,2], DIEGO ELLI-SOTO[1,2], M. TEAGUE O'MARA[1,2], **ddechmann@orn.mpg.de
[1]*Max Planck Institute for Ornithology, Germany;*
[2]*University of Konstanz, Germany.*

In contrast to bird migration, bat migration is rare, but no less intriguing. In an effort to learn more about the remarkable female-biased migration of European bats we have studied the onset of migration of the noctule (*Nyctalus noctula*) for several years in Southern Germany. We find profound differences to bird migration. Females rapidly gain weight in spring, but comparison with the sedentary males shows this is not a behaviour restricted to preparation for migration onset in the females. A comparative model including data from several years shows that the day of the year is the best predictor of migratory onset, with a weak influence of an increase in atmospheric pressure. There was no influence of other environmental variables, such as mean daily temperature, wind speed, or wind direction, that typically modulate migration onset triggers in birds. Migration followed a regular evening foraging session, was uniform in Northeastern direction independent of wind, and appears to be performed in relatively short bouts of up to 100km followed by a stop-over. We postulate that at least at our study site females have no problem in gaining weight quickly after waking up from hibernation. Rapid departure for migration is determined by the highly constrained life cycle of noctule bats, making Julian date the main determinant of migration onset.

TESTING THE PERFOMANCE OF BATS AS INDICATORS OF HABITAT QUALITY IN RIPARIAN ECOSYSTEMS [O*]

CARMELINA DE CONNO[1]**, VALENTINA NARDONE[1], MARCO GUIDA[2], SALVATORE DE BONIS[3], INÊS JORGE[4], UGO SCARPA[1], DANILO RUSSO[1,5],
**deconnoca@gmail.com
[1]Wildlife Research Unit, Dipartimento di Agraria, Università degli Studi di Napoli Federico II, Portici (NA), Italy;
[2]Dipartimento di Biologia Strutturale e Funzionale, Università degli Studi di Napoli Federico II, Napoli, Italy;
[3]ARPA Lazio sezione di Frosinone, Unità risorse idriche, Frosinone, Italy;
[4]University of Porto, Portugal;
[5]School of Biological Sciences, Life Sciences Building, University of Bristol, Bristol, U.K.

Bats are geographically widespread, with over 1300 species covering several ecological niches and providing crucial ecosystem services. Bats have a stable taxonomy and are also highly sensitive to human-driven environmental alteration, so they have all the potential characteristics of a good bioindicator. However, few studies have tested bat bioindicator performances in main ecosystem types, such as farmland, forests or rivers. The aim of this study was to test the performance of bats as bioindicators in river ecosystems. We surveyed bats acoustically at ten rivers in peninsular Italy, using automatically triggered bat detectors, to measure species composition and activity. At each of the sites where we surveyed bats, we also determined water quality independently by using the multimetric STAR_ICM index, the official biological index adopted in the country based on macrobenthic community. Finally, we calculated the Fluvial Functionality Index (IFF), which considers biotic and abiotic factors for a comprehensive assessment of riparian ecosystem functionality. Species richness increased at higher altitudes, but did not respond to environmental quality. However, caution is needed in interpreting these results because the assessment of species richness was inevitably constrained by limitations to species identification posed by the acoustic method. Although no species proved to be exclusive to a particular quality level, we found a clear increase in bat activity at sites where a poorer environmental quality was measured. Generally speaking, responses shown by bat species broadcasting FM-CF echolocation calls were more informative. Our study constitutes a first significant step towards the development of a robust bioacoustic index of riparian habitat quality based on the assessment of activity of the entire foraging bat community or of selected phonic type groups.

PIPISTRELLUS NATHUSII ACTIVITY, ADVERTISEMENT CALLS, AND BAT BOX OCCUPANCY AT THE IJSSELMEER-COAST, THE NETHERLANDS [P]

JASJA J.A. DEKKER[1]**, BOB JONGE POERINK[2], **jasjad@gmail.com
[1]*Jasja Dekker Dierecologie, Arnhem, The Netherlands;.*
[2]*The Fieldwork Company, Groningen, The Netherlands.*

It is often hypothesised that occupancy of bat boxes is a measure of presence of bats in an area. This would be especially useful for tracking migration waves of *Pipistrellus nathusii*, a bat migrating from the Baltics and beyond to the west of Europe. However, autumn migration coincides with the mating period, and bat boxes are used as mating roosts. So, an increase in bat box occupancy might be caused by more bats present, or by use as a mating roost. We test this hypothesis at different sites well-used for migration: the coast of the Noordoostpolder, at the IJsselmeer, the Netherlands, and the Afsluitdijk, a 32 kilometers long dyke separating the Wadden Sea-North sea and the IJsselmeer. Using a combination of bat box monitoring and activity from full season acoustic monitoring as a proxy for bat density, we show that occupancy of boxes is an indicator of higher density of *Pipistrellus nathusii*.

DIVERSITY AND CONSERVATION OF CAVE-DWELLING BATS IN THE BRUNCA REGION OF COSTA RICA [P*]

STANIMIRA DELEVA[1]**, GUSTAVO QUESADA[2], CARLOS GOICOECHEA[2], ANGEL IVANOV[3], GLORIANA CHAVERRI[4], **stanimira.deleva@gmail.com
[1]*University of Costa Rica, San José, Costa Rica;*
[2]*Grupo Espeleológico Anthros (GEA), San José, Costa Rica;*
[3]*Faculty of Computer Science and Engineering, Burgas Free University, Burgas, Bulgaria;*
[4]*University of Costa Rica, Recinto de Golfito, Golfito, Costa Rica.*

The southwestern Brunca region of Costa Rica incorporates a huge diversity of habitats and organisms, including the last preserved lowland rainforests on the Pacific coast of Central America. The Brunca region also contains the largest number of caves in Costa Rica (156), including the longest and the deepest ones in the country. While many of the bat species which inhabit this region are known to use caves for roosting, there is no base information about the bats roosting in the caves of this area. We present the first study to assess the diversity of the cave-dwelling bat species in the Brunca region of Costa Rica in a large number of caves. Between December 2015 and March 2017, we explored 40 underground roosts in the Brunca region of Costa Rica – 37 natural caves and 3 artificial tunnels. We collected data about the bat species diversity and their abundance by direct observation and capturing bats using hand nets inside the roosts. We observed 17 species of bats from the families Phillostomidae (*Artibeus jamaicensis*, *Artibeus lituratus*, *Carollia perspicillata*, *Carollia sowelli*, *Desmodus rotundus*, *Glossophaga soricina*, *Lonchophylla concava*, *Lonchophylla robusta*, *Lonchorhina aurita*, *Phyllostomus discolor* and *Phyllostomus hastatus*), Emballonuridae (*Peropteryx kappleri*, *Peropteryx macrotis* and *Saccopteryx bilineata*), Natalidae (*Natalus mexicanus*) and Mormoopidae (*Pteronotus davyi* and *Pteronotus parnellii*). The most widespread (N=21 roosts) and abundant (c.a., 3930 individuals observed) bat species was *Carollia perspicillata*. To access the potential threats which bats might be exposed to in their roosts, and to help in further conservation actions, we collected information about the human activities carried out in and around the roosts. We observed the potential threats in the caves, whichinclude unregulated visiting, littering and blocking of the entrances.

BATS OF VALSAÍN FOREST (SEGOVIA, SPAIN): HIGH SPECIES RICHNESS AND ACTIVITY USE [P]

ÓSCAR DE PAZ[1], ROBERTO DE LA PEÑA[2], M SOLEDAD REDONDO[3], ELENA TENA[4]**, **etenalopez@gmail.com
[1]Life Sciences Department, Faculty of Biology, Chemistry and Environmental Sciences, University of Alcalá (UAH), Alcalá de Henares, Madrid, Spain;
[2]Treinta y ocho Street, 5, El Escorial, Madrid, Spain;
[3]Centro Montes y Aserradero de Valsaín, National Parks Autonomous Agency (OAPN), Valsaín, Segovia, Spain;
[4]Department of Zoology and Physical Anthropology, Faculty of Biological Science, Complutense University of Madrid (UCM), Madrid, Spain.

From June to September 2016, we carried out a bat community study of Valsaín Forest (La Granja de San Ildefonso, Segovia). National Parks Autonomous Agency manages this forest area of 10,668 hectares, which is located on the northern slope of the Guadarrama Mountains, between 1,100 and 2,130 m asl. In addition, a hydrographic network composed of three main rivers passes through. These provide the presence of water reserves and artificial pools created for firefighting. Valsaín Forest is covered mainly by Scots pine (*Pinus sylvestris*) but also others species such as oak (*Quercus pyrenaica*), holm oak (*Quercus ilex* ssp. *ballota*), montane broom (*Cytisus purgans*), pastures and riparian forest. Three methodologies were used to register all the bat species of the forest community. Eighteen bat species were trapped using mist nets and harp traps, 16 of them with evidence of reproduction; 15 species or acoustic groups were identified using bat detectors and 3 species were found in roost survey. The results for Valsaín forest were 22 species, 71% of the bat species currently known in the Iberian Peninsula, some of them considered as rare or especially threatened. The interpolation of the sampling points for species richness and bat activity to the whole forest highlights the importance of water availability. The river system and the artificial ponds are considered as the hotspots for Chiroptera diversity and activity use in Valsaín Forest community.

NEW DATA ON THE GREATER NOCTULE, *NYCTALUS LASIOPTERUS* (SCHREBER, 1780) IN FRANCE [O]

MARIE-JO DUBOURG-SAVAGE[1,2]**, LIONEL GACHES[1,2], HÉLÈNE DUPUY[1,2], YANNICK BEUCHER[1,2,3], JOËL BEC[1,2], **chirosavage@gmail.com
[1]Coordination Chiroptères Nationale, SFEPM, Toulouse, France;
[2]Groupe Chiroptères de Midi-Pyrénées, Conservatoire d'Espaces Naturels de Midi-Pyrénées, Toulouse, France;
[3]EXEN, Vimenet, France.

Up until 2005 the presence in France of the greater noctule was only documented by a few dead individuals (the most recent ones under wind turbines), some occasional captures of males, and an increasing number of ultrasonic recordings in the southern half of France. This presentation relates the discovery of the first nurseries in the Massif Central area from 2012 onwards and the first results on the species ecology and behaviour obtained by radiotracking, roost monitoring, as well as by ultrasound and video recordings. Two different areas have been studied, but here we will focus mainly on the most southern one on the Levezou plateau (Aveyron Departement), with its minimum population of 159 individuals on 27 June 2016 and 243 on 13 August when young were flying. We will present data on the species' habitat and roosts, the threats it is facing, the discovery of other subpopulations in the Massif Central and discuss about its putative migration status and how to improve its conservation.

THE CURIOUS PHYLOGENETIC PATTERN OF *MYOTIS MYSTACINUS* AND *MYOTIS DAVIDII* IN THE BALKAN PENINSULA [P*]

HELIANA DUNDAROVA[1]**, CHRISTIAN DIETZ[2], SUREN V. GAZARYAN[3], EMRAH ÇORAMAN[4], FRIEDER MAYER[4, 5], **h.vulgaris@gmail.com
[1]*Institute of Biodiversity and Ecosystem Research at the Bulgarian Academy of Sciences, Sofia, Bulgaria;*
[2]*Biologische Gutachten Dietz, Haigerloch, Germany;*
[3]*UNEP/EUROBATS Secretariat, United Nations Campus, Bonn, Germany;*
[4]*Museum für Naturkunde-Leibniz Institute for Evolution and Biodiversity Science, Berlin, Germany;*
[5]*Berlin-Brandenburg Institute of Advanced Biodiversity Research (BBIB), Berlin, Germany.*

The *Myotis mystacinus* species-group is represented by two morphotypes within the Palaearctic region: a larger form described as *M. davidii* in the East and a smaller form, *M. mystacinus*, in the West. We used a novel approach and conducted analysis based on both the mitochondrial ND1 and three nuclear introns (ACOX2, ROGDI and ABHD11). Results demonstrate that *M. davidii* and *M. mystacinus* are separate genetic lineages in all sampled regions, except the Balkan Peninsula. All individuals across the Adriatic region and most Bulgarian animals, assigned to *M. davidii* by the nuclear genetic marker and morphology, carried mitochondria of *M. mystacinus*. *M. davidii* individuals from Bulgaria showed reduced level of mitochondrial variation and their haplotypes resembled those of typical *M. mystacinus* from central Europe. Overall, of 56 analyzed animals from Bulgaria only two carried mitochondrial *M. davidii* haplotype which indicate almost complete replacement of their mtDNA by the *M. mystacinus* mtDNA. Ancient allopatric divergence followed by subsequent secondary contact in the Balkan Peninsula might be the cause for the discrepancy between mitochondrial and nuclear genes. Mitochondrial introgression is hence preceded by hybridization events which raises the question about the effectiveness of the reproductive isolation barriers between both lineages.

EFFECTIVENESS OF BAT MITIGATION ON ROADS - A REVIEW [O]

MORTEN ELMEROS[1]**, JULI D. MØLLER[2], JASJA J.A. DEKKER[3], INAZIO GARIN[4], MORTEN CHRISTENSEN[5], HANS J. BAAGØE[6], **elm@bios.au.dk
[1]*Department of Bioscience, Aarhus University, Rønde, Denmark;*
[2]*Julie Dahl Møller Consult, Frøstrup, Denmark;*
[3]*JD Dierecologie, Arnhem, The Netherlands;*
[4]*Department of Zoology and Animal Cell Biology, University of the Basque Country UPV/EHU,*
48940 Leioa, The Basque Country;
[5]*Orbicon, Roskilde, Denmark;*
[6]*Natural History Museum, Copenhagen University, Copenhagen, Denmark.*

Bats may easily cross over roads but they often do so at traffic height, which puts the bats at risk of vehicle collisions. Roads can also impact bat populations by destroying or degrading habitats and by acting as barriers. To comply with legislative obligation to protect bat populations and to prevent significant numbers of incidental mortalities, road developers in most countries must include mitigation strategies for bats when the road networks are expanded or upgraded. A variety of measures has been implemented on roads during the recent decades to reduce or off-set the negative impacts on bats. The measures aim to facilitate safe crossings, e.g. bat gantries, wildlife overpasses and tunnels, or to compensate for habitat destruction, e.g. bat boxes, afforestation. Many studies have described bats' use of the different types of mitigating measures, but only a few systematic robust evaluations of their effectiveness, i.e. the proportion of bats that used the measures to cross the road safely, have been made. Recent studies have documented that bat gantries are ineffective, and screens can be effective for some bat species but they are ineffective for others. Furthermore, only a couple of studies have monitored and assessed the long-term impact of a road scheme and the mitigation strategy at population levels. As a consequence of the limited documentation on the effectiveness at a site-specific level and at the population scale of the currently advised mitigation strategies, conservationist and road developers may recommend and implement measures that are inadequate or inefficient. To elucidate on bat mitigation strategies on roads, we reviewed scientific papers and reports on the studies on the use and effectiveness of the measures. The talk will present a critical evaluation of the effectiveness of different mitigation measures, and outline further research needs to develop effective mitigation strategies for bats.

PHYSIOLOGICAL PLASTICITY OF *CAROLLIA PERSPICILLATA* (SEBA'S SHORT-TAILED BAT) RELATED TO ECOLOGICAL AND SOCIAL ENVIRONMENT [O]

NICOLAS FASEL[1,2]**, MICHEL GENOUD[2], LAURENT MÈNE-SAFFRANÉ[3], KEVIN MACMILLIAN[2], PHILIPPE CHRISTE[2], **fasel.nicolas@gmail.com
[1]*Leibniz Institute for Zoo and Wildlife Research, Berlin, Germany;*
[2]*Department of Ecology and Evolution, University of Lausanne, Lausanne, Switzerland;*
[3]*Department of Biology, University of Fribourg, Chemin du musée 10, Fribourg, Switzerland.*

Physiological plasticity allows species to occupy varying ecosystems, dealing with seasonal fluctuations or adjust to habitat disturbances. In the Neotropics, *Carollia perspicillata* is abundant, widely distributed and can be found from sea level to high elevations. Males of this species also display alternative reproductive tactics with varying expected energetic costs. To prosper in such a wide range of ecological and social conditions, plasticity is expected to occur. Metabolic rates are partly influenced by the lipid composition of organs and essential poly-unsaturated fatty acids (PUFAs) play crucial roles in different physiological functions. Higher concentration of PUFAs can support a higher rate of metabolism and allow stronger physical efforts. It was further shown that higher PUFA concentration reduces resting metabolic rate (RMR) during torpor, leading to lower body mass losses. Frugivorous species rely on diet poor in fat content, and can also use torpor when food availability is reduced. A careful allocation of PUFAs is therefore expected in these species to adjust their metabolic rates to varying environmental conditions. In this study, we analyzed the relation between RMR of male *C. perspicillata* at different temperatures (15-20-25-32°C) and the red blood cells' lipids, markers of the heart fatty acid composition. In order to trigger variations in torpor expression, we further experimentally mimicked a period of low food abundance and provided the bats with diets varying in PUFA compositions. Finally, we investigated whether males adjust their rate of metabolism based on their social status. This study generates information on the physiological plasticity displayed by this frugivorous species. It further helps to understand the wide distribution of *C. perspicillata* and its complex mating system.

PRELIMINARY RESULTS OF BAT RESEARCH IN THE NORTH SORIA PROVINCE (SPAIN) USING A COMBINATION OF TECHNIQUES [P*]

DANIEL FERNÁNDEZ ALONSO[1]**, ** danielfernandezalonso@gmail.com
[1]*Universidad de Alcalá*

This study presents the preliminary results of an inventory of bats in the north of the Soria province (Spain). The study area covers a surface of 300 squared km, and encompasses a variety of forests, including *Fagus sylvatica*, *Quercus pyrenaica*, *Quercus ilex*, *Juniperus thurifera*, *Pinus sylvestris*… as well as cultivated fields. The altitude of the area ranges between 1000 to 2000 m. Deployed methods were surveys by ultrasound detectors and inventory of roosts. Up to now 16 bat species have been detected, including *Barbastella barbastellus*, *Nyctalus lasiopterus*, *Tadarida teniotis*, *Miniopterus schreibersii*. The specific activity and frequency of detection by habitat unit has been also recorded. Complementarily, the frequency of visits of mammal carnivores to some caves in the field area were recorded, specially of *Martes foina*.

COEXISTENCE OF TWO SYMPATRIC CRYPTIC BAT SPECIES OF FRENCH GUIANA: GENETIC, ACOUSTIC AND ECOLOGICAL CHARACTERIZATION [O]

ONDINE FILIPPI-CODACCIONI[1,2]**, MARIE-PAULINE BEUGIN[2,3], ELODIE PORTANIER[3,4,6,7], CÉCILE KAERLE[5], LINA MUSELET[5], GUILLAUME QUENEY[5], ERIC J. PETIT[4], JEAN-BAPTISTE PONS[2], DOMINIQUE PONTIER[2,3], **seise.ofc@gmail.com

[1]SEISE 12 Carrouet, 33190 Barie, France;
[2]Univ Lyon, LabExEcofect, 92 rue Pasteur, 69361 Lyon Cedex 07, France;
[3]Univ Lyon, Université Lyon 1, CNRS, Laboratoire de Biométrie et Biologie Evolutive UMR5558, F-69622 Villeurbanne, France;
[4]ESE (Ecology and ecosystem health), INRA, Agrocampus Ouest, 65 rue de Saint-Brieuc, 35042 Rennes Cedex, France;
[5]ANTAGENE, Animal Genomics Laboratory, 6 allée du Levant; 69890 La Tour de Salvagny (Lyon), France;
[6]Université de Montpellier, 163 rue Auguste Broussonnet, F-34090, Montpellier, France;
[7]Office National de la Chasse et de la Faune Sauvage - Unité Faune de Montagne, 147 Route de Lodève, Les Portes du Soleil F-34990, Juvignac, France;
[8]Université de Lyon, VetAgro Sup - Campus Vétérinaire de Lyon, 1 Avenue Bourgelat, BP 83, F-69280, Marcy l'Etoile, France.

In order to investigate which mechanisms facilitate coexistence of cryptic species, we assessed genetic, acoustic, morphological and ecological divergences between two neotropical bats from the *Pteronotus parnellii* lineage. The distinction between lineages has been made previously according to i) genetics, and especially to ii) morphology and iii) acoustics in order to separate the two species that live in the same caves in French Guiana, but either sample sizes were too low when genetic and acoustic or morphological data were gathered on the same individuals, or genetic and other data were collected on different individuals. This study first aims to combine all approaches in order to validate genetic, morphologic and acoustic divergence between these two distinct species and secondly, to investigate hybridization between the two species as well as ecological and phenological processes that could explain hybridization. For this, thanks to a long-term study undertaken in French Guiana from 2010 to 2015, we used both mitochondrial and nuclear DNA (20 microsatellites), acoustical records and external measurements of 146 to 748 individuals. Our results support previous findings on the existence of two separate species included in *Pteronotus parnellii* in French Guiana, and suggest that caves have a very low impact regarding the genetic structure of their populations. The extreme low rate of hybridization found could be explained by both differences in life cycle phenology between species as well as morphological and acoustical distinction between sexes in one or the other species. Finally, by combining genetics, acoustics, morphology and ecology, we observed significant differences which could correspond to strategies of co-occurrence.

MODELLING ROOST DISPERSAL OF GREATER HORSESHOE BATS USING LANDSCAPE CONNECTIVITY MODELS [O*]

DOMHNALL FINCH[1,2]**, DIANA P. CORBACHO[3], HENRY SCHOFIELD[2], RICHARD BROUGHTON[4], FIONA MATHEWS[1], **d.finch@exeter.ac.uk
[1]*Biosciences, College of Life & Environmental Sciences, University of Exeter, Exeter, U.K.;*
[2]*The Vincent Wildlife Trust, The Post House, Ham Lane, Powick, Worcestershire,U.K.;*
[3]*Morcegos de Galicia, Drosera, P. do Magdalena, G-2, 2º izquierda 15320 As Pontes, A Coruña, Spain;*
[4]*Centre for Ecology & Hydrology, Maclean Building, Benson Lane, Crowmarsh Gifford, Wallingford, Oxfordshire, U.K.*

Greater horseshoe bat (GHS; *Rhinolophus ferrumequinum*) populations have undergone a dramatic decline during the last century in North-west Europe. This has mainly been attributed to land-use change, which is likely to vary at a local scale. In the face of heightened pressure for new infrastructure, the identification of wildlife 'pinch-points' in landscapes, where such developments are most likely to cause significant negative impacts, is essential. These alterations can lead to a loss of landscape permeability, reducing connectivity between both foraging grounds and meta-populations. The dispersal of GHS in the landscape was modeled spatially, using a connectivity-based approach founded on random walk and graph theories. First, expert opinion was used to rank and score the importance of five landscape features considered likely to influence GHS movements. These scores were used to generate resistance maps, which a program called Circuitscape then used to predict the functional connectivity of the landscape, based on likely GHS movement. The predictions were ground-validated using occurrence data, which were collected using 226 SM2 bat detectors over 1000+ nights of survey effort within 3km roost substance zones. All landscape features from one roost location were assessed as univariate models by varying the expert opinion resistance score until best-fit models were identified; these were then combined into a single multivariate model and assessed again. The predictions of the final best-fit multivariate model based on this single roost were tested against an additional three GHS roost locations to further validate the model. The results confirm that spatially accurate predictions of bat movement can be made. These predictions highlight areas of key importance for bats, 'pinch points', which are critical for their dispersal into the wider landscape. The resultant maps can also be used by planners and decision-makers to inform species management plans and policy.

INVESTIGATING THE ROLE OF ENVIRONMENTAL RESERVOIRS IN THE PERSISTENCE AND TRANSMISSION OF *PSEUDOGYMNOASCUS DESTRUCTANS*, THE CAUSATIVE AGENT OF WHITE-NOSE DISEASE [O*]

NICOLA M. FISCHER[1]**, ANDREA ALTEWISCHER[1],
SÉBASTIEN J. PUECHMAILLE[1], **Fischer.Nicola@yahoo.com
[1]*Zoological Institute and Museum, Ernst-Moritz-Arndt University Greifswald, Greifswald, Germany.*

Hibernation decreases metabolic rate and body temperature, resulting in a severe reduction of the thermal barrier for protection against infection with many fungi. Among them, *Pseudogymnoascus (Geomyces) destructans* (Pd), the causative agent of White-Nose Disease, is unable to grow at temperatures above 20°C and hence only grows on bats during the hibernation period. The particular life cycle of temperate bats in which 5-6 months is spent in hibernation followed by a 6-7-month active period allows them to clear infection. As the bats clear infection after the hibernation period, it remains unclear how they get infected each year and whether transmission rate is exacerbated by inter-individual contacts. To answer these questions, we isolated >600 Pd isolates from bats during hibernation as well as from the environment before and after hibernation over four years and investigated patterns of genetic diversity and distribution. Pd was genotyped at 18 variable microsatellite loci making it possible (via multi-locus genotypes) to follow each fungal individual as it infects bats in different parts of the hibernaculum and over time. The spatio-temporal distribution of Pd individuals shows a clear pattern of infection from the hibernaculum with bat-to-bat infections only playing a minor role. The frequency of each Pd individual on bats is strongly correlated to its frequency in the environment prior to infection. We also demonstrated the survival of spores from April to October on the walls of hibernacula even in the absence of bats. These results show that the environment acts as a passive reservoir allowing yearly re-infection of bats as they enter the hibernacula. The critical role of the environment needs to be considered when planning the management of White-Nose Disease. Once the fungus has been found at a site it will not be eradicated by the absence of bats alone, but needs to be actively removed from the environment to prevent re-infection of bats the next year.

CATALONIA: THE IMPORTANCE OF A GOOD AWARENESS CAMPAIGN TO PROTECT BATS [P]

CARLES FLAQUER[1]**, XAVIER PUIG-MONTSERRAT[1,3], ADRIÀ LÓPEZ-BAUCELLS[1,2,3], MARIA MAS[1], SALVADOR VINYES[1], ANTONI ARRIZABALAGA[1], **carlesflaquer@gmail.com
[1]Natural Sciences Museum of Granollers, Catalonia), Spain;
[2]Centre for Ecology, Evolution and Environmental Changes, University of Lisbon, Portugal;
[3]Galanthus Association (Catalonia), Spain.

At the end of the 20th century, bats in Catalonia (a European country with 7 million inhabitants) were almost totally unknown. None of the Catalan Natural Parks had listed its bat species and there was no indexed paper published about bats in Catalonia. Bats were also ignored in the media. In 2000 we created the Bat Research Department in the Granollers Museum of Natural Sciences. Between 2000 and 2016 the department carried out more than 300 projects that gave, approximately, 500 impacts in the media. Between 2003 and 2016 we carried out 170 Bat Nights in 50 locations. We also published the guide "Bats of Catalonia"; organized the International Symposium on the Importance of Bats as Bioindicators; created an exhibition on bats; produced the international documentary Humans and Bats; conceived a wine dedicated to bats, and also low cost bat detectors (Battune). It is difficult to assess the impact of our campaign to preserve bats in our country, but some numbers are revealing. Now there is no Catalan natural park (n = 18) without bat surveys; some Catalan TV programs, related to bats, had audiences of one million people (15% share). Approximately 18,000 people attended the Catalonian Bat Nights. The first edition of the guide dedicated to Catalan bats was sold out in 2 years (1,500 books); more than 4,000 bottles of the wine dedicated to conserving bats were sold and the wine is sold out, despite being a white wine that costs 15€ per bottle. No less than 300 bat detectors have been sold and more than 35,000 people have visited our bat exhibition in the last three years. Finally, thanks to our research team, 11 papers about Catalonian bats have been published in indexed journals during the last years. One thing is clear; we have changed something when politicians, farmers and families are voicing support for the conservation of our 30 bat species!

RE-ASSESSING THE POTENTIAL BENEFITS OF HEDGEROWS ON BATS – A MULTI-SCALE APPROACH [O*]

JÉRÉMY S.P. FROIDEVAUX[1]**, KATHERINE L. BOUGHEY[2], GARETH JONES[1],
***jeremy.froidevaux@bristol.ac.uk*
[1]School of Biological Sciences, University of Bristol, Life Sciences Building, 24 Tyndall Avenue, Bristol BS8 1TQ, U.K.;
[2]Bat Conservation Trust, Quadrant House, 250 Kennington Lane, London SE11 5RD, U.K.

Hedgerows have been identified as a key landscape feature for insectivorous bats in farmland-dominated landscapes. Bats use hedgerows for both commuting (as acoustic landmarks) and foraging (exploiting food abundance) purposes. Despite the extensive literature on the topic, the potential benefits of hedgerows on bat colony size are less well understood and evidence-based information on their management is crucially lacking. Using the greater horseshoe bat (*Rhinolophus ferrumequinum*) as a case study, we firstly investigated at different spatial scales the role of different landscape features alongside the density of hedgerows to explain maternity colony size in Great Britain. We used summer roost count data from the UK National Bat Monitoring Programme spanning a 10-year period from 2005 to 2014. Then, we assessed at the farm scale the effects of different hedgerow management (trimming regime) on the bat assemblage. We acoustically sampled 64 hedgerows in 20 farms located in South West England during the summer 2016. Our results indicated that maternity colony size of *R. ferrumequinum* was positively related to density of hedgerows at different spatial scales, thus suggesting various benefits of hedgerows for this species. At the farm scale, the potential benefits of different hedgerow management on bats were species-specific and depended on the landscape context. We discuss the implications of these results for the designation of adequate agri-environment schemes to favour bats in agricultural landscapes.

ASSESSING THE POTENTIAL BENEFITS OF ORGANIC FARMING ON BATS AND ARACHNIDS IN MEDITERRANEAN VINEYARDS [P*]

JÉRÉMY S.P. FROIDEVAUX[1]**, BASTIEN LOUBOUTIN[2], GARETH JONES[1],
**jeremy.froidevaux@bristol.ac.uk
[1]School of Biological Sciences, University of Bristol, Life Sciences Building, 24 Tyndall Avenue, Bristol BS8 1TQ, U.K.;
[2]Office pour les insectes et leur environnement (Opie), Antenne Languedoc-Roussillon, 755 avenue du Campus Agropolis, 34 988 Montferrier-sur-Lez, France.

Over the past 60 years, agricultural expansion and intensification have led to a dramatic loss of biodiversity and associated ecosystem services throughout Europe. Organic farming has been proposed as a key agri-environment scheme to counteract the negative impact of agricultural intensification on biodiversity. The high expenditure invested in this conservation programme has led to a rapidly growing number of studies evaluating its effectiveness. However, most of these studies have focused on birds, plants and insects in temperate crops and grasslands which may have led to species- and area-biased conclusions. In this study, we aimed to investigate the effects of organic farming on biodiversity in Mediterranean vineyards. We focused our case study on bats and arachnids given that (i) they are both situated in high tropic level and play an important role in pest suppression in farmland; (ii) they are considered as bioindicators of ecological changes; and (iii) they have different functional traits (in terms of mobility, dispersal ability and home range size) which we hypothesized determine how they respond to organic farming. The experiment was undertaken in the south of France during the summer 2015 at 21 paired sites, involving matched conventional and organic vineyards. We recorded echolocation calls of bats using a passive acoustic method while ground surface arachnids were surveyed using pitfall traps. Our results demonstrate taxon-specific responses towards organic farming implemented in vineyards. Though an appropriate management of the vineyards at the plot scale may enhance low mobility species that have relatively small home range such as arachnids, a landscape-scale approach is required for higher mobility species like bats. We concluded that when designing conservation strategies in Mediterranean farmlands, the implementation of a multi-scale approach is required to assure benefits for a wide range of species.

ARE SECONDARY WOODLANDS PROVIDING SUITABLE RESOURCES FOR BIODIVERSITY? BATS AS A CASE STUDY [O]

ELISA FUENTES-MONTEMAYOR[1]**, RONNY ROTBARTH[1], KEVIN WATTS[1,2], KIRSTY PARK[1], **ef12@stir.ac.uk
[1]*University of Stirling, U.K.;*
[2]*Forest Research, U.K.*

Actions to conserve biodiversity, particularly in areas that have undergone major land transformation, include habitat restoration and creation. These actions are often assumed to benefit biodiversity, but slow habitat development rates coupled with time lags in species responses have resulted in a lack of empirical studies assessing the long-term value of these activities. We used ancient semi-natural woodlands (usually regarded as high quality habitats for many taxa) as reference sites to assess how secondary woodlands created over the last century are performing in terms of their value for bats (a group with many species strongly dependent on woodland for roosting and/or foraging). We conducted vegetation surveys and used ultrasonic detectors to quantify bat activity levels in 30 woodland patches in central Scotland. We used multivariate analyses to identify key differences in habitat structure between ancient and secondary woodlands, and Generalised Linear Models to explore how these related to bat activity levels. There were moderate differences in the vegetation structure of ancient vs. secondary woodlands; these were mainly driven by variation in tree sizes, proportion of native tree species and amount of understorey (all with higher values in ancient than in secondary woodlands). Bat activity levels did not differ significantly between ancient and secondary woodlands, but were influenced by vegetation structure. The activity of *Pipistrellus* species was higher in woodlands with lower tree densities and larger trees. *Myotis* bats displayed higher activity levels in woodlands with larger trees and a relatively open canopy. Our findings suggest that ancient and secondary woodlands can be equally valuable for foraging bats. However, woodland management impacting on vegetation (e.g. reduced tree regeneration due to over-grazing) was apparent at some of our sites and we suggest this is likely to play a major role in determining the suitability of woodlands for bats.

METABARCODING FOR THE PARALLEL IDENTIFICATION OF SEVERAL HUNDRED BATS AND THEIR PREY [P]

MAXIME GALAN[1]**, JEAN-BAPTISTE PONS[2,3], ORIANNE TOURNAYRE[1], ERIC PIERRE[1], MAXIME LEUCHTMANN[4], DOMINIQUE PONTIER[2,3], NATHALIE CHARBONNEL[1], **nathalie.charbonnel@inra.fr
[1]INRA, UMR CBGP, F-34988 Montferrier-sur-Lez, France;
[2]Univ Lyon, Université Lyon 1, CNRS, Laboratoire de Biométrie et Biologie Evolutive UMR5558, F-69622 Villeurbanne, France;
[3]Univ Lyon, LabEx ECOFECT Ecoevolutionary Dynamics of Infectious Diseases, Villeurbanne, F-69365 Lyon, France;
[4]Poitou-Charentes Nature, 14 rue Jean Moulin 86240 Fontaine-le-Comte, France.

Assessing diet variability between individuals and populations is of primary importance to better understand the biology of bats and design relevant conservation strategies. Although the advent of metabarcoding has facilitated such analyses, this molecular approach does not come without challenges. Several biases may occur throughout the whole experiment, from fieldwork to biostatistics, resulting in the detection of false negatives, false positives or to low taxonomic resolution. Here, we detail a rigorous metabarcoding approach based on a two-step PCR protocol and bioinformatic analysis enabling the 'all at once' identification, potentially at the species level, of bats and their arthropod prey for several hundreds of samples. Our study includes faecal pellets collected from 357 bats in eastern France representing 16 species, as well as insect mock communities that mimic bat meals of known composition, negative and positive controls. All samples were analysed in triplicate. We compare the efficiency of DNA extraction commercial kits and we evaluate the effectiveness of our molecular protocol using the rate of bat identification success, taxonomic resolution, sensitivity, and amplification biases. We show that our strategy involves half the steps usually required in the other metabarcoding studies and reduces the probability to mis-assign prey to the wrong bat faecal pellets. The controls included and the bioinformatic approach enable limitation of the risk of a false positive, hence guaranteeing high confidence results for both prey occurrence and bat species assignment. Altogether, our results illustrate the power of this approach to assess diet richness and variability within and between colonies. This study therefore provides a rapid, accurate and cost-effective screening tool for addressing evolutionary ecological issues in particular in the context of Chiroptera conservation biology.

FIRST RECORDS OF *TADARIDA TENIOTIS* IN GEORGIA [P]

SUREN V. GAZARYAN[1]**, IOSEB NATRADZE[2], ALEXANDER BUKHNIKASHVILI[2],
**s.gazaryan@gmail.com
[1]*EUROBATS Secretariat, Bonn, Germany;*
[2]*Institute of Zoology of Ilia State University, Georgia.*

The Caucasus represents the north-eastern range limit of the European free-tailed bat, *Tadarida teniotis*, which has been considered an exceptionally rare species in the region. Until recently, only 6 reliable recorded locations were known from the Caucasus, including 3 locations on the northern slope of the Central Caucasus in the territory of Russia, 2 locations in the northern part of Armenia and one in the territory of Nagorno-Karabakh Autonomy. In 2013-2016, based on acoustic surveys and subsequent analysis, we registered the species at four quite separate locations in Georgia. In September 2014, its calls were recorded at the reservoir near the village of Khopisi, which lies on the Lesser Caucasus in Eastern Georgia. In July 2015, several bats were recorded and observed as they swarmed at the presumed roost in cliffs on the right bank of the Kura River near the historical complex of Uplistsikhe (Eastern Georgia). In September 2015, several passes of free-tailed bats were recorded near the village of Omalo (Tusheti, Northern Caucasus). In September 2016, many sequences of echolocation calls and feeding buzzes were recorded by an automated bat detector installed on the meteorological mast in Imereti Region (Western Georgia). Given the geographical distribution of Georgian records, we assume that the free-tailed bat is rather widespread in central and eastern part of the country where the rarity of prior records stemmed from the difficulty of revealing this species without acoustic methods. However, known absence of records from the western part of the Caucasus can hardly be explained by the lack of acoustic surveys, because this part of the Caucasus has been studied most rigorously with bat detectors both in Russia and Georgia. Our record from the Andi Koisu river basin in proximity to the border with Russia indicates a high probability of the species' occurrence in the adjacent Russian east-Caucasian republics of Dagestan and Chechnia.

ECHO FROM THE SKULLS: IS THERE A TRADE-OFF BETWEEN ECHOLOCATION AND FEEDING FUNCTION IN BATS? [P*]

GIADA GIACOMINI[1]**, DINO SCARAVELLI[2], ANTHONY HERREL[3], RICHARD BROWN[1], CARLO MELORO[1], **giada.giacomini19@gmail.com
[1]*School of Natural Sciences and Psychology, Liverpool John Moores University, Liverpool, U.K.;*
[2]*Department of Veterinary Medical Sciences, University of Bologna, Ozzano dell'Emilia (BO), Italy;*
[3]*UMR 7179 C.N.R.S/M.N.H.N., Département Adaptations du Vivant, Bâtiment d'Anatomie Comparée, Paris, France.*

Bite force and dietary preference seem to play an important role on bat skull morphological variation and species diversification, however the contribution of echolocation to bats ecomorphology remains unclear. In this preliminary study we investigated the functional relationships between skull size and shape and both bite force and echolocation parameters in 18 bat species (5 families). By employing a Nikon D5300 camera and a Nikkor 60 mm macro lens we reconstructed 3D bat skull models following an established photogrammetry protocol (~ 140 high resolution pictures per sample). A unilateral set of 24 three-dimensional landmarks were successively placed on the ventral, dorsal and lateral surfaces of the models to capture general aspects of bat cranial anatomy. Geometric morphometrics and comparative methods were employed to extract size and shape data from 3D coordinates and incorporate species phylogenetic relationship into statistical models. We detected a significant phylogenetic signal in the cranial shape data (Kmultiv=0.9) but not in size (K=0.75, P=0.06) suggesting skull shape evolves according to a Brownian motion model. Allometry did not impact interspecific skull shape variation in our sample. Averaged body mass and bite force values (experimentally taken using a bite force transducer) were strongly correlated with cranial size (r=0.92 and r=0.87, respectively) including after taking phylogeny into account with Phylogenetic Generalised Least Squares. The same parameters did not correlate significantly with skull shape. Using a two-block Partial Least Squares we detected a significant degree of co-variation between echolocation parameters and skull shape (r=0.82, P<0.001). The correlation is still strong after correcting for phylogeny (r=0.72) but not significant (P = 0.36). Despite the small sample size, this study suggests that echolocation plays a role in bat skull diversification and hence should be taken into account in ecomorphological analyses.

BAT SKULL IN THREE DIMENSIONS: PHOTOGRAMMETRY AS A PORTABLE AND RELIABLE SCANNING SOLUTION [O*]

GIADA GIACOMINI[1]**, DINO SCARAVELLI[2], ANTHONY HERREL[3], ALESSIO VENEZIANO[1], CARLO MELORO[1], **giada.giacomini19@gmail.com
[1]*Research Centre in Evolutionary Anthropology and Paleoecology, School of Natural Sciences and Psychology, Liverpool John Moores University, Liverpool, U.K.;*
[2] *Department of Veterinary Medical Sciences, University of Bologna, Ozzano dell'Emilia (BO), Italy;*
[3]*UMR 7179 C.N.R.S/M.N.H.N., Département Adaptations du Vivant, Bâtiment d'Anatomie Comparée, Paris, France.*

The mammalian skull is a complex three dimensional structure. Skull morphology of bats appears to be strongly correlated with feeding and behavioural ecology, but many questions about its micro and macroevolution remain unanswered. Linear measurements were traditionally employed to quantify skull morphology. However, recent advancements in digital photography, CT-scan, and laser scanning have allowed the application of sophisticated statistical methods to explore skull size and shape variation. We explored the potential of 3D photogrammetry to generate reliable virtual 3D models of bat skulls. Photogrammetry represents a cheap and portable alternative to CT and surface laser scanning but its accuracy for very small objects has not been fully tested. Using a digital SLR camera (Nikon D5300) with a macro lens (Nikkor MACRO; focal length 60 mm) we were able to generate 3D skull models for 19 specimens (from the Muséum National d'Histoire Naturelle, Paris) with a range of skull lengths from 10.4 - 22.4 mm (mean = 15.6 mm). These virtual models were compared with those generated using a Breuckmann 3D laser scanner with a scanning resolution of ~ 40 µm. The distances between meshes generated from the photogrammetry models and those from the Breuckmann were very low (mean = 0.04 ± 0.03 mm). We then used 3D geometric morphometrics to compare the size and shape information of the virtual models obtained with both techniques. Matrix correlation for size and shape data were extremely high (r = 1.00, 0.99 respectively) and cluster analyses supported a strong overlap in size and shape data for the same specimens regardless of the scanning method. This was confirmed by a Procrustes ANOVA that showed no differences in skull size and shape variance across the 3D model pairs. Our approach demonstrates that photogrammetry can be effectively employed to investigate skull morphological variation in small bat specimens, and it provides a high degree of accuracy.

SEX RATIO IN ADULTS OF FOUR MIGRATORY BAT SPECIES WITHIN THEIR BREEDING ZONE: THE PREDICTED AND THE UNEXPECTED [P]

LENA V. GODLEVSKA[1]**, SERGIY V. REBROV[1], **LGodlevska@gmail.com
[1]*Schmalhausen Institute of Zoology, NAS of Ukraine, Bohdan Khmelnytskyi 15, 01030 Kyiv, Ukraine.*

It is commonly recognised that in long-distance migratory bat species of the temperate zone a seasonal segregation of sexes occurs in the breeding period. Long distance migrations (up to 1000 km and more) to the breeding places, usually northward, are typical for females, whereas males mostly spend summer within or near the zone of (safe) wintering, at the south. Based on results of nettings and contact examination we consider the summer sex ratio in adults of four bat species (*Nyctalus leisleri*, *N. noctula*, *Pipistrellus pygmaeus*, and *P. nathusii*) in the territory of central and northern Ukraine, lying within their breeding zone. In two species wintering outside the region (*P. pygmaeus* and *N. leisleri*), adult males are almost absent in summer (with only c. 1 and 4 % respectively). That fits the above common scheme of sex-biased migrations. In *N. noctula*, the species which had recently expanded its winter range for 400–500 km northward, now covering the whole territory of Ukraine, the percentage of adult males in summer is up to 25 %. This contrasts with their percentage in winter aggregations in the region, with up to 70%. Such seasonal changes of sex ratio supports an assumption about the "inverted" migration scheme: long-range migrations are made mostly by females (to the south and back), but males commonly stay wintering at the north nearby their place of birth, in the zone of wintering risk. The most unexpected was the percentage of adult males in *P. nathusii*: in total, ca. 40% (and up to 100% for certain localities). The nearest winter records of this species are known only 300–500 km southward. In this case, we may presume that the greatest part of the males migrate with the females to the main breeding zone. Possible explanations for this phenomena are considered.

AN INVESTIGATION OF THE SOCIAL STRUCTURE, SPECIES BOUNDARIES, HYBRIDIZATION AND PHYLOGEOGRAPHY OF THREE *MINIOPTERUS* SPECIES (MAMMALIA: CHIROPTERA) [O*]

KANAT GÜRÜN[1]**, ANDRZEJ FURMAN[1], JAVIER JUSTE[2], MARIA JOÃO RAMOS-PEREIRA[3,4], JORGE M. PALMEIRIM[5], SÉBASTIEN J. PUECHMAILLE[6,7], PAVEL HULVA[8], AHMET KARATAŞ[9], RAŞIT BILGIN[1], **anatgurun@yahoo.com

[1]*Institute of Environmental Sciences, Boğaziçi University, Bebek, Istanbul 34342, Turkey;*

[2]*Estación Biológica de Doñana (CSIC), Avda. Américo Vespucio s/n, Seville 41092, Spain;*

[3]*Department of Zoology, Institute of Biosciences, Universidade Federal do Rio Grande do Sul, Av. Bento Gonçalves 9500, Porto Alegre RS 91540-000, Brazil;*

[4]*Centre for Environmental and Marine Studies Wildlife Research Unit University of Aveiro, Aveiro, Portugal;*

[5]*Center for Eology, Evolution and Environemntal Change Dept. Biologia Animal Faculdade de Ciencias, Universidade de Lisboa 1749-016 Lisboa, Portugal;*

[6]*University College Dublin, School of Biological and Environmental Sciences, Belfield, Dublin 4, Ireland;*

[7]*Zoology Institute, Ernst-Moritz-Arndt University, 17489 Greifswald, Germany;*

[8]*Department of Zoology, Faculty of Science, Charles University in Prague, Viničná 7, CZ-128 44 Praha 2, Czech Republic;*

[9]*Department of Biology, Niğde University, Niğde 51100, Turkey.*

Hybridization among sympatrically occurring species may drastically affect their population structure and genetic make-up. A multi-marker approach is essential for making inferences about the social structure of such species. The interaction among populations of different species may also give rise to interspecific gene-flow, or introgression. *Miniopterus* is a genus of cave-dwelling bats that consists of sister lineages, several of which have been elevated to species level recently, and is well-suited for phylogeographic, hybridization and social structure studies at large geographic scales. In this study, the social structure and its effects on the social genetic make-up and the phylogeography of three *Miniopterus* species, namely, *M. schreibersii*, *M. pallidus* and *M. maghrebensis*, was investigated using 12 nuclear microsatellite markers and mitochondrial DNA data that was previously available, with samples from the entire circum-Mediterranean range of these species. Local structuring that was previously detected among populations of *M. schreibersii* using mitochondrial markers was not observed for microsatellite markers, which indicated male-biased dispersal for the species. In areas where the distributions of sister species overlapped, there were signs of hybridization, introgression and mitochondrial capture.

A NOVEL APPROACH FOR ANALYSING TIME SERIES OF TEMPERATURE DATA IN BAT HIBERNACULA [P]

RALF GYSELINGS[1]**, FILIP BORMS[3,4], BEN VAN DER WIJDEN[2], LUC DE BRUYN[1,2],
**ralf.gyselings@inbo.be
[1]*Research Institute for Nature and Forest, Flemish Government, Brussels, Belgium;*
[2]*Evolutionary Ecology Group, Departement of Biology, University of Antwerp, Antwerp, Belgium;*
[3]*Bat Working Group, Natuurpunt, Mechelen, Belgium;*
[4]*Gotham Nature and Chiropterological Research, Kalmthout, Belgium*.

Bats select specific hibernation sites with regard to their temperature profile. The profile they select is species dependent. Good management of a hibernation site requires knowledge of the available temperature profiles. However, to improve the conditions in a hibernation site, a good understanding of the factors that influence the temperature profile is important as well. Based on system theory and the physics of heat transport, we developed a transfer function model that relates temperature in a hibernaculum to the outside temperature. The transfer function includes parameters for conduction through the wall of the hibernaculum, convective heat transport and mixing with passing air. These parameters are determined by fitting the transfer function to the ratio of the Fourier transforms of inside and outside temperatures. Interpretation of the parameters allows judgement as to what extent air flow or wall thickness of a hibernaculum determine the buffering of the inside environment against fluctuations from the outside temperature. We present the underlying mathematics of the model as well as a case study of some hibernacula in Flanders that were analysed with this model to investigate possible improvements. In the future, this modelling approach can also be used to predict the effect of climate change on the conditions inside the hibernaculum.

WHY AND WHEN DO BATS FLY OUT IN WINTER? A FIELD STUDY IN THE NORTH OF FLANDERS, BELGIUM [O]

RALF GYSELINGS[1]**, GEERT SPANOGHE[1], ERIKA VANDENBERGH[1], LUC DE BRUYN[1,2], **ralf.gyselings@inbo.be
[1]*Research Institute for Nature and Forest, Flemish Government, Brussels, Belgium;* [2]*Evolutionary Ecology Group, Departement of Biology, University of Antwerp, Antwerp, Belgium.*

We investigated winter activity of bats in two riparian areas in the north of Flanders. We recorded bat activity using automated bat detectors during 78 nights in December, January and February. Each recording we noted presence of species and presence of feeding buzzes. Feeding buzzes were only counted as a feeding buzz if we could clearly see a buzz phase II. In addition, for Pipistrellus pipistrellus we could also distinguish drinking buzzes. P. pipistrellus was observed during 63% of the nights. Myotis daubentonii was found 22-30% of the nights depending on the site. Total activity of M. daubentonii per night was very strongly correlated with feeding. For P. pipistrellus activity correlated better with drinking. This is in line with the hypothesis that species that hibernate in buildings where no water is present must fly out to drink, while species that hibernate in objects where drinking water is available fly out to feed. We modelled the total activity per night in function of weather conditions and moon phase. We used one of two temperature measurements: the temperature at sunset and the maximum temperature of the previous day. For P. pipistrellus the latter had a lower AIC. For M. daubentonii the best fit was obtained with the temperature at sunset. This is consistent with the hypothesis that P. pipistrellus can estimate the temperature through the warming of its hibernacula while M. daubentonii that hibernates in more buffered systems has to fly out. The activity of P. pipistrellus was also adversely affected by the illumination of the moon. The fact that bat activity was observed during so many nights indicates that winter activity is an essential part of bat ecology, and riparian areas are an important habitat for bats in winter. Therefore, winter activity of bats should be taken into account in management plans and environmental impact assessments, as it has its own specific conservation implications.

SPECIES-SPECIFIC IMPACT OF HABITAT FRAGMENTATION ON THE POPULATION GENETIC STRUCTURE OF NEOTROPICAL BATS [O*]

TANJA HALCZOK[1]**, STEFAN BRÄNDEL[2,3], RACHEL PAGE[3],
MARCO TSCHAPKA[2,3], SÉBASTIEN J. PUECHMAILLE[1], GERALD KERTH[1],
**Halczokt@uni-greifswald.de
[1]*Zoological Institute and Museum, Ernst-Moritz-Arndt University Greifswald, Greifswald, Germany;*
[2]*Institute of Evolutionary Ecology and Conservation Genomics, University of Ulm, Ulm, Germany;*
[3]*Smithsonian Tropical Research Institute, Balboa, Panama.*

Human-induced landscape modifications are often associated with habitat loss and fragmentation. Specially in the tropics where biodiversity is high, these habitat alterations pose serious threats to wildlife populations as they are known to impact species richness and abundance. Moreover, they may cause reductions in gene flow that might ultimately affect the potential of animals to adapt to environmental change through the loss of genetic diversity. Consequently, populations with low genetic diversity are expected to suffer more severely from diseases and parasites. We investigated six different phyllostomid bat species (*Artibeus jamaicensis*, *Carollia perspicillata*, *Uroderma bilobatum*, *Dermanura watsoni*, *Dermanura phaeotis* and *Trachops cirrhosus*) native to the area around the Panama Canal which has been highly modified by humans. While some of these species exhibit a high mobility, others have been shown to be less mobile which limits their capability to reach isolated forest fragments. We obtained at least 150 genetic samples per investigated species - in some species, data amounts to more than 400 individuals. Using a set of 10 to 16 nuclear microsatellite markers per species we determined levels of genetic differentiation and dispersal patterns for these species. While bat species with a high degree of mobility seem to be resilient to the habitat fragmentation within our study area, gene flow is restricted for less mobile species as indicated by population genetic structure. Our results emphasize the importance of examining the effects of habitat fragmentation at the species level, as differences in responses to habitat alterations appear to be species-specific

BATS AND WINDFARM MONITORING AND IMPLEMENTATION OF MITIGATION MEASURES ACROSS THE WESTERN PALAEARCTIC, AND WHAT CAN BE DONE? [O]

DANIELA HAMIDOVIĆ[1,]**, CHRISTIAN C. VOIGT[2], LUÍSA RODRIGUES[3],
**daniela.hamidovic@dzzp.hr
[1]*Croatian Agency for Environment and Nature, Radnička cesta 80/7, 10000 Zagreb, Croatia;*
[2]*Leibniz Institute for Zoo and Wildlife Research (IZW), Alfred-Kowalke-Str. 17, 10315 Berlin, Germany;*
[3]*Institute for the Conservation of Nature and Forests, ICNF, Avenida da República 16-16B, 1050-191 Lisbon, Portugal.*

In 2016, the Intersessional Working Group on "Wind Turbines and Bat Populations", hosted by UNEP/EUROBATS, developed a questionnaire on post-construction monitoring and implementation of mitigation measures that was sent out to the 63 Range States of the EUROBATS Agreement. The questionnaire focused on evaluation of best practice and legislation that is implemented under the scope of EUROBATS in order to mitigate high mortality rates at wind turbines. Out of 50 states that have windfarms 26 range states returned answers for analysis. The covered time period ranged from 1980 to 2016 depending on the specific country. Numbers of windfarms were reported as zero to more than 5,000, while the number of wind turbines per windfarm ranged from 1 to 165 with most of the medians and averages left unknown. Post-construction monitoring was reported as obligatory in only 11 countries; although it is obligatory, in 6 states it is not done in all windfarms, but is based on the preconstruction assessment. Only 10 countries reported regulations, acts or procedures in which monitoring is prescribed and in 8 it is done according to the EUROBATS guidelines. In 13 range states, avoidance or mitigation measures are prescribed but the effectiveness of mitigation measures is monitored in only 7 countries. There is no regular control of mitigation measures prescribed, and results of such studies are mostly not made available to the public. Although bat mortality rates are reported as high based on the sketchy data available and bats are strictly protected by the Habitats Directive in all EU member states, it seems that there is no unifying procedure with respect to mitigation schemes. We conclude that it is vital to propose changes in the policy, procedures and data availability in order to safeguard bat populations across the Western Palaearctic.

BAT FAUNA OF LOKRUM ISLAND SPECIAL FOREST RESERVE, CROATIA [P]

DANIELA HAMIDOVIĆ[1,**], PETRA ŽVORC[1], MARIJA CRNČEVIĆ[2], DINA RNJAK[3], **bebissima@gmail.com
[1]*Croatian Biospeleological Society, Demetrova 1, 10000 Zagreb, Croatia;*
[2]*Public Institution Lokrum Island, Lokrum Reserve, Od Bosanke 4, 20000 Dubrovnik, Croatia;*
[3]*Geonatura Ltd. Consultancy in Nature Protection, Fallerovo šetalište 22, 10000 Zagreb, Croatia.*

Lokrum Island, Dubrovnik, Croatia, is a special reserve of forest vegetation since 1948. The total surface of the island is 0.7 km^2, while dense vegetation covers 86% of the island, with the forest and maquis dominated by *Quercus ilex* and *Fraxinus ornus*. The island and the seabelt are also a Natura 2000 site. Lokrum Island, as a part of Dubrovnik Old Town, is under the protection of UNESCO as a cultural heritage. The only known data for the bat fauna on the island originate from one source stating that two bat species have nurseries in the Benedictine monastery, without any additional data on dates and numbers of specimens. In June and September 2016 we investigated the bat fauna by placing mist-nets around water bodies, searching overground and underground potential roosting sites and echolocation recording using ultrasound detectors. Overall 7 bat species were mist-netted: *Hypsugo savii, Miniopterus schreibersii*, *Myotis nattereri*, *M. mystacinus, Pipistrellus kuhlii*, *P. nathusii* and *Plecotus kolombatovici*. In the Benedictine monastery a nursery colony of *Rhinolophus hipposideros* was confirmed and one *R. ferrumequinum* specimen was also recorded. The nursery of *Plecotus kolombatovici* was also confirmed, although the exact location in the monastery complex was not found. The echolocation recordings revealed 2 more species: *Tadarida teniotis* and *Nyctalus noctula*. Preserved forest and vegetation of the island, water reservoirs at three localities, a number of overground roosts and sea caves together with the absence of visitors during the night enables a high biodiversity of bat fauna for such a small island, with 11 of the 34 Croatian-recorded bat species. The results were presented at the International Bat Night in 2016, the first ever for that particular county. Bat research results from 2016, together with additional research planned in 2017, will enable further recommendations and actions for the conservation of the bat fauna through the current development of the Lokrum Island Reserve Management Plan.

REFERENCE SCALE OF ACTIVITY LEVELS FOR MICROPHONES INSTALLED ON WIND MASTS IN FRANCE AND BELGIUM [P]

ALEXANDRE HAQUART[1]**, CHARLOTTE ROEMER[1], MARIE-LILITH PATOU[1], THIERRY DISCA[1], FLORIAN LECORPS[1], JULIEN TRANCHARD[1], **ahaquart@biotope.fr
[1]*Biotope, 22 Boulevard Maréchal Foch, 34140 Mèze, France.*

Regulatory studies are conducted throughout Europe in order to assess the impacts of wind turbines on bats. National and international committees notably recommend the use of wind masts to study bat acoustic activity with the aim of estimating collision risks. For this purpose, the evaluation of the quantity of activity for each species can be a difficult task when there is no comparison available. We present here a reference scale of activity levels for microphones installed at 23 wind masts in France and Belgium during 3260 nights between 2011 and 2016. Masts were equipped with SM2BAT recorders and SMX-U1 microphones. We used the "positive minute of activity" to count bat passes. We recorded 16 species and three groups of species. We present their occurrence per site, per night, and the mean amount of activity. The most common species was *Pipistrellus pipistrellus* (occurrence at 100% of sites). *Nyctalus leisleri* was also very common at height (91 % of sites). Species with low activity at height were *Barbastella barbastellus*, *Miniopterus schreibersii*, *Myotis* species, *Nyctalus lasiopterus* and *Plecotus* species. *Rhinolophus* species were never recorded at height. These results are the product of the abundance of a species and its behaviour. Indeed, gleaners will, by definition, be found more often at ground level than at height. This is why it is also important, when interpreting bat activity at height, to put it in perspective with bat activity at ground level. A reference scale for ground activity has already been developed for France.

USING DNA TECHNIQUES TO IMPROVE NATIONAL POPULATION ESTIMATES OF A THREATENED IRISH BAT SPECIES, THE LESSER HORSESHOE BAT [O*]

ANDREW P. HARRINGTON[1]**, PETER TURNER[1], CATHERINE O'REILLY[1],
**andrew.harrington@postgrad.wit.ie
[1]*Department of Science, Waterford Institute of Technology, Waterford, Ireland*.

Ireland contains an internationally important population of the lesser horseshoe bat Rhinolophus hipposideros. This population is increasing but faces threats such as destruction of its woodland habitat, deterioration or damage of its roosting sites, inbreeding in isolated subpopulations, and climate change. Therefore, continued monitoring is essential for this species' conservation. Population estimates are obtained by counting bats present at 142 summer roosts. While all adult females in the national population are assumed to be counted in this way, it is thought that only 25% of bats counted at these sites are male, with the remainder living in smaller dispersed sites. This estimated percentage of males is currently used in the calculation of the national population estimate, but empirical data are lacking. DNA testing of non-invasively collected samples such as droppings has been used studies of other wild mammal species. The aim of this study is to use this method to survey several lesser horseshoe bat maternity roosts and obtain information on the proportion of male bats present. 1,300 bat dropping samples were collected from 6 lesser horseshoe bat roosts in Ireland between May and June 2016. DNA samples were genotyped to identify each individual bat present at each roost. DNA tests were designed to identify male and female bats, and were then applied to the DNA samples collected. Each bat identified was sexed and thus the proportion of male bats in each roost was determined. The proportion of male bats at the sampled roosts ranged from 9% to 72%. At 5 of the sites, the number of males present was found to be higher than the previously assumed level of 25%, and overall males made up approximately 50% of the total number of individuals at the sites that were sampled. This study has found that male lesser horseshoe bats are generally present in much higher proportions at summer maternity sites than previously thought, indicating that the Irish population of this species may have been over-estimated in the past. More data from a larger number of roosts is needed to assess the proportion of males in the monitored Irish population at large to improve the current population estimate, but this method has the potential to be used in other European countries to improve our knowledge of this rare bat species.

WHY ARE ROCKET BOXES FAVORED BY A MATERNITY COLONY OF SOCIAL BARK-ROOSTING BATS? [O*]

JULIA P.S. HOEH[1]**, JOY M. O'KEEFE[1], **jhoeh@sycamores.indstate.edu
[1]*Center for Bat Research, Outreach, and Conservation, Indiana State University, Terre Haute, USA.*

Installing artificial roosts may aid endangered species, but we need more data to find the optimal design for particular bats, e.g. Myotis sodalis. To characterize differences inherent in 3 artificial roost styles (bat box, rocket box, and polyurethane bark mimic), we evaluated roosting surface area, entrance area, volume, and temperature (12 points/roost) while bats were excluded from a cluster containing 1 of each style. We also conducted emergence counts across 1–2 years at 5 more clusters. Rocket boxes provided >2× the entrance and surface area and >5× the volume vs. other roost types. On a daily basis, a greater proportion of the roost remained within the critical temperature range (0–45 °C) in the bat box (92%) and rocket box (93%) than the bark mimic (87%). Possible explanations for this preference include bats choosing larger roosts that are more stable across the day but which offer wider hourly temperature availability.

GENETIC STRUCTURE IN THE MEDITERRANEAN BAT *MYOTIS CAPACCINII*: MULTIPLE REFUGIA, POST GLACIAL DISPERSAL AND MITO-NUCLEAR DISCORDANCE [O]

ELIZABETH M. HEMOND[1]**, ANDREA VIGLINO[2], RAŞIT BILGIN[3], JAVIER JUSTE[4]., MARCO GALAVERNI[2], SÉBASTIEN J. PUECHMAILLE[5,6], EMMANUELLE COSSON[7], ROMOLO CANIGLIA[2], **lizhemond@gmail.com

[1]*Department of Molecular Biology and Genetics, Bahçeşehir University, Beşiktaş 34349 Istanbul, Turkey;*

[2]*Conservation Genetics Laboratory, National Institute for Environmental Protection and Research (ISPRA), Via Cà Fornacetta 9, 40064 Ozzano dell'Emilia (BO), Italy;*

[3]*Institute of Environmental Sciences, Boğaziçi University, 34342 Bebek, Istanbul, Turkey;*

[4]*Doñana Biological Station (CSIC), Avda. Américo Vespucio s/n, Isla de la Cartuja, Seville 41092, Spain;*

[5]*University College Dublin, School of Biological and Environmental Sciences, Belfield, Dublin 4, Ireland;*

[6]*Zoology Institute, Ernst-Moritz-Arndt University, 17489 Greifswald, Germany;.*

[7]*Groupe Chiroptères de Provence, France.*

The genetic structure and the recent evolutionary history of the long-fingered bat, *Myotis capaccinii* Bonaparte 1837, were evaluated analyzing 653 bp of the cytochrome b locus and eight microsatellite loci in more than 200 individuals collected from 20 localities across its known distribution range. Data from both mitochondrial and nuclear markers indicate the presence of at least two discrete evolutionary units within the species and a trend of decreasing genetic diversity from east to west. Whereas the mtDNA data indicate an older genetic break between a western European-Thrace clade and an Asia Minor clade, microsatellite data indicate a genetic break between western and eastern groups. The geographic discordance between the genetic regroupings based on mtDNA versus microsatellites data illustrates the need of using combined data sets to assess comprehensively the conservation status of this vulnerable Mediterranean bat species.

DEVELOPMENT OF A BODY CONDITION SCORING SYSTEM VALIDATED BY DEXA AND DEUTERIUM OXIDE IN BIG BROWN BATS (*EPTESICUS FUSCUS*) [O*]

SARAH E. HOOPER[1]**, JOE FASIG[2], SYBILL K. AMELON[3], **hoopers@missouri.edu
[1]*Department of Veterinary Pathobiology, College of Veterinary Medicine, University of Missouri, Columbia, MO, USA;*
[2]*College of Veterinary Medicine, University of Missouri, Columbia, MO, USA;*
[3]*USDA Forest Service Northern Research Station, Columbia, MO, USA.*

In bats, body condition has historically been assessed by taking two independent measurements, the bat's weight and the length of the forearm. Using these measurements, bats are assigned a body condition index (BCI) score defined as the weight (grams) divided by the forearm (mm). Within a single night, the BCI score of a bat can vary based upon the weight before eating and post-prandial. Additionally, measuring forearm length can be variable among researchers, creating different scores. The purpose of this study was to adapt a numerical body condition scoring (BCS) system to estimate the fat composition, or body energy reserves, of bats, and subsequently compare the body condition and BCI score to the composition measurements in big brown bats (*Eptesicus fuscus*) obtained by dual-energy x-ray absorptiometry (DXA) and deuterium oxide. Big brown bats were assigned a body condition score by five independent observers based upon a scale of 1 to 5 with 1 being emaciated and 5 being excessively fat. Bats were subsequently anesthetized for blood collection, scanned with DXA, and injected with deuterium oxide. Approximately 3 hours post-injection of deuterium oxide, bats were anaesthetized for a second blood collection for determination of deuterium oxide enrichment in the serum after equilibration. Preliminary results from fifteen captive big brown bats weighing 14.1 to 41.9 grams represented BCS of 2 to 5 and had an average percent body fat ranging from 21.1% to 65.5%. Assigning a BCS score of 5 with 60% fat and decreasing the percent fat by 10 for each whole numerical decrease in BCS, revealed there was a high correlation between percent fat measured by DXA and BCS (r2 = 0.86). Additionally, the independent observers assignment of BCS were highly correlative to percent body fat (ρ = 0.93 ± 0.06). Our findings suggest that a numeric body condition scoring system can be a useful management tool.

WHEN THE EXTANT BATS AROSE? FOSSIL RECORD AND MOLECULES ILLUMINATE THE HISTORY OF THE BAT FAUNA IN WESTERN PALEARCTICS [O]

IVAN HORACEK[1]**, EVA TRAVNICKOVA[1], PAVEL HULVA[1], **horacek@natur.cuni.cz
[1]*Department of Zoology, Charles University, Prague, Czech Republic.*

The new fossil records and detailed time-calibrated outputs of molecular phylogenetic analyses appearing during the recent decade reappraised former ideas on history of the Western Palearctic bats in essential way. The fossils show that at least five modern families begun their radiation already during the late Early Eocene in N-Africa; 57 species of 10 families from Quercy Phosphorites demonstrate excessive diversification of the Middle to Late Eocene bat fauna in Europe, divergent from the Late Eocene radiations in N-Africa. The leading taxa of these local radiations, mostly without any relation to extant clades, disappeared along the "Grand Coupure" with onset of Oligocene. Just from that time FAD of the genus *Myotis* s.str. (33 Ma) has been reported, i.e. more than twice older than that proposed by molecular analyses of the genus. We will discuss aspects of the discrepancy incl. alternative calibrations of molecular clocks. Yet, the main question is: when the extant species appeared? The Vallesian and Turolian stages (11-5.4 Ma) with a rise of vespertilionid clades, *Myotis* in particular, could be a turning point. A scarce bat record of that time (with some new data) will be reviewed. Since beginning of the Pliocene the situation dramatically changed both as concerns the structure of bat communities (roughly conforming to extant fauna), and reliability of the fossil record with even very abundant community samples. In several of them we examined aspects of phenotype variation, particularly in Myotis spp., and compared to that in extant species. In most cases, the patterns conforming to extant populations were achieved only during the late Pliocene and Early Pleistocene. Specificities of particular clades and discrepancies with the molecular dates of speciations (ca 10 Ma on average) will be discussed.

CALL ACTIVITY AND SPECIES DIVERSITY OF BATS AT NACELLE HEIGHT IN WIND FARMS OF AUSTRIAN MONTANE FORESTS [O]

SENTA HUEMER[1]**, BRIGITTE KOMPOSCH[1], **b.komposch@oekoteam.at
[1]*Oekoteam - Institute for Animal Ecology and Landscape Planning, Graz, Austria.*

Montane forests are important habitats for many of the 28 Austrian bat species. In the last decade, these habitats are increasingly utilised by wind farms - due to the rapidly-growing demand for renewable energy sources. To reduce the number of bat fatalities, curtailment algorithms are used for mitigation measures. As these algorithms are usually deduced from lowland conditions, we here address the following questions: How is bat activity in montane forests influenced by environmental conditions? Are there significant differences between bat activity in lowland and montainous forests? We studied the bat activity in four wind parks situated in Austrian montane spruce forests (1,200 – 1,700 m a.s.l.) by using batcorders (EcoObs) in nacelles from April to October. We recorded bat calls and measured wind speed and air temperature. Our results indicate that bat activity in montane forests is different from lowland conditions: montane bats cope with higher wind speed and lower temperatures than their lowland relatives. We could also record activity peaks of their migration periods in June. The fluctuations between daily call activities is very high, so long-term recording is essential for significant conclusions on bat activities

NEUTRAL AND ADAPTIVE EVOLUTION IN *P. PIPISTRELLUS* SPECIES COMPLEX: INTEGRATION OF THE GENETIC AND BIOACOUSTIC APPROACH [P*]

PAVEL HULVA[1,2], JAN DEMJANOVIC[1]*, KLARA JANIKOVA[1]**,
TOMAS BARTONICKA[3], **jan.demjanovic@seznam.cz
[1]*Department of Biology and Ecology, Faculty of Science, University of Ostrava, Chittussiho 10, 710 00 Slezská OstravaCzech Republic;*
[2]*Department of Zoology, Faculty of Science, Charles University, Viničná 7, 128 44 Praha 2, Czech Republic;*
[3]*Department of Botany and Zoology, Faculty of Science, Masaryk University, Kotlarska 2, 611 37 Brno, Czech Republic.*

Pipistrelle bats are often a feature of island communities due to their good dispersal capabilities, thus they are interesting model organisms for research into the role of population isolation and other insular effects on speciation. Active flight is associated with a fast metabolism, therefore trophic adaptations play an important role in bats' evolution. The parameters of the echolocation can be very useful in the characterization of the trophic niche in insectivorous bats. In this study, we present a combination of genetic and bioacoustic approaches to bats of the *Pipistrellus pipistrellus* species-complex from the Mediterranean islands and continental sympatric populations. The genetic approach was used to assign individuals to cryptic lineages, and to measure population diversity and degree of introgression. Neutral mitochondrial and nuclear microsatellite markers and candidate genes associated with echolocation were investigated. Bioacoustic data were obtained for particular individuals by recording them in a flight tent, which allowed the obtaining of standardized data and avoidance of the plastic reaction of echolocating animals to their immediate environment. By integration of both types of data, information about the polarity of ongoing changes and the processes acting in insular populations and continental siblings was ascertained.

INTELLIGENT VIRTUAL PERSONAL ASSISTANT FOR BAT SCIENTISTS [O*]

ANGEL IVANOV[1]**, STANIMIRA DELEVA[2], DANIELA OROZOVA[1],
**angelivanov@bfu.bg
[1]*Faculty of Computer Science and Engineering, Burgas Free University, Burgas, Bulgaria;*
[2]*Faculty of Biology, University of Costa Rica, San Jose, Costa Rica.*

Our life is benefiting from the use of contemporary technologies. Most of these technologies are widely used in scientific studies. Many bat researchers, however, still follow traditional methods of collecting and processing data, not taking advantage of the potential of modern inventions. Some of these methods include collecting data first on paper, and then having it digitized long after the end of the fieldwork. Another common practice is the use of several digital devices such as cameras and sound recorders in combination with paper notebooks. These practices often cause long delays before the completion of processing the gathered information. Manual data transfer often leads to typographical errors, and during the period from obtaining the information to digitizing it, valuable notes and observations could be lost or remain undetected. The data collection process will be significantly eased if a researcher could use a single entity for collecting, storing and processing data. Here we present such an entity – Virtual Intelligent Personal Assistant (VIPA) designed to facilitate the field work of bat researchers. VIPAs are software agents designed to assist users in performing specific tasks. They are able to communicate, co-operate, discuss, and guide people. One major advantage of VIPAs is that they collaborate with the user in different ways, and in virtually unlimited tasks and applications, by hiding the complexity of difficult tasks, performing tasks on behalf of the user, and teaching the user to monitor events and procedures. The presented VIPA is a BDI-based, mobile software developed using freely available Open Source technologies. Its initial version includes some basic functionalities such as gathering of fully customizable field data, processing of this data, analysis and reports. Future plans include integrating this software into a Virtual Collaboration Space for Bat Scientist as an additional abstraction layer of interoperation.

PURPOSE-BUILT HIBERNACULA FOR BATS – ARE THEY FUNCTIONAL? [P]

ERIC A. JANSEN[1], VITA J.A. HOMMERSEN[1]**, HERMAN J.G.A. LIMPENS [1], MARCEL J. SCHILLEMANS[1], MAURICE LA HAYE[1], MARTIJN VAN OENE[1],
**vita.hommersen@zoogdiervereniging.nl
[1]*Dutch Mammal Society, Nijmegen, The Netherlands.*

In many lowland areas bats are mostly restricted to artificial buildings and other underground structures for hibernation. An increasing economic pressure stimulates either the re-use of these structures or their demolition to make space for new developments. This results in bats loosing many of their (to us unknown) hibernation sites. To compensate for this loss of hibernation sites, the first purpose built hibernation structures were built in 1984. Between 1984 and1991, on average two structures intended as underground bat hibernacula, were built per year. Change in subsidy policies and the discovery of cheaper ways to build underground sites accelerated the construction of new hibernacula. Between 1991 and 2015, between 6 and 12 structures were built annually. These structures were mainly built as active conservation measures, often as a part of local landscape enhancements. We estimate at present 200 purpose-built bat hibernation structures exist in the Netherlands. However, the effectiveness of these purpose-built hibernation structures is often debated between conservationists. To gain insight in the effectiveness of these structures in the Netherlands, we analyzed the database containing all hibernation counts of the Dutch Mammal Society, which is managed within the framework of the Network Ecological Monitoring (NEM). Among all hibernation sites we focused on purpose-built structures. The structures used in our analysis varied from smaller square concrete profiles covered with earth (4– 20 m^2) to larger and more complex structures (> 50 m^2). We checked what proportion of these purpose-built structures is used by hibernating bats, calculated the time since construction and what proportion seems not to be used even after prolonged waiting times. We try to correlate these data with volume, type of surrounding landscape, distances to known traditional hibernacula, differences in regional densities of different bat species (in winter) and on-site climate conditions.

THE DUTCH MONITORING SCHEME FOR FOUR COMMON BAT SPECIES NOT COVERED IN THE HIBERNATION AND SUMMER ROOST COUNTS [P]

ERIC A. JANSEN[1]**, VITA J.A. HOMMERSEN[1], MARTIJN VAN OENE[1], NEELTJE HUIZENGA[1], MARCEL J. SCHILLEMANS[1], HERMAN J.A.G. LIMPENS[1], TON VAN DER MEIJ[2], HANS HOLLANDER[3], **eric.jansen@zoogdiervereniging.nl
[1]*Dutch Mammal Society, Nijmegen, The Netherlands;*
[2]*Statistics Netherlands, The Netherland;*
[3]*Arcadis, The Netherlands.*

The goal of this project is to identify the national trend within five years of four bat species currently not covered in other monitoring schemes. Three species, common pipistrelle (*P. pipistrellus*), common noctule (*N. noctula*) and serotine (*E. serotinus*), are widespread and common but differ in landscape use and regional densities. The fourth species, Nathusius's pipistrelle (*P. nathusii*), is a migratory species. Our aim is to get at least 90 fixed car-transects of 30 km outside urban areas, sampled twice per year. We expect that within five years we can generate reliable trends for these species. Within each transect there should be at least 7 contacts with all four target species. The transects are sampled twice during favourable weather within a 10-day period during the post lactation period. We choose not to use a random design. We pre-selected our sampling areas by allowing transects only in areas were the four species are present simultaneously (based on previous distribution data). We stratified the design further towards serotine bat and noctule, by using the time window Sun Set +1/4hr to Sun Set +1½ hour and having transects alongside more favourable habitats. The transects should not run close to (known) roost-sites. We chose to do car transects with newly recruited volunteers using real-time recorders with onboard GPS system. Furthermore we chose to have groups of 4-7 volunteers managing 3 transects per year. This reduces volunteer management-time and enhances the groups' responsibility to deliver collectively. We invest time in training volunteers in plotting the transect and in analysing the recordings and to upload the results of the analyses. We offer them different forms of additional help; Manuals, FAQ, Helpline, Forum. We regularly make contact to improve our volunteer management. Raw data is scrubbed and identified by volunteers to species level or to species-group level by use of freeware software. Wave-files containing bat calls and metadata are uploaded to a server. Species are verified manually by a bat expert. Individual volunteer skill and level of species difficulty are explicitly taken into account. Verified data is checked against a set of constraints. Detection probabilities are calculated per species and per year by Statistics Netherlands, as also are population and distribution trends based upon occupancy modelling and N-mixture models. Arguments for use of this sampling method are: 1) can be applied in many landscapes nationwide, 2) all four species in one effort, 3) both quantitative and distribution data. Results are: 1) widespread scheme, with 120 volunteers, 2) enough contacts for all four species on transect, 3) good reproduction of results (high detection probability of target species), 4) bonus species: *N. leisleri*, *M. dascyneme*, *M. myotis*, *V. murinus*, *P. pygmeus*.

THE IMPORTANCE OF DUTCH DIKES AND COASTAL AREAS FOR MIGRATING BATS: FIVE YEARS OF BAT MONITORING AT THE COASTAL ZONE OF THE NETHERLANDS [P]

BOB JONGE POERINK[1]**, JASJA J.A. DEKKER[2], JANNES HEUSINKVELD[1],
**bob@fieldworkcompany.nl
[1]The Fieldwork Company. Van Schendelstraat 1, 9721 GV Groningen, The Netherlands;
[2]Jasja Dekker Dierecologie, Enkhuizenstraat 26, 6843 WZ Arnhem, The Netherlands.

In the last few years passive ultrasonic recorders have given bat researchers the possibility to monitor bat activity at remote areas during the entire bat season. In 2011 we started to monitor bats with passive recorders at several survey sites along the coast of the Netherlands. Coastal areas previously thought to be of minor importance for bats appeared to be of major importance for bats during the migration season. Especially Nathusius's pipistrelle (*Pipistrellus nat*husii) was found in large numbers in the coastal region, as well as parti-coloured bat (*Vespertilio murinus*) and noctule bat (*Nyctalus noctula*). Bats are highly dependent on sufficient food availability during migration. Specific ecosystems and landscape elements serve as an important food source for these bats, as they provide massive numbers of insects, in particular non-biting midges (Chironomidae). The importance of chironomid rich environments like dikes, estuaries and reed beds for migrating bats in the coastal zone of the Netherlands needs to be incorporated into bat-friendly infrastructure and habitat design and management.

SANGER AND NEXT-GENERATION SEQUENCING BASED NUCLEAR GENETIC ANALYSES OF THE LONG-FINGERED BAT, *MYOTIS CAPACCINII* AROUND THE MEDITERRANEAN BASIN [P*]

KÜBRA KARAMAN[1]**, ASLI SALCIOĞLU[1], KANAT GÜRÜN[1], EMRAH ÇORAMAN[1], ANDRZEJ FURMAN[1], AHMET KARATAŞ[2], RAŞIT BİLGIN[1], **krmn.kubra@gmail.com
[1]*Institute of Environmental Sciences, Boğaziçi University, 34342 Bebek, İstanbul, Turkey;*
[2]*Department of Biology, Niğde University, Niğde, Turkey.*

Myotis capaccinii, the long-fingered bat, has a wide distribution in the western Palearctic, covering the Mediterranean basin and spreads into North Africa, and reaching Anatolia and Iran to the east. It is considered to be polytypic with a taxonomic break in the former Yugoslavia. A recent mitochondrial DNA analysis with samples from the Mediterranean coasts of Europe, North Africa, Anatolia and Iran showed the presence of two genetic breaks; a deeper one in southeastern Europe, and a more recent one around the Alps, potentially corresponding to species and subspecies level differentiation, respectively. In this study, first, using a nuclear intron marker, we aimed to see whether these mitochondrial DNA breaks were reflected in the nuclear DNA as well. The results indicated no parallel differentiation in nuclear DNA, suggesting conspecificity of all three mitochondrial groups. However, the lack of differentiation could be due to the lack of resolution of the intron marker. Therefore, more detailed analyses with ddRAD-seq which is a higher resolution marker were conducted. The ddRAD structure, spanning over 3000 loci, paralleled the mtDNA differentiation. The ddRAD and mtDNA structure suggests that the three lineages could be considered different species, although further morphological analyses are necessary for their confirmation.

**SITKA SPRUCE PLANTATIONS:
A POTENTIAL OPPORTUNITY FOR BAT POPULATIONS? [O]**

LUCINDA KIRKPATRICK[1]**, KIRSTY PARK[2], **lucinda.kirkpatrick@uantwerpen.be
[1]*University of Antwerp, Belgium;*
[2]*University of Stirling, U.K.*

Despite their large size, and predominance in some landscapes, commercial coniferous plantations are probably one of the least studied bat habitats. Therefore, although there is some evidence of bat associations with plantations, forest managers have relatively little information about the effects of management on the provision of foraging and roosting sites for bats. In this study, we surveyed three large, intensively managed Sitka spruce dominated plantations in Scotland and North England to determine bat composition in the plantations, assess how *Pipistrellus pygmaeus* makes use of plantations during pregnancy and lactation, and we assess the impact of alternative energy generation through wind turbines on bats in commercial plantations. We recorded 9 species, although activity was dominated by *P. pygmaeus* and *P. pipistrellus*. We found that bats were using commercial coniferous plantations extensively, with activity concentrated in low density or felled areas. This was confirmed through acoustic surveys, trapping and radiotracking. Lactating female *P. pygmaeus* roosted in large (500 plus) colonies in and around the plantation area, with individuals flying up to 40km in a single night to access preferred foraging areas, suggesting that food availability is sufficient to render such a journey energetically viable. Finally, we found that bat responses to clearfelling were species-specific and determined to some extent by the scale of felling. We suggest that bat use of commercial plantations is limited by roost availability and may be linked to the high seasonal abundance of the highland midge, *Culicoides impunctatus*. We provide some recommendations for management practice that will benefit bat populations, including the provision of alternative roosts. Keyhole felling for wind turbine installation may pose a direct threat for bat populations in commercial plantations and further research is necessary to determine the potential impacts of siting wind turbines in commercial plantations.

HABITAT SELECTION OF THE BARBASTELLE BAT (*BARBASTELLA BARBASTELLUS*) DURING LACTATION IN SWEDEN – PRELIMINARY RESULTS [P]

TOMASZ KOKUREWICZ[1]**, GRZEGORZ APOZNÁNSKI[1], STEFAN PETTERSSON[2], SONIA SÁNCHEZ-NAVARRO[3,4], JENS RYDELL[4], **tkokur@gmail.com
[1]Wrocław University of Environmental and Life Sciences, Institute of Biology, Department of Vertebrate Ecology and Paleontology, Kożuchowska 5b, 51-631 Wrocław, Poland;
[2]EnviroPlanning AB, SE-411 04 Göteborg, Sweden;
[3]Department of Evolutionary Ecology, Estación Biológica de Doñana-CSIC, Américo Vespucio s.n., Sevilla 41092, Spain;
[4]Lund University, Biology Department, SE-223 62 Lund, Sweden.

The province of Halland in southwestern Sweden is a stronghold for the barbastelle bat in northern Europe. Bats (2 males and 8 females) were captured in mist nets, measured, weighed and checked for sex and reproductive status. LB-2X transmitters (0.32 g; Holohil Systems) were attached to them by using bonding adhesive (Torbot). Tagged bats were subsequently followed by three tracking teams during 13 consecutive nights (25 July - 7 August 2016) using three Australis 26k receivers with Y-3 antennae (Titley Electronics). We identified 47 feeding sites used by the bats, most of them located in or near pockets of mature deciduous woodland or wooded wetland including bogs and mires and, in a few cases, in stands of mature spruce trees. Many regularly used feeding sites were located 10-14 km west of the maternity roost, about 3 km on either side of the boundary between forest and open farmland to the west, and included several small isolated patches of woodland on open farmland. The bats freely crossed quite extensive (1-2 km) open areas, including crop fields, young spruce plantations and lakes on their commuting flights. Minimum convex polygons encompassing all fix points of the eight females and two males separately, showed that the females used an area of 64 km^2, while each of the two males used 11 km^2. Current practices for the conservation of barbastelles in Sweden and elsewhere in Europe are based on establishment of a protected zone around each known maternity colony. The suggested areas of the zones are based on radio-telemetry studies and vary from 2 km radius in Sweden to 7 km in England. In our case, this approach would be inefficient, regardless of chosen zone size, because most of the area used by the females and all of that used by the males would fall outside of the protected circle. We suggest that the conservation efforts should instead focus on the preservation and restoration of the remaining woodland patches maintaining a diverse tree species and age structure.

AN INFLUENCE OF CLIMATIC FACTORS ON NUMBERS OF BATS HIBERNATING UNDERGROUND – THE CONSEQUENCES FOR METHODOLOGY OF WINTER MONITORING [O]

TOMASZ KOKUREWICZ[1]**, LUCINDA KIRKPATRICK[2], ANITA GLOVER[3], JOHN HADDOW[4], CHRISTIANE SCHMIDT[5], HENRY SCHOFIELD[3], FONS BONGERS[6], KAMILA WILLEMS[7], GRZEGORZ APOZNAŃSKI[1],
**tkokur@gmail.com
[1]*Wrocław University of Environmental and Life Sciences, Institute of Biology, Department of Vertebrate Ecology and Paleontology, Kożuchowska 5b, 51-631 Wrocław, Poland;*
[2]*Evolutionary Ecology Group, University of Antwerp, Prinsstraat 13, 2000 Antwerp, Belgium;*
[3]*The Vincent Wildlife Trust, 3 & 4 Bronsil Courtyard, Eastnor, Ledbury, Herefordshire HR8 1EP, U.K.;*
[4]*Auritus Wildlife Consultancy Ltd, 27 Balmoral Court, FK15 9HQ, Dunblane, U.K;*
[5]*Landesfachausschuss Fledermausschutz, Fachgruppe Fledermausschutz, Dresden, Germany;*
[6]*Schoolweg 15, 1191 JP Ouderkerk a/d Amstel, The Netherlands;*
[7]*Masaryk University, Faculty of Science, Department of Botany and Zoology, Kamenice 753/5, 625 00 Brno, Czech Republic.*

Significant fluctuations in numbers of bats hibernating underground, exceeding 30% of the values recorded in previous years, indicates that environmental factors affecting hibernation strategies are masking the real population trends. Additionally, global warming, making it possible for cold-dwelling species to hibernate in less insulated hibernacula (e.g. tree holes), makes these estimations more difficult than in the past. There is an urgent need to model these factors to obtain reliable data about the conservation status of bat species and to apply successful protection measures in proper time. We applied generalized linear mixed effect models to the results of the bat monitoring programme carried out from 1999 in the Natura 2000 site "Nietoperek" (Poland), to describe the influence of autumn and winter temperatures and precipitation on bat numbers recorded during bat censuses in January. We hypothesised that climatic factors may influence: (1) autumn fat accumulation, leaving some bats with low body reserves and in consequence forcing them to hibernate in more stable microclimatic conditions in crevices where the animals are less likely to be detected by observers, (2) long distance autumn migrations, bats resting at stopovers before reaching the final hibernation place, (3) winter feeding, making it possible for bats to leave underground sites in winter, (4) winter bat movements from less insulated to better insulated hibernacula when the ambient temperatures are staying below freezing point for prolonged periods. Unexpectedly, the strongest influence on numbers of *M. myotis*, *M. daubentonii*, *M. bechsteinii*, *M. dasycneme*, *B. barbastellus* and *P. auritus* in January were precipitation and temperatures in September and October (r^2 = from 0.57 to 0.76) probably affecting long distance migrations and fat accumulation. The number of frosty days (Tdaily max <0°C) and temperatures in December and January, previously considered as important, did not have significant influence in the used models.

EVOLUTION OF MOVEMENT MODE AND OF LONGEVITY [P]

KLEMEN KOSELJ[1]**, KAMIL A. BARTOŃ[2], IRENEUSZ RUCZYŃSKI[3]**,
**koselj@orn.mpg.de
[1]*Max Planck Institute for Ornithology, Seewiesen, Germany;*
[2]*Institute of Nature Conservation, Polish Academy of Sciences, Kraków, Poland;*
[3]*Mammal Research Institute, Polish Academy of Sciences, Białowieża, Poland.*

According to evolutionary theory of ageing, longevity can only evolve in species with low mortality due to extrinsic factors. Namely, if early death by predation, disease etc. is probable, the animals with costly adaptations for longevity are mostly prevented from receiving their fitness benefits. After correction for the low body size, bats are the record holders in longevity among mammals. Together with the lifespans of other endotherms capable of flight or climbing (birds, arboreal and gliding mammals), the longevity of bats appears to support evolutionary theory of ageing. Ageing rate is directly related to mortality risk in birds and mammals and active flight enables birds and bats to be more successful at avoiding predators. But is this the only mechanism by which flight can contribute to the evolution of longevity? We used individual-based models to disentangle confounding effects of flight on life span evolution. We tested if increased foraging efficiency and resource availability enable flying animals to reduce the risk of starvation, thereby favouring longevity evolution. In our simulations alleles determining movement mode, offspring size and longevity were allowed to mutate. Aerial foragers had higher metabolic cost of movement per unit time and lower per unit distance than ground foragers and were moving faster. We manipulated energy content and regrowth time of prey, energy capacity of foragers, offspring cost, prey distribution (patchiness) and predation rate. Foragers could die either of age, by predation or by starvation. Evolution of longevity was connected with high costs of offspring and was more likely in aerial than ground foragers. We found that beside high predation, intense competition for food can prevent evolution of longevity. Our results demonstrate that the interplay of factors ranging from environmental parameters to movement mode and physiology, influences evolution of life histories in a more complex manner than previously assumed.

FOOD AVAILABILITY AFFECTS ENERGY MANAGEMENT AND REPRODUCTIVE TISSUE DEVELOPMENT IN MALE PARTI-COLOURED BATS, *VESPERTILIO MURINUS* [O]

EWA KOMAR[1], DINA K.N. DECHMANN[2], MAAREK ZEGAREK[1], PAULINE SZAFRAŃSKA[1], IRENEUSZ RUCZYŃSKI[1]**, **iruczyns@ibs.bialowieza.pl
[1]*Mammal Research Institute PAS, Białowieża, Poland;*
[2]*Max Planck Institute for Ornithology, Radolfzell, Germany.*

Bats can reduce metabolic rate and decrease body temperature to allocate more energy to fat deposition during unfavourable conditions. However, torpor also affects and slows down important processes, such as foetal development or potentially sperm production. This might be crucial for male reproductive success due to high sperm competition. Rare social groups of male temperate bats are postulated to be a counter-strategy to this to increase foraging success and reduce the need for daily torpor, allowing earlier sperm production. We experimentally manipulated food availability for captive male parti-coloured bats, to verify the effect on their thermoregulatory patterns as well as the development of testes, filling of the epididymis and body condition. We found no significant correlation between food regime and the duration or depth of torpor bouts. Regardless of the food restriction all males maintained relatively high body temperature until sperm had been produced. However, ad libitum-fed males finished spermatogenesis up to half a month earlier. From then on they rapidly gained weight as well as decreased their resting metabolic rate. Males that maintained more stable and higher body temperature finished sperm production earlier. Our results indicate that bats under limited food availability are forced to trade-off between investment into reproductive tissue or fat. The project was funded by the Polish National Science Centre grant: DEC-2013/10/E/NZ8/00725.

REPRODUCTION AND POST-NATAL GROWTH OF *RHINOLOPHUS HIPPOSIDEROS* ROOSTING IN ILLUMINATED BUILDINGS [O]

JASMINA KOTNIK[1]**, KLEMEN KOSELJ[2], MAJA ZAGMAJSTER[3],
**jasmina.kotnik89@gmail.com
[1]*Department of Biology, Biotechnical Faculty, University of Ljubljana, Jamnikarjeva 101, SI-1000 Ljubljana, Slovenia;*
[2]*Max Planck Institute for Ornithology, Eberhard-Gwinner-Straße, D-82319 Seewiesen, Germany;*
[3]*Department of Biology, Biotechnical Faculty, University of Ljubljana, Jamnikarjeva 101, SI-1000 Ljubljana, Slovenia.*

Human influences on the planet are ubiquitous and they affect wildlife in multiple ways. For many bat species, human buildings provide additional roosting sites. These are particularly abundant in older buildings that are part of the cultural heritage. In the past few decades, such buildings have been increasingly illuminated at night. It has been shown that illuminating the flight access points can delay the emergence of bats from the roost and that artificial light at night affects food availability outside the roost. However, it is still poorly understood to what extent these effects influence reproductive success of bat populations. Here, we manipulated the illumination of three churches with nurseries of *Rhinolophus hipposideros* in central Slovenia, to investigate its effect on several parameters of reproductive success, e.g. the number of juveniles present and their growth. Each church has been illuminated either with very intensive light as originally present, or with adjusted illumination that is shaded bluish light or shaded yellowish light. These treatments were exchanged among the churches over three consecutive years. We visited each roost at least ten times per season and when juveniles were present, measured their body mass and forearm length. The start of parturition varied more strongly between the years than between the churches. Up to one day old bats (umbilical cord present) were recorded in a period of up to 15 days per roost, and juvenile bats with closed eyes even up to 31 days in a single roost. Growth rate varied little among illumination treatments; however we always observed a lower mass of nursing females in one church that had the lowest forest cover in the surroundings. This shows that multiple factors can influence reproductive success in a complex and intertwined manner. Our study demonstrates that addressing these factors in a systematically controlled manner is necessary to provide a reliable support for conservation strategies.

UNHEEDED DIVERSITY: ATTEMPT TO REVISE GENUS BARBASTELLA (PLECOTINI, VESPERTILIONIDAE) [P]

SERGEI V. KRUSKOP[1]**, KUNIKO KAWAI[2], MIKHAIL P. TIUNOV[3],
**selysius@mail.ru
[1]*Zoological Museum, Moscow State University, Moscow, Russia;*
[2]*Field Science Center for Northern Biosphere, Hokkaido University, Sapporo, Japan*
[3]*Instiutute of Biology and Soil Sciences RAS, Vladivostok, Russia*

The genus *Barbastella* has a vast distribution area from Great Britain and Canary Islands to Japan and Taiwan. Nonetheless, for many decades only two species were accepted occurring in all that range, with very limited total number of named forms. However, first serious morphological approach had shown that Asian *B. darjelingensis* and *B. leucomelas* from Sinai are not conspecific. Following studies from an isolated population in Beijing revealed a fourth separate species. Our analyses of mitochondrial genes cox I and cyt-b, demonstrate that the specimen from the Nepalese Himalayas (tentatively represent typical *B. darjelingensis*) is different from Asian specimens, usually assigned to the same species. Morphological comparison of 118 collection specimens, mainly from the *Barbastella* genus´ distribution range, let us reveal some undescribed or unaccepted taxa. Firstly, independent status of the Central Asian barbastelles was shown and the species name *B. caspica* was revived. All the other lineages within the genus inhabit mainly in forested areas and are similar in overall size and fur coloration. Two of them – one from south-west China, northern Indochina and Taiwan, and another from Japan and Kuril Islands – have no less than 10% divergence of mtDNA from other named forms. Principal Component analysis demonstrates quite limited overlap between Japanese race and "typical" *B. darjelingensis*. Discriminant Function analysis significantly discriminates Japanese samples from all other, and demonstrates that samples from Hokkaido and Honshu definitely belong to the same set. Besides, fur coloration and structure of Japanese animals differ somewhat from those of Asian mainland. Thus, there is no doubt about the separate taxonomic status of the Japanese form. Finally, despite being Chinese/Vietnamese lineage different, it is hardly distinguishable from *B. darjelingensis* and its status requires further revision.
The work was done with partial support thanks to RFBR 17-04-00689 and RNF 14-50-00029 grants.

TWINS OR COUSINS: TWO SPECIES OF "DESERT" LONG-EARED BATS (*PLECOTUS*; VESPERTILIONIDAE, CHIROPTERA) COEXISTING IN MONGOLIA [O]

SERGEI V. KRUSKOP[1]**, IRINA V. KURDYUKOVA[3], ILIYA V. ATRYUSHIN[2], VLADIMIR S. LEBEDEV[1], **kruskop@zmmu.msu.ru
[1]*Zoological Museum, Moscow M.V. Lomonosov State University, Moscow, Russia;*
[2]*Department of Vertebrate Zoology, Biological Faculty, Moscow M.V. Lomonosov State University, Moscow, Russia;*
[3]*Faculty of Biology and Chemistry, Moscow State University of Education, Moscow, Russia.*

The use of molecular methods totally changed the understanding of the genus *Plecotus*. Instead of the 2 to 4 previously accepted species, the presence of up to 19 putative species was shown, and later this amount has been even further enlarged. Though some of these species possess overlapping distribution areas and are sympatric in some territories (which implies their species status), most of Asiatic members of the genus demonstrate allopatric or parapatric distribution. Meantime, interrelations between some of those forms seem to be unclear and require revision. Studies in Mongolia reveal the presence of two putative *Plecotus* species in this country, adapted to the arid climate. According to some features, these two forms were provisionally associated with names *Plecotus kozlovi* and *P. turkmenicus*. Further studies have shown that both forms in southern Mongolia coexist in some areas and even in the same habitats, though little is known about their natural history. The two taxa are very close morphologically. They possess some qualitative features in dentition and baculum shape, which however may be treated as either interspecific or interpopulation characteristics, due to additional arguments. Morphometric PCA analysis did not reveal any difference in skull shape between the two forms, though well-discriminates them from two other Asian species – *P. ognevi* and *P. strelkovi*. Mitochondrial DNA divides these forms very substantially, making *P. kozlovi* a sister lineage to Siberian *P. ognevi*. In that case one may suppose that "*P. kozlovi*" represents a *P. turkmenicus* population with introgression of mtDNA from *P. ognevi*. However, preliminary data on nuclear DNA have also shown differences between the two forms, suggesting a more complicated microevolutionary scenario than just occasional ancient hybridization. This work was done with partial support from grants RFBR 17-04-00689 A and RNF 14-50-00029.

WHAT PROPORTIONS MAY TELL: CRANIO-DENTAL MORPHOMETRY IN COMMON SEROTINES *(EPTESICUS SEROTINUS S.* LATO; VESPERTILIONIDAE, CHIROPTERA) [P]

SERGEI V. KRUSKOP[1]**, VLADIMIR S. LEBEDEV[1], **kruskop@zmmu.msu.ru
[1] *Zoological Museum, Moscow M.V. Lomonosov State University, Moscow, Russia.*

In the last decade true serotines and in particular *Eptesicus serotinus* species complex became subjects of heated discussions in respect to their taxonomy. However, the majority of recent taxonomic conclusions were made mostly on genetic data (in accordance to the "genetic species concept"). To understand how morphological and genetic variability correlate within the complex, a set of 22 cranial and dental measurements was analyzed. Measurements were taken from 298 full-grown specimens, most of which were examined genetically or can be unequivocally assigned to a particular genetic clade. We used the model-based clustering algorithm as implemented in MCLUST software to determine the number and composition of clusters present in the morphometric data. For the complete data set as well as for size-adjusted data the optimal delimitation suggests the existence of three clusters that correspond essentially to the major taxonomic subdivisions of *E. serotinus s.*lato: *E. s. serotinus, E. s. turcomanus* and *E.* [*s.*] *pachyomus.* Less than 14% of specimens were identified incorrectly (i.e. not in agreement with a priori expectations). All Taiwanese and Korean specimens and most of specimens from India, Pakistan and south-east Iran were included in the "pachyomus" cluster. Generally, *"serotinus"* and *"turcomanus"* clusters seem to be slightly more similar to each other than to "pachyomus". The sample of *"shirazensis"* from Syria demonstrates strong association with the *"serotinus"* cluster. Samples from the Caucasus and, surprisingly, from the Syrdariya valley (central Kazakhstan) fall close to both *"serotinus"* and *"turcomanus"* clusters. Some of the analyses based on a reduced set of dimensions produced a larger number of clusters. New clusters are associated with several local samples otherwise belonging to *"pachyomus",* thus, indicating pronounced geographic variation within *E.* [*s.*] *pachyomus.* The work was done with support from grants RFBR 17-04-00689 А and RNF 14-50-00029.

THE UTILIZATION OF BAT HIBERNATION ROOSTS BETWEEN MAY AND AUGUST IN GERMANY [P]

KARL KUGELSCHAFTER[1]**, EDMUND HENSLE[2], HERBERT FRIEDRICH[3], MARKUS SCHMID[2], **karl.kugelschafter@chirotec.de
[1]ChiroTEC - Monitoring Technology & Ecological Consultancy, Germany;
[2]Bat Working Group Baden-Wuerttemberg, Germany;
[3]Bat Working Group Hessen, Germany;
[4]Bat Working Group Baden-Wuerttemberg, Germany.

Sampling procedures using mist nets at the entrance of hibernation roosts have revealed that bats are most abundant in late summer during autumn swarming. Systematic investigations of bat abundance at winter roosts in summer time have not been carried out. During our studies three hibernation sites have been investigated: two karst caves in southern Germany with 300 and 600 hibernators respectively and a slate mine in West Germany with 1,700 hibernating bats. Species dominance varied between *Myotis myotis*, M. *emarginatus* and *M. bechsteinii* in combination with *M. nattereri*. All three roosts were equipped with automatic light barriers and additional camera systems to register bat activity and document species abundance on photos. Most striking was the huge difference in species abundance at the roosts among the dominant species. While *M. emarginatus* showed a continuously high activity at the hibernation site, *M. myotis*, *M. bechsteinii* and *M. nattereri* were much less active in summer time. This summer gap was especially pronounced in *M. myotis* which only returned to the hibernation site in early August. Swarming activity at the winter roosts was registered for *M. bechsteinii* and *M. nattereri* in springtime. While autumn swarming in *M. bechsteinii* started already in the second half of July, *M. nattereri* returned to the hibernation site only by mid-August.

HOW PRECISE ARE POPULATION COUNTS AT HIBERNATION SITES? [P]

KARL KUGELSCHAFTER[1]**, THOMAS HORVATH[1], BJÖRN SPRUCK[1],
THOMAS VOLK[1], **karl.kugelschafter@chirotec.de
[1]*ChiroTEC - Monitoring Technology & Ecological Consultancy, Germany.*

Visual population counts of hibernation colonies have a long tradition in Germany. They are usually carried out in January/February when each roost is visited once and, depending on its size and accessibility, parts of it or the complete site are searched for bats. The established data form the basis for population trends. Until the recent past no method existed to verify the count results. Using automatic light barrier systems, which are installed in the roost openings, arriving and departing bats are counted and can be subtracted to calculate the number of hibernators. In this poster the results of visual and automatic hibernation counts will be presented. Roosts investigated were natural caves, mines with tunnel systems of several kilometres and bunkers that, from visual estimations, contained between several dozen and several hundred bats. The most important result was that the automatically established population sizes were always higher than the visually estimated ones. In the bunker "Krusenkoppel" in northern Germany, 125 bats were counted visually in 2015, while automatic counts revealed a population of 274 bats. The highest discrepancy was revealed in the slate mine "Hörre", where the highest visually established number was 60 bats in 1994 (53 in 2004) while automatic counts revealed a population of 3,500 individuals in 2016 (60 times higher than visual counts in the same year). Unfortunately, a constant factor cannot be applied, since it is different for every roost. The huge discrepancy between manually and automatically established data highlights the necessity to apply modern techniques in order to reach realistic results and evaluate the importance of spacious roosts.

NEW INSIGHTS INTO THE HIBERNATION STRATEGY OF BECHSTEIN'S BAT (*MYOTIS BECHSTEINII*) IN GERMANY [O]

KARL KUGELSCHAFTER[1]**, CHRISTIAN KREIDLER[1], HERBERT FRIEDRICH[2], JOSEF KÖTTNITZ[2], **karl.kugelschafter@chirotec.de
[1]*ChiroTEC - Monitoring Technology & Ecological Consultancy, Germany;*
[2]*Bat Working Group Hessen, Germany.*

Little is known about how and where Bechstein's bat spends its winter. For example, it has been suggested they hibernate in tree cavities, as in the region of highest abundance within Central Hessen/Rhineland Palatinate only few individuals were detected in the many subterranean hibernation sites investigated. Recent results of our studies, using infrared light barrier systems, show that Bechstein's do use the regionally very abundant slate mines as hibernation roosts where they gather in "mass-aggregations" of up to several hundred individuals. The number of hibernating Bechstein's in the mine "Grube Abendstern" in Central Hessen regularly reaches up to 600 individuals. Some other underground roosts, surveyed with the same method, provide shelter for a similar number of individuals. A particular characteristic of this species is that it can be found at its hibernation site all year round. Their activity peak was between mid-August and mid-September, while already in early September the first individuals started hibernating. By the end of November the last hibernators entered the roost, where they disappeared for several months and only re-appeared from their hiding places in the first half of March. In the last third of April, until early May, most of the Bechstein's left the hibernation site. Shortly afterwards, they reappeared at the roost. This "visitation phase" lasted until June, followed by a short phase of absence, and the cycle started over again.

BATS AND PESTS: ECOSYSTEM SERVICES AT PARQUE NATURAL DO VALE DO TUA, PORTUGAL [P]

PEDRO LEOTE[1]**, VANESSA MATA[2], HUGO REBELO[2,3,4], ARTUR CASCAREJO[1], PEDRO BEJA[2,3], **pedroleote@valetua.pt
[1]PNRVT, Parque Natural Regional do Vale do Tua, Mirandela, Portugal;
[2]CIBIO-InBIO, Centro de Investigação em Biodiversidade Recursos e Genéticos, Universidade do Porto, Vairão, Portugal;
[3]CEABN-InBIO, Centro de Ecologia Aplicada "Prof. Baeta Neves", Instituto Superior de Agronomia, Lisboa, Portugal;
[4]School of Biological Sciences, University of Bristol, Bristol, U.K.

A project to promote pest control ecosystem services by bats has been implemented by the Parque Natural Regional do Vale do Tua (PNRVT) and Centro de Investigação em Biodiversidade e Recursos Genéticos (CIBIO) in the Trás-os-Montes region, northwest Portugal, to compensate for the ecological impact of the construction of the Tua river mouth dam. Owing to the flooding of the basin, a considerable amount of land has been lost, both ecologically and economically, since the region's economy is heavily based on the production of wine, olive oil and cork. To counter this loss of land and the impacts it has on landowners and wildlife, PNRVT has begun to set up integrative projects that will benefit stake-holders and ecosystems alike. The first one to take place aims to increase pest control by bats and to supply the existing populations with shelters to reduce the impact of habitat loss, simultaneously reducing the costs of production for landowners. Fifty wooden poles have been placed, each with two different bat box models, Schwegler 2FN and 2F, in land with vineyards, olive tree orchards and cork tree woods, to facilitate the establishment and increase of bat populations. The boxes are regularly monitored for the presence of guano, to evaluate which bat species are more relevant to pest control in each cropland, and environmental education workshops will be carried out to raise awareness in the local population. This project aims to help in preserving the biodiversity within the PNRVT, whilst working closely with the landowners and providing them with a service that translates into measurable financial gains. A study of the diet of bats using cutting-edge molecular tools will further our current knowledge regarding the role of bats as pest regulators in fragmented agricultural landscapes. The project will minimize the impact of agriculture by reducing the use of pesticides, providing information to guide management and ensure a sustainable development of the region.

DIFFERENCES IN WHOLE-TRANSCRIPTOME GENE EXPRESSION CONTROL SUSCEPTIBILITY TO WHITE-NOSE SYNDROME IN *MYOTIS LUCIFUGUS* AND *EPTESICUS FUSCUS* [O]

THOMAS M. LILLEY[1,2]**, DEEANN M. REEDER[2], JENNI M. PROKKOLA[2], KEN A. FIELD[2], **tmlill@liverpool.ac.uk
[1] *University of Liverpool, U.K.;*
[2] *Bucknell University, U.K.*

White-nose syndrome in North America bats is caused by *Pseudogymnoascus destructans* (Pd), a psychrophilic fungus that grows in the cold hibernacula and causes cutaneous infections in bats while they hibernate. The infection disrupts hibernation behaviour and leads to more frequent arousals from torpor, premature energy depletion, and death of susceptible bats. Susceptible species, such as *Myotis lucifugus* have shown population declines greater than 90% in affected hibernacula. Populations of some other North American species, such as *Eptesicus fuscus* are not affected as severely. In this experiment, we look at differences in responses to Pd-infection in two species of bats, one susceptible (*M. lucifugus*) and the other apparently resistant (*E. fuscus*). By measuring gene expression at the whole-transcriptome level, we compared expression patterns between experimentally hibernated, infected and uninfected bats of both species during the hibernation period. We hypothesize that components of the immune system, which are up-regulated in hibernating Pd-infected *M. lucifugus*, could respectively contribute to resistance in *E. fuscus* by being down-regulated. Results will be presented on differences in gene expression between species during hibernation, while cutaneous infections were observed by histopathology. We discuss how the responses of the immune system in infected *M. lucifugus* play a role in events that lead to the drastic population declines in this species.

A MODEL FOR THE ASSESSMENT OF FAVOURABLE CONSERVATION STATUS OF BATS IN A SPECIFIC PLANNING PROPOSAL AREA [O]

HERMAN J.G.A. LIMPENS[1]**, MARCEL J. SCHILLEMANS[1], ERIC A. JANSEN[1], VITA J.A. HOMMERSEN[1], **herman.limpens@zoogdiervereniging.nl
[1]*Dutch Mammal Society, Nijmegen, The Netherlands*.

Conservation decisions and licensing in the EU are dependent on Favourable Conservation Status (FCS) of species. Criteria for assessment of FCS can be deduced from the European Habitats Directive. The criteria are formulated from the viewpoint of assessment on a larger national scale, and in development and planning need to be translated to a smaller and practically applicable scale. Criteria for assessment of FCS of a species are data on population dynamics (size, trend), range, size and quality of habitat. Population data need to indicate a long-term viability of the species and its natural habitats. At present and in the foreseeable future, the natural range (occurrence and distribution) needs to be maintained, and the habitat needs to be of sufficient size and quality to maintain its populations on a long-term basis. For the smaller scale of an individual development project, or e.g. a municipality, assessment of population size and trend of a species in absolute numbers is difficult to achieve. The range of a species will rather reflect the available habitat, where the available habitat (size and quality of roosting, foraging habitat and connective habitat) is a relevant criterion, which can be surveyed and monitored. The long-term aspects of the requirements demonstrate the need to ensure availability of key habitats and measures to maintain these. We developed a table to score available information reviewing population size, trend, and occurrence, distribution and quality of the habitat(s) in five classes. Through assessment on different scale levels, the information used to evaluate criteria on the level of an individual development proposal is put into a larger context. Through assessing information for different time periods, both instant and long-term effects and requirements are incorporated. Cells that cannot be scored illustrate data deficiency and the need for further active survey and/or research. Scoring with/without mitigation measures reveal the need for mitigation measures.

COMPLEX HYBRIDIZATION BEFORE COMPLETE SPECIATION: INTERESTING MITO-NUCLEAR DISCORDANCES AMONG THREE *RHINOLOPHUS* SPECIES [O*]

TONG LIU**, KEPING SUN, JIANG FENG, **liut035@nenu.edu.cn
[1]*Northeast Normal University, China;*
[2]*Jilin Agricultural University, China.*

Increasingly studies uncovered hybridization between mammalian taxa in recent years, but the roles hybridization play during speciation are still unclear. Horseshoe bats have diverse phenotypes, disperse by flight, roost in mixed colonies, and are thought to have undergone rapid speciation, and so may present good candidates. In this study, we combined morphological (external, craniodental, baculum), genetic (mtDNA and ncDNA) and acoustic data to clarify relationships among *Rhinolophus macrotis*, *Rhinolophus huananus* and a closely related unidentified species, *Rhinolophus* sp. nov. Based on an integrative taxonomy approach, 155 individuals were divided into eight groups. MtDNA and ncDNA lineages of *R. macrotis* and *R*. sp. nov indicated these two species derived from a common ancestor, and diverged at ca. 1.30 Mya. With the coming of the glacial epoch, part of *R. macrotis* migrated to a southern refuge, and hybridized with *R*. sp. nov, causing mtDNA introgression. Some *R. macrotis* adapted to the environment of southern China, and formed small forms *R. huananus* at ca. 0.50 Mya. Another part of *R. macrotis* migrated eastward, forming *R. m. caldwelli* at ca. 0.08 Mya. More recently, some *R. macrotis* migrated to the south, hybridized with *R. huananus*, and produced a new group. The individuals of this new group have similar ncDNA genetics with *R. macrotis*, and similar mtDNA with *R. huananus*, but the phenotypes and acoustic characters are intermediate. All the collected bacula are similar, indicating an incomplete reproductive isolation. Our studies suggest that these three bat species have a complex history of evolution and speciation, and need more studies in future.

SHOULD WE USE *MYOTIS DAUBENTONII* AS AN ECOLOGICAL INDICATOR TO EVALUATE RIPARIAN ECOSYSTEM HEALTH? [O*]

ADRIÀ LÓPEZ-BAUCELLS[1,2]**, LAURA CASANOVA[1],
XAVIER PUIG-MONTSERRAT[3], ANNA ESPINAL[4], FERRAN PÁRAMO[1],
CARLES FLAQUER[1], **adria.baucells@gmail.com
[1]*Granollers Museum of Natural Sciences, Granollers, Catalonia, Spain;*
[2]*Center for Ecology , Evolution and Environmental Changes, FCUL, Lisboa, Portugal;*
[3]*Galanthus Association, Celrà, Catalonia, Spain;*
[4]*Servei d'Estadística Aplicada, UAB, Catalonia, Spain.*

Daubenton's bat, *Myotis daubentonii*, is one of the bat species most closely associated with riparian habitats in the north-east Iberian Peninsula, and is used as an ecological indicator in specific monitoring programmes, such as the Waterway Survey (United Kingdom) and the QuiroRius (Spain). Nonetheless, there is still great controversy in Europe as to whether *M. daubentonii* is a good biological indicator or not. Due to the lack of information regarding habitat-quality requirements in Daubenton's bats in the Mediterranean region and the species' potential as a bioindicator in riparian habitats, in this study we addressed the following questions: a) does QuiroRius data match other well-established biological indicators? (IBMWP for invertebrates and QBR for riparian forests), b) how do environmental variables affect the presence of *M. daubentonii* at both local and landscape scales?, and c) how do environmental traits influence the local activity of *M. daubentonii*? A total of 104 streams below 1,000 m a.s.l. were simultaneously sampled using bat, macroinvertebrate and vegetation ecological indicators. Although they share similar conservation aims, the three bioindicators did not provide consistent images of overall riparian ecosystem quality and thus a multidisciplinary approach is necessary for a full analysis of the health of these ecosystems. While *M. daubentonii* were found more frequently in wide rivers with well-structured native riparian forests, landscape composition at broader scales and altitude had no influence on this bat's presence/activity. We suggest that QuiroRius could be used as a complementary ecological indicator for analysing riparian forest quality, but should not be used alone as a tool for evaluating overall riparian ecosystem health. Both relative abundance and/or presence/absence could be used as bioindicator surrogates given that the effect of microhabitat environmental predictors had similar impact on both these measures.

A NEW MAMMAL SPECIES FOR ALGERIA, *RHINOPOMA MICROPHYLLUM* (CHIROPTERA: RHINOPOMATIDAE): MORPHOLOGICAL AND ACOUSTIC IDENTIFICATION [P*]

HIBAT-ELLAH LOUMASSINE[1]**, BENJAMIN ALLEGRIN[2], FARID BOUNACEUR[1], OLIVIER PEYRE[2], STEPHANE AULAGNIER[3], **loumassine_bouz@hotmail.fr
[1]Laboratory of Agro-Biotechnology and Nutrition in Semi-Arid areas, Faculté des Sciences, Université Ibn Khaldoun, Tiaret 14000, Algeria;
[2]Naturalia Environment, Green Park – Bât C, 149, Avenue du Golf, Baillargues 34670, France;
[3]Behavior and Ecology of Wild Fauna, National Institute of Agronomic Research, University of Toulouse, CS 52627, 31326 Castanet Tolosan cedex, France.

In 2015 and 2016, the Chiroptera fauna in the arid region of north-western Algeria has been investigated for the first time. We present here the original data for a new species to this area. The Greater mouse-tailed bat (*Rhinopoma microphyllum* Brunnich, 1782) was recorded for the first time in Algeria from two caves of the Boukaïs region (Bechar). Noseleaf shape, forearm and tail lengths clearly identified this species. The frequency of maximal energy of echolocation calls varied from 28.2 to 31.2 kHz for hand-released individuals.

LONG-TERM BAT POPULATION TRENDS IN EAST, CENTRAL AND SOUTH-WEST ROMANIA [O]

GEORGIANA MĂRGINEAN[1], OANA MIRELA CHACHULA[1]**, ADRIAN DONE[2], ADRIAN SOPINCEAN[3], IONUȚ CREȚU[4], IOAN COROIU[5], **oana_chachula@yahoo.com
[1]*Department of Biology, Bucharest University, Splaiul Independenței 95-97, Bucharest, Romania;*
[2]*Speological Foundation Club Speo Bucovina, M. Viteazu street, no 56, bl. L, sc. C / 4, Suceava, Romania;*
[3]*Mountain Sports Club, Sarmizegetusa 36, Hunedoara, Romania;*
[4]*Freelancer, Râului 23, Zărnești, Brașov, Romania;*
[5]*Faculty of Biology and Geology, Babes-Bolyai University, Clinicilor 5-7, Cluj-Napoca, Romania.*

Our research was conducted from 2000 to 2017 with the focus being on the identification, inventory and monitoring of bat roost sites that had been previously studied up until 1980, and to observe possible differences in the structure and population numbers. The research also identified shelters and caves not previously studied. The investigation was done mainly in the North of Orientali Carpathians (13 bat roosts, of which 6 were new), Transylvanian Alps and Banat Mountain (150 bat roosts, of which 58 were new, namely: 37 hibernacula, 18 nurseries and 5 anthropic sites). Four of the bats roost are of National and European interest. In Liliecilor Cave from Rarău Mountain one of the largest bat colonies was found comprising of about 3740 *Myotis myotis/blythii* during hibernation time (2017). Șura Mare Cave is also unique in Europe because of the largest bat colonies and hibernacula for *Pipistrellus pipistrellus* and *Miniopterus schreibersii*. The second important hibernating roost was in Peștera Mare de la Ștălitrari Cave with 2300 *Rhinolohus euryale* and also Topolnița Cave with one of the largest *R.euryale* nursery colonies of about 1740 individuals. Bucegi Mountain is remarkable with 12 bat roosts never before investigated and the discovery of two hibernating colonies of *M. emarginatus* and another one with about 40 *Barbastella barbastellus*. Piedmont and Făgăraș Mountain ranks in second place with the most rich bat fauna, along with Șureanu Mountains with 12 species. Our data identified an important European bat hot-spot from the West of the Transylvanian Alps (Șureanu, Cernei, Mehedinți Mountains). This occurs because of many reasons as karst is dominant in all three Massifs and there is the existence of an excellent mosaic of natural habitats and low level of anthropic disturbance of the area.

USE OF BODY CONDITION INDEX TO DESCRIBE PHENOLOGY OF FRENCH BATS POPULATIONS FROM MIST-NETTING DATA [O]

JULIE MARMET[1]**, YVES BAS[1], JEAN-FRANÇOIS JULIEN[1], CHRISTIAN KERBIRIOU[1], **jmarmet@mnhn.fr
[1]*UMR7204 "Centre d'Ecologie et de Sciences de la Conservation" Muséum national d'Histoire naturelle, Paris, France.*

In 2013, the French national action plan for bat conservation started a program for the exploitation and valorisation of the mist-netting data available in the whole country. Thanks to bat workers and volunteers, more than 60000 data have been collected. The first step of this study was to investigate the quality of the data set and to model seasonal phenology (activity, reproduction, mating…) of each species. Further analyses were then conducted on Body condition Index, based on weight and forearm length ratio. This metric is known to be a good index to describe activity pattern and fat accumulation strategy. We analysed how BCI changes during the night according to the species, sex, season and habitat. Seasonal variations of BCI were particularly powerful in highlighting the different stages of bat biological cycle, from reproduction to fat accumulation just before hibernation. These analyses showed how mist-netting data contain quantitative and relevant data on bat biology that could hardly been collected by other means. This exploratory work opens up many opportunities to better understand bat activity pattern and to test biological factors as climate change that could have an impact on it.

BAT BOXES AND CLIMATE CHANGE: TESTING THE THERMIC RESPONSE DURING EXTREME HEAT EVENTS IN THE MEDITERRANEAN REGION [O*]

GARAZI MARTIN[1]**, ADRIÀ LÓPEZ BAUCELLS[1,2], XAVIER PUIG-MONTSERRAT[1,3], MARIA MAS[1], XAVIER PORRES[4], CARLES FLAQUER[1], **garazimartin025@gmail.com
[1]Natural Sciences Museum of Granollers, Granollers, Catalonia, Spain;
[2]Centre for Ecology, Evolution and Environmental Changes, University of Lisbon, Portugal;
[3]Galanthus Association, Catalonia, Spain;
[4]Delta de l'Ebre Natural Park, Catalonia, Spain.

Impact mitigation practices are currently one of the hottest topics in conservation and regarded as priorities worldwide. Habitat loss is one of the most important threats to biodiversity and forest fragmentation reduces bat natural roost site availability. Since bat populations are known to provide important ecosystem services, such as pest control, bat boxes have become one of the most popular management options amongst scientists for counteracting roost loss. However, some evidence shows that in warmer regions, where temperatures can easily reach 40ºC, bat boxes could also act as death traps due to overheating. The lack of guidelines for building and siting bat boxes, together with the absence of specific regional regulations, make them a conservation tool that might bring undesired consequences for conservation in these areas. Only few studies have investigated how extreme heat events affect the microclimate of boxes, testing different types of boxes, orientations, materials or colors. The aims of this study were to i) test the effect of boxes structural variables on the internal temperatures, ii) quantify the frequency of overheating events for different bat box models, and iii) describe how the influence of these structural variables vary across an altitude gradient within a Mediterranean region. From July-September 2014-2016, temperatures from 94 bat boxes of 21 models, 5 different materials, facing all orientations, placed in 11 localities in the north-east of the Iberian Peninsula across an altitude gradient, have been hourly and simultaneously monitored and pair compared. Both, material and model had strong effect on the internal temperatures. Black-cement bat boxes could easily reach temperatures of above 40^{o} and 50ºC (several times per month in almost all altitudes), while wood and rice boxes rarely reached these values. Rice represented a new recycled material, prepared with the rice chaff, boxes proved to be cooler and as insulating as other models, potentially reducing the risk of overheating events.

THE POOP EXPERIMENT: DEFINING SAMPLING PROCEDURES FOR METABARCODING DIETARY STUDIES IN BATS [O*]

VANESSA A. MATA[1]**, FRANCISCO AMORIM[1], HUGO REBELO[1,2,3], GARY F. MCCRACKEN[4], SIMON JARMAN[1], PEDRO BEJA[1,3],
**vanessamata@hotmail.com
[1]CIBIO-InBIO, Research Center in Biodiversity and Genetic Resources, University of Porto, Porto, Portugal;
[2]School of Biological Sciences, University of Bristol, Bristol, U.K.;
[3]CEABN-InBIO, Centre for Applied Ecology "Prof. Baeta Neves", Institute of Agronomy, University of Lisbon, Lisbon, Portugal;
[4]Department of Ecology and Evolutionary Biology, University of Tennessee, Knoxville, USA.

Dietary studies based on DNA metabarcoding have boomed during recent decades. This technique offers a powerful tool to tackle old ecological questions by providing ecologists with unprecedented data resolution. At the moment, diet analysis based on DNA metabarcoding techniques is commonly limited to the use of frequencies of occurrence (FO), i.e., the frequency a prey is present in a number of samples. This means that in order to have good FO estimates, an adequate number of samples is required. However few studies have assessed the impact of sampling design on molecular diet analysis and the advantages and disadvantages of the different approaches. Here we aim to assess how different experimental designs affect the accurate estimation of FO in metabarcoding studies of bat diets. We investigated the effects on FO estimates of: sequencing depth, number of PCR replicates per faecal sample, number of faecal samples per individual, and pooling of samples before extraction. One of the main goals is to understand the sources of variability in FO estimates, thereby devising sampling and analytic strategies that maximize FO estimate accuracy. For this we assessed the diet of the European free-tailed bat, *Tadarida teniotis*, in an orthogonal set-up, and sequenced a small fragment of the COI gene of 20 bat individuals, using 15 pellets per individual as well as a pool of 15 pellets (all from the same foraging night), 3 PCR replicates, and 2 levels of sequencing depth. Overall, results suggest that maximizing the number of individuals analyzed is the most important factor for accurately estimating FO, with the number of pellets per individual also significantly affecting FO estimates for each given sample size of individuals. PCR replicates were fairly consistent given similar sequencing depths, with rarer species disappearing at lower sequencing depths. These results will give us fundamental baseline information to propose guidelines for the sampling design of future studies.

WHAT IS WRONG WITH BAT ACTIVITY ASSESSMENTS DEVELOPMENT SITES, AND HOW WE CAN MAKE THINGS BETTER: A PLEA FOR IMPROVED INTERNATIONAL STANDARDS [P]

FIONA MATHEWS[1]**, PAUL LINTOTT[1], **f.mathews@exeter.ac.uk
[1]*University of Exeter, Hatherly Laboratories, Prince of Wales Road, Exeter, EX4 4PS, U.K.*

To meet the legislative requirements, bat activity is frequently measured at development sites. However, the questions that the surveys seek to address are frequently poorly defined, and the survey methodologies fail to provide information useful to bat monitoring or mitigation. Given the scarce resources available for bat conservation, and the ever increasing pressure on bat populations from development, it is vital that better approaches are used. This poster will outline a free tool, developed in the UK, that helps consultant and decision-makers to move away from interpreting survey results on an anecdotal basis, by providing a facility to contextualise information relative to a large dataset. This helps users to judge, in a transparent and defensible way, whether bat activity is high or low at a particular site. We also argue that there needs to be standardisation of data collection and a sharing of data across the community. This will create a resources which can then be used to answer key questions that currently hamper our ability to mitigate the effects of development on bats.

A NATIONAL-SCALE ASSESSMENT OF THE EFFECTS OF WIND ENERGY INSTALLATIONS ON BATS: WHAT HAVE WE LEARNT, AND HOW USEFUL ARE CURRENT APPROACHES TO MINIMISING RISK? [O]

FIONA MATHEWS[1]**, SUZANNE RICHARDSON[1], PAUL LINTOTT[1], ALISTAIR MOYLE[1], DAVID HOSKEN[2], **f.mathews@exeter.ac.uk
[1]*University of Exeter, Prince of Wales Road, EX4 4PS, U.K.;*
[2]*University of Exeter, Penryn Campus, Cornwall, TR10 9FE, U.K.*

Bat fatalities at wind energy installations are of international concern. Due to the logistical issues of obtaining access to sites, most research uses detailed assessments of small numbers of sites. This means it can be difficult to estimate the impacts of wind turbines on national populations; or to be sure that findings from focal studies apply elsewhere. We have studied 46 wind farms, and a further 30 single installations of small-medium sized turbines, in the UK. At each site, bat carcasses were located using trained search dogs, and bat activity was recorded using acoustic detectors at the turbine nacelle and at ground level. Features linked with increased casualty rates included increased blade length, low wind speeds, and increasing the number of turbines per site. However, an important finding of the project is that fatality rates are highly variable. No casualties were found at a third of sites, whilst a small number had casualty rates sufficiently large to generate concern for local populations. It was also difficult to predict casualties on the basis of habitat: indeed high casualty rates were sometimes found at high altitude moorland sites that would generally be considered of low suitability for bats. Similarly, whilst low bat activity was associated with a low casualty risk, casualty rates were variable at sites with moderate-high activity. By reviewing pre-construction assessments reported in EIAs, and comparing the results with observed fatality rates, we show that EIAs – at least as performed currently – are insensitive indicators of true risk levels. This may partly be explained by our observation that *Pipistrellus pipistrellus* activity is higher at turbine locations than in matched habitat: if bat activity is altered by the presence of a turbine, then the concept of relying on pre-construction activities to assess risk could be flawed.

BEHAVIOURAL AND PHYSIOLOGICAL RESPONSES IN *RHINOLOPHUS EURYALE* IN HIBERNATION [O*]

EDITA MAXINOVÁ[1,2]**, INAZIO GARIN[2], MARCEL UHRIN[1],
**edita.maxinova@gmail.com
[1]*Department of Zoology, Faculty of Science, Pavol Jozef Šafárik University in Košice, Košice, Slovakia;*
[2]*Dep*artment of Zoology and Animal Cell Biology, University of The Basque Country UPV/EHU, Leioa, The Basque Country.

We studied behavioural and physiological features related to foraging during winter arousals from torpor in the Mediterranean horseshoe bat, *Rhinolophus euryale*. The observed colony hibernated in a cave located on the border between Slovakia and Hungary during four hibernation periods from autumn 2011 until spring 2015. We analyzed foraging, digestion, defaecation and microbial flora of bats by non-invasive methods from the faeces and based on morphological analysis, DNA analysis, proteonomic analysis, petrographic analysis, cytological analysis, microbiological cultivation and non-cultivation analyses and biochemical analyses of digestion enzymes. We found that *R. euryale* intermittently aroused during winter and produced both typical consumptive as well as non-consumptive faeces (produced after no feeding activity). This species became active and emerged from the cave mainly when the outside temperature was mild. Consumptive faeces during the winter contained only the order Lepidoptera. Non-consumptive faeces contained high concentration of inorganic material of cave origin and the virtual lack of prey indicates that drinking as well as direct sediment consumption occurred. Enterobacteria and enterococci in the faecal samples decreased during hibernation and only reached pre-hibernation numbers at the end of hibernation. There were time-dependent changes in the gut microflora and the decrease in bacterial variability was dependent on the hibernation stage. The activity of digestive enzymes (amylase, chitobiase, endochitinase, glucosaminidase) was detected in fresh feaces during the whole winter. Activity of chitinases was relatively stable during the winter, but activity of amylase was highest during late November and December. We conclude that *R. euryale* is physiologically ready to hunt during the winter when suitable conditions occur, but winter arousals are unlikely to be directed towards gaining energy through foraging, but more likely are aimed at active drinking.

THE GENETICS OF MIGRATION OF THE TEQUILA BAT (*LEPTONYCTERIS YERBABUENAE*) [O*]

ANGELICA MENCHACA RODRIGUEZ[1]**, GARETH JONES[1], RODRIGO MEDELLIN[2],
**am14886@bristol.ac.uk
[1]*University of Bristol, Bristol, U.K.;*
[2]*Universidad Nacional Autonoma de Mexico, Mexico.*

Migration is a fundamental life-history strategy essential for the reproduction and survival of many animals. Heritable components have been identified as major causes of differences in the expression of specific migratory behaviour, yet our knowledge of its molecular bases remains limited. Describing mechanistic links between genetic and behavioural variation in free-living animals presents a major scientific challenge. Bats exhibit strikingly different scales and patterns of migration as latitudinal, altitudinal and regional migration. The tequila bat (*Leptonycteris yerbabuenae*) exhibits contrasting intraspecific migratory strategies with a long-distance migratory population and a resident population that maintain gene flow mediated by males. We used the tequila bat as a model to investigate the genetic basis and evolution of different aspects of migratory behaviour in bats. We compared variation in behaviour and related it to gene expression in brain and blood among ten individual bats. We used the information from differentially expressed transcripts among individuals to identify potential candidate genes responsible of the migratory behaviour. In addition, morphological differences between these two populations were evaluated with geometric morphometrics to assess variation in wing shape and compare flight efficiency. Our findings confirm that genetic and environmental interactions are shaping the migratory phenotypic diversity in the species.

GENETIC AND ECHOLOCATION DIVERGENCE IN *RHINOLOPHUS HIPPOSIDEROS*: IS THE POPULATION OF THE MALTESE ISLANDS DISTINCT? [O*]

CLARE M. MIFSUD[1]**, ADRIANA VELLA[1], **cmifsud2@gmail.com
[1]*Conservation Biology Research Group, Department of Biology, University of Malta, Msida, Malta.*

Rhinolophus hipposideros is the only extant species representing the family Rhinolophidae in the Maltese Islands. Prior to this research, knowledge on this species was limited to population monitoring of known roosting sites. The population of this species in Malta is very close to the southern border of its distribution within the Mediterranean region. Given that bat species are predicted to shift their range northwards due to future climate change, with possible extinctions from the southern distribution, the Maltese *R. hipposideros* population may be ranked at a higher extinction risk. In this respect obtaining scientific knowledge on various biological aspects of this species is of utmost importance for the formulation of effective conservation management strategies. The *R. hipposideros* population inhabiting the archipelago was investigated through underground site and cave surveys to identify major nurseries and hibernation sites. Acoustic surveys were conducted to determine habitat use and record echolocation calls, while morphological information and wing biopsies for genetic analyses were obtained by mist-netting. During this research effort, the first major maternity colony for this species was discovered in Malta. During acoustic surveys, this species was recorded along cliff faces, shrublands, valley sites and woodlands; however, it was never recorded in urban and agricultural sites. Comparing echolocation calls of *R. hipposideros* from Malta to those of mainland regions revealed variation in the range of the echolocation call frequencies. The differences in echolocation of the local population are also coupled with divergent mitochondrial DNA sequences and morphological characters. The echolocation, morphological and genetic differences observed between the population of *R. hipposideros* on the Maltese Islands and mainland regions have various ecological and conservation implications which need to be integrated within conservation strategies.

TRACKING VIRAL AND BAT HOSTS INTERACTIONS: SUPPORT FOR PARALLEL EVOLUTION BETWEEN SEROTINE BATS AND LYSSAVIRUS [P]

PATRICIA MINGO-CASAS[1], JUAN E. ECHEVARRIA[1,2], SONIA VÁZQUEZ-MORÓN[1], THOMAS MÜLLER[3], CONRAD FREULING[3], ENGBERT A. KOOI[4], FLORENCE CLIQUET[5], EVELYNE PICARD-MEYER[5], JAVIER JUSTE[2,6]**, **juste@ebd.csic.es

[1]*National Center of Microbiology (ISCIII), Madrid 28220, Spain;*
[2]*CIBER of Epidemiology and Public Health (CIBERESP), Madrid 28029, Spain;*
[3]*Friedrich-Loeffler-Institute - Federal Research Institute for Animal Health, D-16868 Wusterhausen, Germany;*
[4]*Central Veterinary Institute of the Wageningen University, 8200 AB Lelystad, The Netherlands;*
[5]*Nancy Laboratoire de la rage et de la faune sauvage, ANSèS, Technopole Agricole et Vétérinaire, 54 220 Malzeville, France;*
[6]*Estación Biológica de Doñana (CSIC), Seville, Spain.*

Rabies is a lethal zoonosis caused by several lyssaviruses. One of them is the European Bat Lyssavirus type-1 (EBLV-1), which is endemic to a large part of Europe. Two different subtypes (EBLV-1a and EBLV-1b) have been described for this virus, which is usually found associated with the bat *Eptesicus serotinus*, which accounts for more than 95% of the rabid bats detected in Europe. The Iberian Peninsula is the only area known where *E. serotinus* meets its sibling species *E. isabellinus*, which occupies only the southern half of the peninsula. Previously, EBLV-1 virus was known in Iberia only in the species *E. isabellinus* and forming a monophyletic clade, but recently, we have detected EBLV-1 also in *E. serotinus* bats from the north of the Iberian Peninsula. A total of 81 sequences of a 400 bp fragment of the Nucleoprotein gene of EBLV-1 detected in the brain of *Eptesicus* sp. across Europe, were studied together with bats' sequences of the mtDNA HVII obtained from the specific bats from which each virus was detected. The aim was to test for a possible pattern of parallel evolution between EBLV-1 rabies viruses and their *Eptesicus* sp bat hosts. The analyses comprised comparisons of the topologies of phylogenetic reconstructions for viruses and bats' genetic markers and comparisons by Mantel's Tests of the matrices of genetic distances for both viruses and rabies positive bats and were performed independently for the lineages EBLV-1a, European EBLV-1b and Iberian EBLV-1b. Although the phylogenetic analyses did not reveal any correlation between virus and host bats topologies, Mantel's Tests showed significant correlation for the genetic distances between European EBLV-1b and its serotine bat hosts suggesting the existence of parallel evolution between rabies virus and their hosts, at least within this strain.

DETECTION DISTANCES FOR BATS IN SOUTHERN AFRICAN SAVANNAS [O]

ARA MONADJEM[1]**, JULIE T. SHAPIRO[2], FEZILE MTSETFWA[3], APRIL RESIDE[4], ROBERT A. McCLEERY[3], **aramonadjem@gmail.com
[1]Department of Biological Sciences, University of Swaziland, Swaziland;
[2]School of Natural Resources and Environment, University of Florida, Gainesville, USA;
[3]Department of Wildlife Ecology and Conservation, University of Florida, Gainesville, USA;
[4]Centre for Biodiversity and Conservation Science, University of Queensland, Brisbane, Queensland, Australia.

Bats are a critical component of most terrestrial systems, yet accurately assessing species richness and abundances remains a challenge, especially in Africa. The use of acoustic monitoring has increasingly been used to assess bat communities. Compared with more traditional trapping surveys, acoustic monitoring is relatively easy to use and vastly increases the amount of data collected. However, the ability to accurately identify bat calls from acoustic detectors is limited by the availability of regional call libraries describing the calls of local species. Further, the lack of knowledge of detection distances for different species limits the ability to compare activity levels or abundances between species. We developed an echolocation call library based on zero-crossing recordings with Anabat Express detectors that can be applied broadly to bat acoustic detector surveys across the savanna systems of Swaziland and South Africa, and potentially the broader region of Southern Africa. We also compared detection distances for different species and provide a correction factor that will increase our ability to accurately compare activity between different species. We apply this correction factor to a large acoustic dataset collected in this region and demonstrate the enormous difference it makes to interpretation of the data.

PHYLOGEOGRAPHY OF DAUBENTON'S BAT, *MYOTIS DAUBENTONII*, IN EUROPE [O]

VALENTINA NARDONE[1]**, DANILO RUSSO[1, 2], PAVEL HULVA[3,4], JAN DEMJANOVIČ[4], KLARA JANIKOVA[4], CARLOS IBÁÑEZ[5], DINO SCARAVELLI[6], JAVIER JUSTE[5], **valentina.nardone@unina.it

[1]*Wildlife Research Unit, Laboratorio di Ecologia Applicata, Dipartimento di Agraria, Università degli Studi di Napoli Federico II, Italy;*

[2]*School of Biological Sciences, University of Bristol, U.K.;*

[3]*Department of Zoology, Faculty of Science, Charles University in Prague, Praha, Czech Republic;*

[4]*Department of Biology and Ecology, Faculty of Science, University of Ostrava, Chittussiho, Slezská Ostrava, Czech Republic;*

[5]*Estación Biólogica de Doñana, Consejo Superior de Investigaciones Científicas, Sevilla, Spain;*

[6]*Dipartimento di Scienze Mediche Veterinarie, Università degli Studi di Bologna, Ozzano dell'Emilia, Bologna, Italy.*

We combined mitochondrial and nuclear markers to explore the phylogeography of *Myotis daubentonii* in Europe. We collected 229 samples from 96 sites and analyzed genetic diversity of mtDNA cytocrome b; we also genotyped 11 microsatellite loci of 121 samples. We found a remarkable differentiation with >60 Cyt b haplotypes. Phylogenetic reconstructions revealed three distinct, highly structured mitochondrial lineages: 1) located only in the Iberian Peninsula (Iberian lineage); 2) found across Italy, France, Switzerland, Germany, Sweden, Czech Republic and in Central and N Iberia (Italian lineage); 3) widespread through Serbia, Montenegro, Greece, Czech Republic, Ukraine, the Netherlands, N. Iberia (Balkan lineage). In the Iberian lineage, the parsimony network showed no haplotype sharing by subgroups, suggesting a pattern of refugia-within-refugia and demographic indices revealed that no expansion occurred. On the contrary, possible past events of demographic expansions were supported by the genetic variation patterns for the Balkan and Italian lineages. Microsatellite analyses (PCAs and Structure Bayesian assignment) revealed only two main clusters with the two lineages identified as Italian and Balkan through mtDNA analysis showing just very shallow differentiation in nuclear markers through Europe. The other cluster confirmed the presence of an isolated Iberian lineage sympatric with the other two lineages in the northern half of Iberia. Mediterranean peninsulas acted as glacial refugia for *M. daubentonii*: European populations originated from the postglacial Palaearctic expansion of the Italian and Balkan lineages, which then merged along this secondary post-glacial expansion. The Iberian clade never crossed the Pyrenees, remaining genetically distinct, and showed a possible pattern of refugia-within-refugia as a consequence of the climatic cycles from the Pleistocene. These results imply the reinstatement of *M. nathalinae* (1977) as a valid species for the European bat fauna.

ACOUSTIC SURVEYS IN THE WESTERN SOUTH CAUCASUS (GEORGIA) IMPLY SEASONAL BAT MIGRATIONS [P]

IOSEB NATRADZE[1]**, ALEXANDER BUKHNIKASHVILI[1],
***ioseb.natradze@iliauni.edu.ge*
[1]*Institute of Zoology of Ilia State University, Tbilisi, Georgia.*

In 2016, the study of seasonal movements of bats in the western South Caucasus was initiated, employing passive acoustic surveys by automated bat detectors with subsequent estimation of activity indices (calculated per hour), complemented by mist netting, active surveys with handheld detectors and inspection of roosts at potential stopover sites. Recordings were analyzed by Kaleidoscope Pro4 Software. Six automated detectors - two Song Meter SM3BAT, two Song Meter SM4BAT FS and two Anabat Express, were installed at two distinct areas. Four detectors were installed in the first study area (SA1) – the Likhi Range, a watershed which divides the Caucasus into western and eastern parts. The other two detectors were placed in the second study area (SA2) located on the Black Sea coast between the rivers Tikori and Churia. The area is known as an important bird migration route - the Eastern Black Sea Flyway. Preliminary results indicate that among recorded species, most numerous were *Nyctalus* sp. followed by *Pipistrellus pipistrellus*, *Eptesicus serotinus* and *Vespertilio murinus*. The bat activity indices (BAI) for the SA1 increased almost twofold in the autumn compared with the summer time, however whether this was caused by flying young animals or seasonal movements is not yet clear. At the SA2, the BAI was calculated for each night during a two-month research period, reaching the highest BAI 51.04. Among species recorded at the SA2, the most numerous was *P. nathusii*, followed by *Nyctalus* sp., *P. pygmaeus* and *V. murinus*. Considering the observed changes in the BAI and the most numerous recorded species as well as the facts that *P. nathusii*, *Nyctalus* sp. and *V. murinus* are generally known as long-distance migrants reproducing outside the western South Caucasus, and seasonal movements are known for *P. pygmaeus*, we can assume that migration/seasonal movements take place in western South Caucasus. Research is continuing to confirm migration of bats across western South Caucasus.

THE ROLE OF BIOTIC INTERACTIONS IN SHAPING THE RANGE OF CRYPTIC BAT SPECIES [O*]

ROBERTO NOVELLA FERNANDEZ[1]**, JAVIER JUSTE[2], CARLOS IBANEZ[2], HUGO REBELO[3], DANILO RUSSO [4], ANTTON ALBERDI[5], ANDREAS KIEFER[6], PATRICK DONCASTER[1], ORLY RAZGOUR[1], **r.novella-fernandez@soton.ac.uk
[1]*Biological Sciences, University of Southampton, Southampton, U.K.;*
[2]*Estacion Biológica de Doñana (CSIC), Seville, Spain;*
[3]*CIBIO/Inbio, University of Porto, Vairão, Portugal;*
[4]*Dipartimento di Agraria, Università degli Studi di Napoli Federico II, Napoli, Italy;*
[5]*Natural History Museum of Denmark, University of Copenhagen, Copenhagen, Denmark;*
[6]*Universität Trier, Trier, Germany.*

Understanding the factors that shape species ranges is one of the main aims of Biogeography. Species ranges are primarily thought to be constrained by the effects of climatic factors. Only recently it has been recognized that biotic interactions can also play a role at both the fine and broad spatial scales. Nevertheless, there is still a knowledge gap on how generalised is their effect, and a methodological framework to measure this effect and include it in models is still poorly developed. While species distribution models (SDMs) are commonly used to better understand species ranges and predict responses to climate change, they have thus far largely failed to consider the effect of biotic interactions. Because of their shared morphology, cryptic species constitute an excellent model system to study competitive interactions. We use SDMs to study the effect of interspecific competition on shaping the range of four sets of Palaeartic cryptic bat species of the genera *Eptesicus* (*E. serotinus* and *E. isabellinus*), *Myotis* (*M. nattereri*, *M. escalerai*, *Myotis* sp A), *Plecotus* (*P. auritus*, *P. austriacus*, *P. macrobullaris*, *P. kolombatovici*), and *Rhinolophus* (*R. euryale* and *R. mehelyi*). We modelled the continental range for all species and identified their main ecological requirements. Then, we studied interacting pairs of potentially competing species by analysing differences in suitable and realised range overlap and the proportion of the realised range within overlapping and non-overlapping suitable areas. We relate patterns of range overlap to ecological niche differences. Cryptic species groups showed differences in the extent of niche and range overlap, indicating that for some pairs of interacting species competition could have been a major driver limiting their distributions. Thus, we highlight the need for including biotic interactions in SDMs in order to produce more realist models and better forecasts of future suitable ranges.

THE IMPACTS OF ACOUSTIC INTERFERENCE FROM CONSPECIFICS DURING FLIGHT OF *MYOTIS DAUBENTONII* [P]

MADS OLSEN[1]**, ANNEMARIE SURLYKKE[1], LASSE JAKOBSEN[1],
**madsolsen@biology.sdu.dk
[1]*Institute of Biology, Faculty of Natural Science, University of Southern Denmark*.

Echolocating bats often encounter and interact with conspecifics in their search for food. This has long been believed to be problematic for the bats due to acoustical interference. Several theories explaining how to adapt and avoid this problem have been proposed, especially the use of jamming avoidance response (JAR). Recent studies have questioned this theory and conclude that some species of bats are not actively using JAR. Our study focuses on how Daubenton's bat (*Myotis daubentonii*) overcomes the issue of acoustical interference from conspecifics and how this affects its acoustical behaviour during navigation. Observations made in the field seem to support the newly concluded hypothesis and indicate that *M. daubentonii* does not use JAR. For our study we recorded several wild *M. daubentonii* in its natural habitat hunting over open water using a multi-microphone array. We analyzed the acoustical behaviour of bats flying alone and bats hunting in groups. Preliminary data indicate that *M. daubentonii* does not use any clear JAR. Source level and beam directionality stayed the same with no significant difference when conspecifics were nearby. Further analysis is needed to clarify our observations. If in fact the bats do not use JAR and their hunting success is not affected it strongly indicates that the echolocation system is more robust than previously assumed.

QUANTIFYING THE IMPACT OF LIGHT POLLUTION AT THE CITY SCALE: URBAN-DWELLER BATS ARE NEGATIVELY AFFECTED BY ARTIFICIAL LIGHT [O*]

JULIE PAUWELS[1,2]**, ISABELLE LE VIOL[1], CLÉMENTINE AZAM[1], NICOLAS VALET[2], CHRISTIAN KERBIRIOU[1], **julie.pauwels@edu.mnhn.fr
[1]*Centre d'Ecologie et des Sciences de la Conservation, MNHN-UMPC-CNRS UMR 7204, Paris, France;*
[2]*Auddicé environnement, Roost-Warendin, France.*

Light pollution, i.e. the alteration of natural light levels due to artificial light sources, constitutes a major threat to biodiversity and especially to nocturnal species. Indeed artificial illuminations cause habitat loss and fragmentation as it represents a barrier to animals' movement and decreases the quality of habitats. Only a few bat species, such as *Pipistrellus pipistrellus*, adapt to live in a highly urbanized ecosystem. However, artificial lights are densely implanted in cities, which causes them to be areas with high levels of light pollution and might threaten urban-dwelling bats. This issue is beginning to be included in environmental policies, but we lack quantitative information to guide land managers in possible enhancement of public lighting. The aim of this study is to define a simple measure of the effect of light pollution on bats behaviour to enable its use as a tool in urban planning. We studied the activity of *P. pipistrellus* in three highly urbanized cities of France using standardized citizen-science data (1149 recordings). We used two different sources of information to describe light pollution: the geolocation of street lamps and nocturnal satellite pictures. Overall, we show that at the city scale the light variables indicate that *P. pipistrellus* activity is negatively impacted by light pollution. This deleterious effect is better described by the variables based on nocturnal satellite pictures than the ones based on the geolocation of street lamps. As nocturnal satellite pictures are more and more accessible, they represent an interesting source of information to measure the impact of light pollution on bats at the scale of a city or a group of cities. These variables could be incorporated in land management plans as an important environmental factor to help in promoting urban biodiversity. Moreover, they can be used to take light pollution into account while assessing the landscape connectivity and determining the best ecological corridors.

NO EVIDENCE OF POPULATION DECLINE IN A LONG-DISTANCE MIGRATORY BAT, NATHUSIUS'S PIPISTRELLE BAT (*PIPISTRELLUS NATHUSII*), IN NORTH-EASTERN EUROPE [P]

GUNĀRS PĒTERSONS[1]**, VIESTURS VINTULIS[2], ILZE BRILA[1],
**Gunars.Petersons@llu.lv
[1]*Latvia University of Agriculture, Jelgava. Latvia;*
[2]*University of Latvia, Riga, Latvia*.

The Nathusius's pipistrelle bat, *Pipistrellus nathusii*, is one of the most frequently killed bat species at wind turbines throughout Europe. The Nathusius's pipistrelles breeding in north-eastern Europe hibernate in western and central Europe. Thus they have to pass through areas with a high risk of collisions with wind turbines, both during the autumn and the spring migration. This raises serious concerns about possible negative impact on breeding populations of this species. Here, we present data of long-term acoustic monitoring of the species carried out at the Pape Ornithological Research Centre located at the eastern coast of the Baltic Sea (SW Latvia). Annual nightly counts of bats were carried out in 1993-2016 during the peak period of the autumn migration between the 10 August and 10 September. Several models of the Pettersson Elektronik heterodyne ultrasound detectors were used during the monitoring period. Bat passes per year were used as an indicator of the yearly bat activity. TRIM analyses of the monitoring data show a strong increase of the bat activity throughout the study period. However the permanent increase of the activity of the Nathusius's pipistrelles has changed to a stable trend during the last eight years. Thus our data do not support the expected decline of the Nathusius's pipistrelle bat populations during the last 23 years.

ACTIVITY PATTERNS OF BATS AT THE TOP OF WIND TURBINES HAS IMPLICATIONS FOR EFFICIENT MITIGATION [O]

STEFAN PETTERSSON[1], JENS RYDELL[2]**, JOHAN EKLOF[3], JONN LANZ[4],
**jens.rydell@telia.com
[1]EnviroPlanning AB, SE-411 04 Göteborg, Sweden;
[2]Biology Department, Lund University, SE-223 62 Lund, Sweden;
[3]Graptolit Ord och Natur, Krokdalsvägen 88, SE-157 34 Bollebygd, Sweden;
[4]Department of Applied Physics, Chalmers University, SE-412 96 Göteborg, Sweden.

Bats are killed at wind turbine facilities worldwide, apparently at a scale that threatens the long-term survival of some populations. Action to halt or minimize the killing is probably urgent, but mitigation measures are often hard to implement because of high costs and low efficiency. Acoustic surveys from the ground before construction are of limited value for predicting the risk that bats will later be killed by the turbines and this also means that mitigation measures based on such surveys become ineffective or meaningless. More efficient may be to base the mitigation scheme on bat activity as measured from the operating nacelle, i.e. where and when the bats are actually at risk. We monitored bat activity, wind and temperature at the top of wind turbines in southern Sweden more or less continuously over three seasons with 10 minute precision. Bat activity differed by a hundredfold between the wind farms (N=7), reflecting geographical variation in bat species diversity and abundance, but always showed the same pattern with respect to seasonal timing and weather factors. Activity represented open-air bats (*Nyctalus*, *Vespertilio*, *Eptesicus* and *Pipistrellus* spp.) and a single long-eared bat (*Plecotus* sp.). Most activity (90%) occurred during specific nights between late July and early September with prevailing low wind speed and high temperature. Overall, the 90 percentiles for wind speed and temperature were 5.8 m/s and 14.6ºC, respectively. The strong temperature dependence is an important novel finding, suggesting that mitigation measures may be restricted to a few warm nights annually, at least in northern Europe. This would lower the cost (production loss) considerably and increase the efficiency of the mitigation. Agreement with data from other countries suggests that our results have direct and wide applications.

CAVERS FOR BAT MONITORING IN THE SULCIS IGLESIENTE PROJECT (SOUTHERN SARDINIA, ITALY) [P]

PAMELA PRIORI[1], DINO SCARAVELLI[1,2]**,
FEDERAZIONE SPELEOLOGICA[3] SARDA[3], **dino.scaravelli@unibo.it
[1]ST.E.R.N.A. and Ornithological Museum F. Foschi, via Pedriali 12, 47121 Forlì, Italy;
[2]Department of Veterinary Medical Science, University of Bologna, Via Tolara di Sopra 50, 40064 Ozzano dell'Emilia, Bologna, Italy;
[3]Sardinian Speleological Federation (Federazione Speleologica Sarda), Ex direzione miniera San Giovanni, Regione San Giovanni, 09016 Iglesias CI, Italy.

Thanks to the support of the Sardinia Region and of the Carbonia Iglesias Province, with funds from the Regional law n°4 of 7/08/2007, a bat monitoring project was started in 2015 involving the speleological groups of the Sulcis Iglesiente area. The aim of the project was to involve all the cavers interested in conservation in the importance of bats' presence and the necessity of cave environment protection, including training them in bat identification and in the use of sound analysis. Participants came from the different local speleological groups, as well as other volunteers associated with the Sardinia Speleological Federation. These actions will allow the identification of bat species in caves and their phenology, in an area of particular biospeleological interest. The necessity to protect the bats helps in protect underground habitats, caves and mines, including preventing them being blocked when worked out. Geologically, Sulcis Iglesiente is a complex of Palaeozoic lithologies and deep carbonate layers where massive karstic complexes develop, creating 1289 caves, as well as hundreds of km of mine galleries created over a thousand-year period of extraction of minerals. These underground sites are inhabited by bats and many different large colonies are already known. In Sardinia 21 bat species are present and most of them are related to caves in all or some parts of their phenology. After a course to learn about bat species, recognition, collection of information, bioacoustic and ethics, 35 volunteers have monitored for a year, every month, the caves Cava Romana (Nuxis), Corona Sa Craba (Carbonia), Grotta dei Fiori (Carbonia), Sa Crovassa de Pranu Pirastu (Domusnovas), San Giovanni (Domusnovas). After a year an impressive series of data about colony structure and phenology has been collected for *M. schreibersii*, *M. punicus*, *M. emarginatus*, *R. euryale*, *R. mehelyi*, *R. ferrumequinum*, *R. hipposideros*, (all in Annex II of the Habitats Directive), giving no excuse in the necessity to protect all the areas where the caves are located.

CONTRASTING PHYLOGEOGRAPHY AND POPULATION STRUCTURE IN TWO ECOLOGICALLY SIMILAR *RHINOLOPHUS* SPECIES, *R. EURYALE* AND *R. MEHELYI* [O]

SÉBASTIEN J. PUECHMAILLE[1,2,3]**, BENJAMIN ALLEGRINI[4], RAŞIT BILGIN[5], A ABIADH[6], CARLOS IBAÑEZ[7], JAVIER JUSTE[7], ELENA PAPADATOU[8], PANAGIOTIS GEORGIAKAKIS[9], DANILO RUSSO[10], M SAPHIRI[11], EGOITZ SALSAMENDI[12], INAZIO GARIN[12], HUGO REBELO[13], R TOFFOLI[14], JY COUTOIS[15], D RAMBAUT[16], BJORN SIEMERS[2], EMMA TEELING[1], **s.puechmaille@gmail.com
[1]*School of Biology and Environmental Science, University College Dublin, Dublin, Ireland;*
[2]*Sensory Ecology Group, Max Planck Institute for Ornithology, Seewiesen, Germany;*
[3]*Zoology Institute & Museum, Greifswald University, Greifswald, Germany;*
[4]Naturalia environnement, Baillargues, France;
[5]Institute of Environmental Sciences, Boğaziçi University, Istanbul, Turkey;
[6]Association des Amis du Belvédère, Tunis Belvédère, Tunisia;
[7]Evolutionary Ecology Dpt., Estacion Biologica de Donana (CSIC), Seville, Spain;
[8]Athens, Greece;
[9]Natural History Museum of Crete, University of Crete, Irakleion, Greece;
[10]Wildlife Research Unit, Dipartimento di Agraria, Università degli Studi di Napoli Federico II, Portici, Italy;
[11]Department of Biology, Razi University Center for Environmental Studies, Baghabrisham, Kermanshah, Iran;
[12]Department of Zoology and Animal Cell Biology, University of the Basque Country (UPV/EHU), Leioa, The Basque Country;
[13]CIBIO/InBIO, University of Porto, Vairão, Portugal;
[14]CHIROSPHERA, Associazione per lo studio e la tutela dei Chirotteri e l'ambiente, Torino, Italy;
[15]Groupe Chiroptères Corse, Corte, France;
[16]Correns, France;

Rhinolophus euryale and *Rhinolophus mehelyi* are sibling cryptic species with very similar morphology, diet, echolocation calls and habitat use. Given these similarities and their largely sympatric distribution, we hypothesized that these two species would have a similar post-glacial recolonisation history and current population structure across their range in Europe, Northern Africa and the Middle East. To test this hypothesis and better inform conservation for these two endangered species, we collected a dataset of >1,000 samples from across the range of the two species between 2009 and 2016. These samples were then sequenced for the highly variable D-loop region (mitochondrial DNA) and genotyped for 19 microsatellite loci. This multi-marker approach was used to provide information at different spatio-temporal scales. We found that although the two species showed some similarities (an east/west differentiation), their post-glacial recolonisation history, including the re-colonisation of Mediterranean islands, and current population structure differed vastly. Additionally, for each species we identified isolated populations and populations that are undergoing pronounced genetic drift. Such populations are of particular concern for conservation. Our study highlights that although these two *Rhinolophus* species are ecologically very similar, they reacted very differently when exposed to similar situations such as climate change (i.e. the post-glacial period) and possibly past and current anthropogenic activities modifying their roosting and foraging habitats.

POPULATION GENETIC STRUCTURE OF *PSEUDOGYMNOASCUS DESTRUCTANS* IN THE WESTERN PALEARCTIC:

WHERE DID IT ALL START? [O]

SÉBASTIEN J. PUECHMAILLE[1]**, S. RANPAL [1], R.-M. STECKER[1], N. M. FISCHER[1], A. ALTEWISCHER [1], N. TOSHKOVA[1], V. ZHELYAZKOVA[1], M. FRITZE[1], SERENA E. DOOL[1], **s.puechmaille@gmail.com
[1]*Zoology Institute & Museum, Greifswald University, Greifswald, Germany.*

The longstanding utility of fungi to all life on earth has often been matched by their 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 to North America from Europe. To prevent such an event from happening again, elucidating the precise source in Europe and knowing when the introduction happened would provide us with critical information to infer the mode of introduction. Hence the first objective of this project is to elucidate the location of the source population in Europe and the timing of introduction. The second objective is to characterise population structure of the fungus across Europe and to evaluate whether intra-European movements of the fungus are of concern (e.g. if different geographically separated lineages exist). We used an unprecedented number of samples (n >2,000) collected from 21 countries in Europe and genotyped for a set of 18 variable microsatellites, to build a genetic reference collection that is critical for identifying the source population of the North American introduction. Based on this reference dataset, we developed a novel method that allows precise identification of the origin of any sample based on its genetic fingerprint. This large genetic dataset also revealed a surprisingly strong population structure of the fungus across Europe, suggesting that movements of the fungus across Europe via anthropogenic activities might be of concern.

DIFFERENTIAL EFFECTS OF CLIMATE CHANGE ON THE BODY CONDITION OF BATS [O]

XAVIER PUIG-MONTSERRAT [1,3]**, ADRIÀ LÓPEZ BAUCELLS[1,2], MARIA MAS[1], CARLES FLAQUER[1], **xavierpuigm@gmail.com
[1]*Natural Sciences Museum of Granollers, Granollers, Catalonia, Spain;*
[2]*Centre for Ecology, Evolution and Environmental Changes, University of Lisbon, Portugal;*
[3]*Galanthus Association, Catalonia, Spain.*

The effects of climate change on the distribution and viability of both habitats and species has received increasing attention during the last decade. The physiological responses of bats to climate change have received some attention, mainly regarding the changes in reproductive rates, though it remains unclear whether it compromises their fitness. We used four species that were sampled in Catalonia (NE Iberia) during the period 2001-2012, along with daily climate data from a network of 72 automated weather stations spread across the survey area, to test for the effect of climatic variables on the body condition of bats. Sets of separate data were built grouping adult individuals of the same gender and species that were captured between 15 May and 15 June (before reproduction). Only those sets containing at least 20 records per year for a minimum of 4 years were included. Linear models were build using body condition as dependent variable (1411 individuals from 958 locations) and data from the nearest weather station (minimum, maximum and average temperature, relative humidity, aridity, mean precipitation and cumulated precipitation). Since there is no general agreement on the best index of body condition, four different indexes were tested. Daily models were built for the data set, starting from the day of capture of each individual and going back 365 days. Weak though significant correlations (r2 = -0.403, p< 1e-20) were found between male *Hypsugo savis's* body condition and winter average temperature, with the effect stronger in December. Cumulated precipitation during winter had an inverse effect on this species (r^2 = 3.12, p< 1e-10). Male *Miniopterus schreibersii*'s body condition showed a very weak positive correlation with winter temperatures (r^2 = -0.212, p< 1e-15). No significant relations were found for the remaining groups. Though further research is needed, we suggest that climate change may affect the fitness of some temperate bat species.

IMPORTANCE OF BIA□OWIE□A PRIMAEVAL FOREST, POLAND, AS A PRIMARY SITE FOR WESTERN BARBASTELLE BAT, *BARBASTELLA BARBASTELLUS* (SCHREBER, 1774) [P]

ALEK RACHWALD[1]**, ANETA ZAPART[2], WOJCIECH NOWAKOWSKI[3],
**a.rachwald@ibles.waw.pl
[1]*Forest Research Institute, Forest Ecology Department, Sękocin, Poland;*
[2]*Gdańsk University, Department of Zoology and Ecology of Vertebrates, Gdańsk, Poland;*
[3]*Warsaw, Poland.*

The occurrence of the barbastelle bat, *Barbastella barbastellus*, in the woodland areas of the Białowieża Primaeval Forest, Poland, during July 2016 was examined. Earlier observations of barbastelles in this area were mostly connected with riverine and village areas, with a few records from strict woodland, but this was due to the research methods. In this study, we were able to record and distinguish barbastelle passes by means of bat detecting techniques, as well as to catch barbastelles with mist nets inside forest stands. Also 20 wooden buildings in close vicinity to the forested area were checked for the presence of barbastelle colonies. Field recordings were based on using LunaBat DFR-1 full-range ultrasound detectors (Animal Sound Labs). Barbastelles were found at all 11 netting locations and at 18 of 19 detecting transects (both in National Park and in the managed forests). Barbastelle was a highly dominant species during the netting: the ratio of barbastelles to all remaining species was 57:14, which is a surprising result. Lactating females were present in all locations. On the other hand, no colony was found in the buildings. According to these results, it is very likely that this species is much more widely distributed in the Białowieża Forest area than was expected from previous data. Thus, Białowieża Forest can be considered as one of most important, European woodland sites for this endangered species.

THE IMPORTANCE OF BIOTIC AND ABIOTIC INTERACTIONS FOR UNDERSTANDING BAT SPECIES DISTRIBUTIONS IN AN INSULAR SYSTEM [O]

ANA RAINHO[1]**, **amrainho@fc.ul.pt
[1]*Departamento de Biologia Animal & Centre for Ecology, Evolution and Environmental Change. Faculdade de Ciências, Universidade de Lisboa. 1749-016 Lisbon, Portugal.*

The Azores is a volcanic archipelago located in the North Atlantic Ocean astride the mid-Atlantic ridge, within the biogeographic region of Macaronesia. These isolated islands are unique and much of their natural values are endangered or extinct. Bats are probably the only mammals native to these islands and to the Azores; two species were recorded during a survey performed during the early 2000s: *Nyctalus azoreum*, endemic to this archipelago, and *Pipistrellus maderensis*, endemic to Macaronesia. Both species are listed as Vulnerable by the IUCN Red List. *N. azoreum* is present in seven of the nine islands of the archipelago, while *P. maderensis* was initially recorded only in three, but recently was confirmed in a further three islands. The two species only coexist on four islands, and *P. maderensis* shows very small populations and restricted distribution on these islands. Competition may be one of the main mechanisms to achieve permanent or temporal coexistence for multiple species and we hypothesized that this biotic interaction is one of the main drivers defining the patterns of distribution of these two species in the islands. Islands are largely recognized as natural laboratories and the patterns of co-occurrence observed provided an excellent scenario to test this hypothesis. We used null-model (co-occurrence), species distribution modelling and niche estimation methods to evaluate the roles of several landscape descriptors and competition, and compared the potential and realized niche of the two species. Results suggest that adaptation to abiotic conditions has been a major force underpinning the distribution of these species. However, competition may also be an important driver, limiting the spread of any one species. The results obtained will be discussed in a conservation biology framework.

LIFETIME REPRODUCTIVE SUCCESS OF FECUND FEMALE GREATER HORSESHOE BATS IS AFFECTED BY MATRILINEAL RANK AND GRANDMOTHER'S PARTURITION [O]

ROGER D. RANSOME[1]**, HELEN WARD[2], STEPHEN J. ROSSITER[2], GARETH JONES[1], **rogerransome@hotmail.com
[1]*School of Biological Sciences, University of Bristol, Bristol, BS8 1UG, U.K.;*
[2]*School of Biological Sciences, Queen Mary, University of London, London, E1 4NS, U.K.*

The reproductive performance of cohorts of female bats born over 14 years was followed through 3 generations. The 21 matrilines identified were split into two mega ranks (MR1 & MR2) for comparison. MR division was based on matrilineal lifetime reproductive success (LRS) over these years. MR1 matrilines showed longer lifespans and LRS (median 11 years; 8 pups) and MR2 matrilines showed shorter lifespans (median 7 years; 5 pups). A total of 22 highly successful female bats, producing 10 or more pups in their lifespan (= stars) were selected for detailed analysis. Star LRS was related to pup sex ratio, and to parturition sequences of mother and grandmother to better understand the mechanisms that regulate bat populations. Greater horseshoe bats were studied in the UK at the northern edge of their range. Stars were individuals born in favourable summers and did not show stunted growth due to adverse climate. Stunted growth after cold springs is a key factor reducing longevity and LRS. Most stars were born into MR1 matrilines, but some were from MR2. Stars from both MRs produced a mean of 12 pups over their lifespan. However, MR1 stars had significantly more female pups than MR2 stars. The latter had more male pups. The mean parturition sequence of star mothers was significantly greater (mean 4.82) than that of grandmothers (mean 2.63). Stepdown regression analysis of number of female pups born to all stars was related to 7 factors, including survival, total pup numbers, mother's & grandmother's parturition sequence. Female pup number reduced with both MR and increasing grandmother's parturition sequence. Grandmother's parturition sequence was the sole factor affecting male pup number positively. The importance of mega rank and a grandmother's parturition sequence will be discussed in relation to stress resistance, senescence in female bats and population recovery. Our study highlights the value of long-term ringing studies in helping to understand population changes.

PREDICTING COMMUTING CORRIDORS OF BATS [O]

THOMAS RAVESSOUD[1,2], KLAUS ECKER[1], FABIO BONTADINA[1,3], CLAUDE STECK[4], STEFFI VON FELTEN[5], LUCRETIA DEPLAZES[3], HUBERT KRÄTTLI[6], MARTIN K. OBRIST[1]**, **martin.obrist@wsl.ch
[1]Swiss Federal Research Institute WSL; Birmensdorf, Switzerland;
[2]University of Lausanne; Lausanne, Switzerland;
[3]SWILD - Urban Ecology & Wildlife Research; Zürich, Switzerland;
[4]FrInaT - Freiburg's Institute of Applied Animal Ecology; Freiburg, Germany;
[5]Oikostat - Ecological Statistics; Ettiswil, Aarau, Birwinken, Zürich, Switzerland;
[6]Bat Conservation Switzerland; Zürich, Switzerland.

Three main targets for the conservation of bats exist: roosts, foraging areas and commuting corridors. Roosts can be relatively well targeted at least in house-dwelling bats, and foraging areas often profit from other habitat conservation measures. But commuting corridors are difficult to protect due to limited knowledge about their location and importance. We aimed at finding models for predicting the commuting activity of bats in agricultural landscapes, focussing on two bat species with different navigational adaptations: *Rhinolophus hipposideros*, known to depend strongly on vertical structures, and *Myotis myotis*, less reliant on such features. We recorded acoustic activity at 30 sites around six roosts per species, twice before and after the juveniles were flying, at vertically structured and more open recording sites. Species-specific passes during peak activity of dawn emergence and dusk return were considered as commuting. In a first analytical step, we modelled the relation between the commuting activity and 170 environmental predictors per recording site. The most relevant predictors were identified with automatic Least Absolute Shrinkage and Selection Operator (LASSO) model selection, cross-validated using training and testing sets to evaluate the predictive model performance. Activity of both species was mainly related to three-dimensional arrangement of landscape features, terrain ruggedness, open spaces, and distance to structures, highlighting the importance of fine-scaled spatial parameters. Using the inverse of these habitat selection predictions as cost matrix, we modelled Least-Cost Distance corridors and critical features therein (pinch-points in current flow). The resulting corridor models allow the visualizing and targeting of important commuting corridors for landscape planning and conservation. In a final step, model calculations will be compared with expert's nomination of corridors, to assess necessary effort and yield in corridor identification.

USING LANDSCAPE GENETICS TO UNDERSTAND BAT RESPONSES TO CLIMATE CHANGE [O]

ORLY RAZGOUR[1]**, JOHN TAGGART[2], MICHAËL BEKAERT[2], JAVIER JUSTE[3], CARLOS IBÁÑEZ[3], SÉBASTIEN J. PUECHMAILLE[4], ANTTON ALBERDI[5], STEPHANIE MANEL[6],
**Orly.Razgour@soton.ac.uk
[1]*Biological Sciences, University of Southampton, Southampton, U.K.;*
[2]*Institute of Aquaculture, University of Stirling, Stirling, U.K.;*
[3]*Estacion Biológica de Doñana (CSIC), Seville, Spain;*
[4]*Ernst-Moritz-Arndt University, Greifswald, Zoological Institute and Museum, Germany;*
[5]*Natural History Museum of Denmark, University of Copenhagen, Copenhagen, Denmark;*
[6]*EPHE, PSL Research University, CNRS, Montpellier, France*.

Climate change is a major threat to global biodiversity that is predicted to force many species to move in search of suitable conditions. The ability of species to shift their ranges in response to future changes is likely to be limited by landscape barriers to movement and anthropogenic land cover changes. We integrated genomic tools with geographic data and modelling approaches to understand and predict the responses of bats to climate change based on the effects of the landscape on their movement potential. We focus on two recently-confirmed cryptic forest bat species of the Natterer's species complex, *Myotis escalerai* and *Myotis* spA, that are sympatric in the Iberian Peninsula, but whose distributions appear to be limited by interspecific competition. We used ddRAD-sequencing to generate genomic datasets of ~20,000 SNPs for each species. Using the landscape genetics approach we statistically related spatial patterns of genetic variation to landscape variables likely to affect movement in forest bats. We found that landscape connectivity between *M. escalerai* populations is a function of habitat suitability, slope and tree cover, while *M.* spA is affected by land cover type, distance to forests and rugged landscapes. We identified isolated populations and population clusters based on landscape connectivity. Next, using species distribution modelling we predicted shifts in the suitable climatic ranges of both species to higher latitudes and altitudes under future climate change, with *M.* spA, in particular, losing most of its Iberian range. We modelled the ability of the two species to shift their ranges and reach climatically suitable areas given the effects of the landscape on their movement potential and population connectivity. Our study highlights the importance of understanding movement ecology and limits to future landscape connectivity for predicting the ability of bats to persist under climate change.

INVESTIGATING THE ATTITUDE OF PRIESTS TOWARD BATS TO IMPROVE THE CONSERVATION OF BAT ROOSTS IN CHURCHES [P]

KAROLINA REBERNIK[1], MAJA ZAGMAJSTER[2]**, **maja.zagmajster@bf.uni-lj.si
[1]Institute of the Republic of Slovenia for Nature Conservation, Regional Unit Ljubljana, Cankarjeva cesta 10, SI 1000 Ljubljana, Slovenia;
[2]Department of Biology, Biotechnical Faculty, University of Ljubljana, Jamnikarjeva 101, SI 1000 Ljubljana, Slovenia.

Improving the protection of bat roosts in churches is one of the bat conservation priorities in Slovenia. Many bat species have nursery colonies in buildings, especially church attics and belfries. Moreover, some species rely almost exclusively on such sites. The most common problem is closure of bat access points, sometimes even at the beginning of the nursery period. Next is the renovation of churches in a time and/or manner unsuitable for bats. In this study, we aimed to investigate what were the main factors leading to destruction of bat roosts. The main managers responsible for the churches are priests, so they were the target group of our study. We conducted semi-structured interviews with 21 priests, who were separated into two groups: those responsible for churches with already destroyed or negatively affected bat roosts, and those responsible for intact bat roosts. Their answers were analysed using text coding and interpretation approach. Our results showed that the attitude and behaviour toward bats were better in priests that were familiar with the biology of bats and who rejected the myths and superstitions about bats. If bats were considered as the source of damage to sacred buildings, this negatively affected priests' attitude toward protection of bat roosts in churches. Priests were willing to improve their future actions, if they were informed that their past actions were not appropriate for bat conservation. Besides the legislative acts and financial aid, raising awareness is a key to improving the knowledge, attitude and behaviour of priests towards bats and the protection of their roosts in churches. These findings support the need to put more time and energy into informing the priests about bats and conservation issues. But, it was also stressed by some priests that a more regular presence of state conservation authorities at the sites would be needed and appreciated.

FLORENCE LOVES BATS … AND BATS LOVE FLORENCE! ARCHITECTS AND NATURALISTS DURING THE MEDICI RENAISSANCE PERIOD AND TODAY'S BAT CONSERVATION [P]

MARCO RICCUCCI[1]**, **marco.riccucci@gmail.com
[1]*Museum of Natural History of the University of Florence, Zoological Section «La Specola», Italy.*

Florence is regarded as the birthplace of the Renaissance. Conrad Gessner's (1516–1565) "Historiae animalium" (History of the Animals) is an encyclopaedic "inventory of Renaissance zoology". Some renowned artists such as Bernardo Buontalenti (1531-1608), Gherardo Silvani (1579-1675) and even Michelangelo Buonarroti (1475-1564) used the image of bats in their artistic works. Buontalenti owned a vegetable garden bordering on the famous Giardino dei Boboli (Boboli Garden) and also built the "Grotta Grande" in the same garden. This city park is visited by many bats (*Pipistrellus kuhlii*, *Hypsugo savii*, *Plecotus austriacus*) that also colonized the bat boxes placed on the "Torrino" (astronomical observatory) on the top of the adjoining Museum of Natural History. Some examples: Palazzo di Bianca Cappello - Buontalenti built two new windows on the ground floor and under the sills inserted a bat motif carved with outspread wings; Casino Mediceo di San Marco - here Buontalenti created motifs that characterize the terminal stage of the Renaissance: zoomorphic decorations such as bats with outspread wings above the entrance portal and under the window-sills; similar decorations are in the nearby Palazzo Capponi-Covoni, by Silvani. Here again we find the motif of the bat in the four ground floor windows; the Ritratto (portrait) di Lorenzo de' Medici duca di Urbino is a marble sculpture by Michelangelo for the tomb of Lorenzo in the Sacrestia Nuova (New Sacristy) of the Basilica di San Lorenzo (Basilica of St Lawrence). Lorenzo is deep in thought and his left elbow rests on a locked chest decorated with the head of a bat. The project "BAT BOX: Un pipistrello per amico" (Be a bat's friend) by the Museum of Natural History of the University of Florence was launched in 2006 and about 100 bat boxes have been placed within the boundaries of the city of Florence (over 40,000 bat boxes throughout Italy). A farm just south of Florence has succeeded in restoring the indigenous Tuscan grapes of the Renaissance and has installed 600 bat boxes to protect its vineyards from pests.

ARE ALL MOUNTAINS THE SAME? CHANGES IN SOUTH AMERICAN BAT DIVERSITY PATTERNS ALONG ENVIRONMENTAL GRADIENTS [O*]

CRISTINA RIOS-BLANCO[1]**, RICHARD D. STEVENS[1,2], **makris88@gmail.com
[1]*Department of Natural Resources Management, Texas Tech University, Lubbock, TX 79409 USA;*
[2]*Museum of Texas Tech University, USA.*

Biodiversity patterns are often related to environmental gradients. Typical approaches to understanding the relationship between biodiversity and environmental gradients evaluate changes in species richness. However, different aspects of biodiversity may elicit different patterns along the same gradient. Using other dimensions of biodiversity may provide a more comprehensive understanding of biodiversity along environmental gradients. However, biodiversity changes along one gradient may also vary with respect other gradients. For example, patterns of different dimensions of biodiversity along elevation gradients may change with latitude. Thus, it is important to consider whether biodiversity patterns along one gradient could be affected by variation along another. We examined change in four dimensions (taxonomic, phylogenetic, functional and phenetic) of bat biodiversity across elevational gradients that differ based on their latitudinal position in South America. We characterized biodiversity of 16 bat metacommunities using 12 diversity indices. We determined significance of diversity indices by comparing our measurements against index values from random communities. To examine whether diversity changes were similar across metacommunities we used analysis of covariance. Most metacommunities exhibit a decrease in biodiversity towards higher elevations. Decreases are more evident in the taxonomic dimension. However, these changes depended upon latitude. Metacommunities at lower latitudes exhibit a more rapid decline in biodiversity relative to higher latitude metacommunities. Our results suggest that biodiversity patterns along elevational gradients cannot be generalized along latitudinal gradients. Biodiversity changes in the tropics are more related to shifts in dominance of phylogenetic and functional groups with increasing elevation. In contrast, elevational changes in biodiversity at higher latitudes are primarily explained by changes in taxonomic diversity.

THE IMPACT OF CLIMATE ON TRENDS IN COMMON BAT SPECIES [O]

NIAMH ROCHE[1]**, TINA AUGHNEY[1], STEVE LANGTON[2], DEIRDRE LYNN[3], FERDIA MARNELL[3], **niamhr@batconservationireland.org
[1]*Bat Conservation Ireland, Virginia, Ireland;*
[2]*Steve Langton Statistical Consultancy, Malton, England;*
[3]*National Parks and Wildlife Service, Dublin, Ireland.*

The Irish car-based bat monitoring scheme was established in 2003. Three species are targeted for annual monitoring: *Pipistrellus pipistrellus*, *P. pygmaeus* and *Nyctalus leisleri*. All three species are common in Ireland and are considered habitat generalists. Data has been collected by volunteers from the same locations (30 x 30 km survey squares) using the same time expansion detectors every July and August. The 28 survey squares were originally randomly selected and the same route, each with 15 x 1.6 km transects, is followed each year. Acoustic data are analysed using Bat Sound. All three bat species have shown increasing trends since 2004. For this study we aimed to determine whether observed bat trends, island-wide and/or within survey squares, have been influenced by weather. Weather data for 14 years of the survey was gathered from 68 Met Éireann weather stations. Met data was calculated as a weighted average so that stations within or closest to the survey square had greatest influence. Temperature and rainfall data were combined into quarterly figures representing seasons. Data were examined both spatially and temporally. Spatially, while some positive significant relationships were found between temperature and both *P. pipistrellus* and *N. leisleri* the significance of the relationships was lost when factors for eastings and northings were included. Temporally, with bat and weather data averaged over all the squares, significant relationships were found between temperature and yearly island-wide *P. pipistrellus* levels, and between *P. pygmaeus* and rainfall. At the level of survey square, with year as a fixed factor, similar relationships between the three species and weather variables were found, however. These results showed that warmer temperatures, in particular seasons of the previous year, positively impact on bat activity levels for all three target species. We will discuss our findings in relation to predicted climate change models for Ireland.

REGIONAL MISMATCHES BETWEEN AGRICULTURAL PEST AND BIOCONTROL SERVICES BY BATS: AN EXAMPLE FROM CONTINENTAL PORTUGAL [O]

JAVIER RODRÍGUEZ-PÉREZ[1]**, GERARDO JIMÉNEZ-NAVARRO[1], BRUNO SILVA [1], TIAGO MARQUES[1], ANTÓNIO MIRA[1], JOSÉ M. HERRERA[1],
**jvr.rodriguez@gmail.com
[1]*CIBIO-InBIO/UE, Research Center in Biodiversity and Genetic Resources, University of Évora, Casa Cordovil 2a Andar, Rua Dr. Joaquim Hemrique da Fonseca, 7002-554, Évora, Portugal*.

The increasing expansion of agriculture intensification has driven a scenario of decline of biodiversity and ecosystem functions. Currently, it is important to coordinate efforts using strategies and incentives for maintaining and recovering biodiversity at the landscape scale. Here, we study the functional value of a bat species community on potentially maintaining natural pest control in agroecosystems in continental Portugal, with the aim of potentially identifying regional mismatches between bat diversity and ecosystem functions. Specifically, we aim to evaluate the role of the region's bats in biological control, as areas with high probability of species' occurrence and pest-control service. In addition, we aim to identify regions for potentially restoring biocontrol, as areas suitable to be restored and colonized by bat species. Using censuses of bat species throughout continental Portugal, we first calibrated Species Distribution Models (SDM) to predict the potential distribution of bat species by environmental factors (i.e. land-cover and geoclimatic variables). The potential area of (insect) pest species was based on the pest-crop specificity and the land-use area of each crop. We assessed the potentially species-specific consumption of pests by bats from literature. Finally, we calculated the ecosystem service by bats as areas of mutual occurrence of both biocontrollers and pest species. We found regional mismatches between bat and pest distribution, which identifies areas of high bat richness in northern Portugal and high pest richness in southern Portugal. Concerning ecosystem services provided by bats, we identify areas of high probability of pest biocontrol in north-western and southern Portugal agreeing with areas rich in tree-like plantations, open agricultural areas and agroforests, respectively. Finally, we calculated the potential area biologically controlled by bats and the area with potential to be restored for pest biocontrol.

INFLUENCE OF LOCAL LANDSCAPE FEATURES ON ROAD COLLISION RISKS [O*]

CHARLOTTE ROEMER[1,2]**, YVES BAS[1], THIERRY DISCA[2], AURÉLIE COULON[1,3],
**croemer@biotope.fr
[1]*Muséum national d'Histoire naturelle, France;*
[2]*Biotope, France;*
[3]*CNRS, France.*

Bat species make use of a particular type of sonar, depending on their niche specialisation, which allows aerial-hawkers to fly at heights, while gleaners' sonar is better suited to fly close to the ground. Knowledge of bat movement ecology has mainly been developed at intermediate spatial scales for the study of home ranges. Little is known at a very small scale, where obstacle avoidance can be observed. This lack of information is problematic when it comes to assessing and mitigating collision risks. Many assumptions are formulated concerning the reaction of each species to landscape features and hence their role in road mortality. Gleaners are described as flying close to the ground and vegetation whereas aerial-hawkers are supposedly more plastic. However, these elements rely mainly on bat experts' experience and may lead to hazardous impact assessment studies. The aim of this study was to determine how several types of local landscape configuration (simple or double hedges, forest, no three-dimensional element) and site characteristics (road size, vegetation height, distance to the vegetation edge) alter collision risks. Acoustic flight path tracking was performed at 58 road locations in southern France, during two whole nights per site. This allowed us to estimate species activity and presence in risky areas (i.e. above the road). We then used conditional probabilities to model how local landscape configuration affect species activity and presence at risk. Results are presented for the most common species (*Pipistrellus pipistrellus*, *Nyctalus leisleri*, *Miniopterus schreibersii* and the group of small *Myotis* spp.). These results shed more light on the understanding of how local landscape influences collision risks by distinguishing the contributions of bat activity and bat position in space. The identification of the role of road features and maintenance strategies is important in order to give guidance for road collision mitigation.

THE EFFECTS OF LED STREET LIGHTING ON BAT ACTIVITY [O*]

ELIZABETH G. ROWSE[1]**, STEPHEN HARRIS[1], GARETH JONES[1],
**liz.rowse@bristol.ac.uk
[1]*School of Biological Sciences, Life Sciences Building, University of Bristol, 24 Tyndall Avenue, Bristol, U.K.*

Bats show species-specific responses to artificial lighting: some feed on the insects that are attracted to street lights, whereas others avoid light. Many street lights across Britain, and elsewhere in the world, are being switched from older lighting technologies, such as low-pressure sodium (LPS) to light emitting diode (LED) lights. LED lights have a number of advantages over older lighting technologies, including energy efficiency, increased flexibility and longevity. LED lights also allow for the implementation of management schemes, such as dimming. Dimming not only reduces the intensity of the street light, but also the amount of light distributed from the light source. Reducing the spread of light may be less detrimental to light-intolerant bats, by creating dark refuges and corridors which light-intolerant bats may use. Understanding how these changes in spectral output and light intensity affect bat behaviour will help inform conservation strategies. We used a before-after-control-impact paired design to examine the effects of the switch-over from LPS to LED street lights on bat activity across southern England. We found no significant differences in either bat activity or feeding behaviour around LPS and LED lights. This is positive from a conservation perspective as many existing street lights are being, or have been, switched to LED lights before the ecological consequences have been assessed. However, it is important that these results are viewed alongside the wider impacts of artificial lighting on bats. Artificial lighting generally has a negative impact on slow-flying bats, many of these species are already vulnerable to extinction, and changes in lighting technology do not address this issue. We will also present results from a dimming study, to determine if reducing the light intensity of LED lamps is an effective mitigation strategy for light-intolerant bats.

DETECTING BAT DIVERSITY HOTSPOTS AND ECOLOGICAL CORRIDORS AS A TOOL FOR CONSERVATION PLANNING: ITALY'S PROTECTED AREA NETWORK AS A CASE STUDY [P]

DANILO RUSSO[1, 2], LEONARDO ANCILLOTTO[1], LUCIANO BOSSO[1], LUCA CISTRONE[3], VALENTINA NARDONE[1]**, PAOLA CONTI[4],
**valentina.nardone@unina.it
[1]*Wildlife Research Unit, Laboratorio di Ecologia Applicata, Dipartimento di Agraria, Università degli Studi di Napoli Federico II, Italy;*
[2]*School of Biological Sciences, University of Bristol, U.K.;*
[3]*Forestry and Conservation, Italy;*
[4]*Ente Parco Nazionale del Vesuvio, Italy.*

Parks and reserves still represent one of the main approaches to in situ conservation of animal populations threatened by human action. However, if sufficient connectivity is not offered by the landscapes surrounding sites where important populations occur, gene flow between such sites may be difficult or impossible, weakening the functioning of protected areas. Italy has a significant network of parks, reserves and Natura 2000 sites, but ecological corridors connecting them are often jeopardized by urbanization, agricultural intensification and road development. In this project, we focus on the Italian bat fauna (35 species in the whole country, several of which are classified as threatened in the national Red List). The project involves one academic institution (WRU, Department of Agriculture, University of Naples Federico II) as well as seven of the country's main national parks (Vesuvius National Park, Abruzzo, Lazio and Molise National Park, Circeo National Park, Tuscan Archipelago National Park, Aspromonte National Park, Alta Murgia National Park, Gargano National Park). In 2017-2018 extensive surveys will be carried out in the parks to collect occurrence records for all bat species present in their territories. The data will be integrated with records already available for the remaining parks, reserves and Natura 2000 sites. The dataset will be used to develop species distribution models whose outputs will be overlaid to identify diversity hotspots within protected areas. We will then model the corridor network to detect areas both within and between protected areas which bear high value for bats as ecological corridors, as well as areas that might be restored to improve connectivity. The project represents a best practice example of nationwide collaboration among academic and conservation institutions leading to guidelines that might be of crucial importance for the large-scale management of bat populations.

SOCIALITY AS A DRIVER OF THERMOREGULATORY AND ROOST-SWITCHING BEHAVIOUR IN A FOREST BAT [O]

DANILO RUSSO[1,2]*, LUCA CISTRONE[3], IVANA BUDINSKI[4], GIULIA CONSOLE[5], CLAUDIA MILIGHETTI[6], IVY DI SALVO[1], VALENTINA NARDONE[1], MARK BRIGHAM[7], LEONARDO ANCILLOTTO[1]**, **leonardoancillotto86@gmail.com
[1]*Wildlife Research Unit, Dipartimento di Agraria, Università degli Studi di Napoli Federico II, Portici, Italy;*
[2]*School of Biological Sciences, University of Bristol, Bristol, U.K.;*
[3]*Forestry and Conservation, Cassino, Italy;*
[4]*Department of Genetic Research, Institute for Biological Research "Siniša Stanković", University of Belgrade, Serbia;*
[5]*Dipartimento di Biologia, Università degli Studi di Firenze, Firenze, Italy;*
[6]*Dipartimento di Biologia e Biotecnologie "Charles Darwin", Università degli Studi di Roma "La Sapienza", Roma, Italy;*
[7]*Department of Biology, University of Regina, Regina, Canada.*

In summer, many temperate bat species use daytime torpor, but breeding females do so less, to avoid interference with reproduction. In forest-roosting bats, deep tree cavities buffer roost microclimate from abrupt temperature oscillations and facilitate thermoregulation. Forest bats also switch roosts frequently, so thermally suitable cavities may be limiting. We tested how barbastelle bats (*Barbastella barbastellus*), often roosting beneath flaking bark in snags, may thermoregulate successfully despite the unstable microclimate of their preferred cavities. We assessed thermoregulation patterns of bats roosting in trees in a beech forest of central Italy. Although all bats used torpor, females were more often normothermic. Cavities were poorly insulated but social thermoregulation probably overcomes this problem: a model incorporating the presence of roost mates and group size explained thermoregulation patterns better than others based respectively on the location and structural characteristics of tree roosts and cavities, weather, or sex, reproductive or body condition. Homeothermy was recorded for all subjects, including non-reproductive females: this probably ensures availability of a warm roosting environment for non-volant juveniles. Homeothermy may also represent a lifesaver for bats roosting beneath loose bark, very exposed to predators, since homeothermic bats may react quickly in case of emergency. We also found that barbastelle bats maintain group cohesion when switching roosts: this probably accelerates roost occupation at the end of a night, quickly securing a stable microclimate in the newly occupied cavity. Overall, both thermoregulation and roost switching patterns were satisfactorily explained as adaptations to a structurally and thermally labile roosting environment.

LONG-TERM EFFECTS OF FLOOD-LIGHTS ON BROWN LONG-EARED BATS IN CHURCHES [O]

SONIA SÁNCHEZ-NAVARRO[1,3]**, JOHAN EKLÖF[2], JENS RYDELL[1],
**sonia_san_na@hotmail.com
[1]*Biology Department, Lund University,Lund, Sweden;*
[2]*Krokdalsvägen 88, SE-517 34 Bollebygd, Sweden;*
[3]*Estación Biológica de Doñana-CSIC, Sevilla, Spain.*

We surveyed 110 country churches in south-western Sweden for the presence of brown long-eared bats, *Plecotus auritus*, in summer 2016 by visual inspection and/or evening emergence counts. Each church was also classified according to the presence and amount of aesthetical directional lights (flood-lights) aimed on its walls and tower. Sixty-two of the churches had been surveyed by one of us (JR) between 1980 and 1990, before lights were installed, using the same methods. Churches with bat colonies had decreased significantly in frequency from 61% in the 1980s to 38% by 2016. All abandoned churches had been fitted with aesthetic lights in the period between the two surveys, and bat colonies remained significantly less frequently in those that were lit from all directions, compared to those that were partly lit. In churches that remained unlit, bat colonies (N=12) showed extraordinary roost fidelity and every colony remained after 25+ years between the surveys. Our results suggest that churches were abandoned by *P. auritus* colonies following installation of flood-lights, particularly when this occurred from all sides of the church. Lighting of churches and other historical buildings is a serious threat to the long-term survival and reproduction of light-averse bats such as *Plecotus* spp. Bat roosts are strictly protected according to the EU Habitats Directive and the EUROBATS Agreement. Lighting of buildings for aesthetic purposes is already a serious environmental issue, because important bat roosts are destroyed in large numbers, and the problem should be handled accordingly. As a start, installation of flood-lights on buildings should require an environmental impact assessment (EIA).

IMPORTANCE OF HOST ECOLOGY FOR THE PRESENCE OF *BARTONELLA* SPP. IN THE ECTOPARASITES OF INSECTIVOROUS BATS IN CENTRAL AND SE EUROPE [O]

ATTILA D. SÁNDOR[1]**, ALEXANDRA CORDUNEANU[1], LEVENTE BARTI[2], PÉTER ESTÓK[3], TAMÁS GÖRFÖL[4], MIHÁLY FÖLDVÁRI[5], HEIN SPRONG[6], ZOLTÁN LÁSZLÓ[7], GÁBOR FÖLDVÁRI[8], **adsandor@gmail.com

[1]*Department of Parasitology and Parasitic Diseases, University of Agricultural Sciences and Veterinary Medicine, Cluj-Napoca, Romania;*

[2]*Romanian Bat Protection Association – Central Branch, Odorheiu Secuiesc, Romania;*

[3]*Department of Zoology, Eszterházy Károly University, Eger, Hungary;*

[4]*Department of Zoology, Hungarian Natural History Museum, Budapest, Hungary;*

[5]*Department of Evolutionary Zoology and Human Biology, University of Debrecen, Debrecen, Hungary;*

[6]*Centre for Zoonoses & Environmental Microbiology, Centre for Infectious Disease Control, National Institute for Public Health and the Environment, Bilthoven, The Netherlands;*

[7]*Hungarian Department of Biology and Ecology, Babeş-Bolyai University, Cluj-Napoca, Romania;*

[8]*Department of Parasitology and Zoology, University of Veterinary Medicine, Budapest, Hungary.*

Bats are ideal hosts for a number of specialised arthropod ectoparasites, such as mites, ticks, fleas and flies. Their most specialised ectoparasites are the hippoboscoid flies, mostly flightless flies occurring only on bats. Throughout their blood-feeding, these ectoparasites are able to transmit a number of pathogens, and are known vectors of a number of viral, bacterial or protozoan diseases. Among these, a wide variety of bacteria of *Bartonella* spp. are known to parasitize bats and their ectoparasites. The aim of the present work was to assess, by PCR and sequencing, the prevalence and diversity of *Bartonella* spp. in hippoboscoid flies of bats occurring naturally in Hungary and Romania, and to find factors contributing to the high diversity recorded. In order to achieve this, we made molecular identification of *Bartonella* sequences from parasitic flies and compared them to sequences deposited in GenBankTM and evaluated the importance of host and vector ecology for the presence and prevalence of these bacteria. In our study 158 bat flies tested positive for *Bartonella* spp. DNA (29.1%). *Bartonella* spp. sequences were identified in 8 out of 10 Nycteribiidae fly species, collected from 11 out of the 14 bat species studied. Polyxenous bat flies had the lowest prevalence. Individual nycteribiid fly species explained the distribution of *Bartonella* spp. only marginally; with only 4 species contributing significantly to the observed pattern. Bat host species explained most of the variance found in *Bartonella* spp. distribution, with 6 individual species significantly contributing to the modelled distribution. Bat gender was another significant factor, with males carrying more than twice as many *Bartonella*-positive bat flies than females. The bat roost site also made an important contribution, as significantly higher number of *Bartonella*-infected bat flies were collected on bats using underground shelters, than from bats roosting either in buildings or in trees.

INTEGRATING LANDSCAPE GENETICS WITH CONNECTIVITY ANALYSES TO PRIORITIZE REGIONAL CONSERVATION OF *PLECOTUS AURITUS BEGOGNAE* IN THE IBERIAN PENINSULA [O]

HELENA SANTOS[1], RAQUEL GODINHO[1], ORLY RAZGOUR[2,3,4], JAVIER JUSTE[5], CARLOS IBÁÑEZ[5], HUGO REBELO[1,3,6]**, **hugo.rebelo@cibio.up.pt
[1]CIBIO/InBIO, University of Porto, Vairão, Portugal;
[2]Biological Sciences, University of Southampton, Life Sciences Building, Southampton, U.K.;
[3]School of Biological Sciences, University of Bristol, Life Sciences Building, Bristol, U.K.;
[4]Biological & Environmental Sciences, University of Stirling, Stirling, Scotland, U.K.;
[5]EBD–Estación Biológica de Doñana (CSIC), Seville, Spain;
[6]CEABN/InBIO, Instituto Superior de Agronomia, University of Lisboa, Lisbon, Portugal.

Landscape composition plays a significant role in shaping species distributions, population structure and connectivity. Currently, one of the main methodological challenges is the integration of these themes into a single analytical approach. Landscape genetics tests the effect of landscape and environmental variables on the spatial genetic structure of populations. While this approach allows the identification of the main drivers and barriers to gene flow, it does not consider the connectivity between populations. Thus, areas susceptible to isolation may be overlooked. Here, we identified the main environmental drivers of the population structure and connectivity of *Plecotus auritus begognae* in the Iberian Peninsula. We gathered over 360 samples covering the whole Iberian range of the species and genotyped those samples for 19 microsatellite loci. For the spatial analyses we considered over 50 environmental variables divided into three sets: land cover, topography and climatic. Our results show that there was no spatial structure of the populations within the bat's range in Iberia (k=1 populations), i.e. high levels of gene flow were detected. However, the landscape variables distance to forests and to cliffs seemed to contribute marginally to the maintenance of current gene flow patterns. The large extent of forests in the northern and central regions of Iberia seem to prevent the fragmentation of the populations of this bat. Nonetheless, the connectivity analyses showed that areas in the north-west and south-east of Iberia are susceptible to becoming isolated, because their connectivity with the bat's core distribution is dependent on the occurrence of small forests in between. In conclusion, the integration of landscape genetics with connectivity analyses has provided spatially explicit results that have identified areas sensitive to genetic isolation. This information can also be used to develop conservation measures tailored for the species.

BATS IN THE ATLAS OF MAMMALS OF THE REPUBLIC OF SAN MARINO [P]

DINO SCARAVELLI[1,2]**, PAMELA PRIORI[2]*, SANDRO CASALI[3],
GLAUCO BUSIGNANI[3], DANILO LANCI[3], ANDREA SUZZI VALLI[3],
**dino.scaravelli@unibo.it
[1]*Department of Veterinary Medical Science, University of Bologna, Via Tolara di Sopra 50, 40064 Ozzano dell'Emilia, Bologna, Italy;*
[2]*ST.E.R.N.A. and Ornithological Museum F. Foschi, via Pedriali 12, 47121 Forlì, Italy;*
[3]*San Marino Nature Centre (Centro Naturalistico Sammarinese) Via Valdes De Carli 21, 47893 Borgo Maggiore, Republic of San Marino.*

The Republic of San Marino covers 61 km^2 entirely surrounded by Italy. Mainly hilly, it reaches 750m of elevation with the Titano mountain. The oldest Republic of the world, established in 1600, is collecting information on his natural heritage thanks to the effort of San Marino Nature Centre. In 2016 was published the Mammal Atlas, collecting the work of the last ten years on the presence and distribution of 46 species. After urban settlements, the most common landscape is the mosaic of crops, hedgerows and gardens, with scattered rural buildings, and ruderal and shrub vegetation. Some xeric areas as well as a few remnant woods are the wildest small landscapes, together with the high cliff of the Titano and the karstic caves in this limestone. Other caves are located in the gypsum embedded in the hills of clay on the southern and western border. Old railway tunnels are really important for bats as in Piagge where more than 2000 *Miniopterusschreibersii* winter, and during summer it hosts a breeding colony of *Rhinolophuseuryale*. The Atlas covers the distribution of the 17 bat species now recorded based on a grid of 75 1x1 km squares, that cover the 10x10 km UTM UJ06, UJ07, TJ96, TJ97. For each species a bilingual card with local notes and the distribution map is included: there are widespread species, present in all the squares, as *P. kuhlii* and *H.savii*, but others are recorded in only one square (*M. emarginatus*, *M. bechsteinii*, *M. daubentonii*, *M. blythii*, *P. auritus*),a few squares (*M. nattereri* 2, *M. myotis* 2, *P. austriacus* 3, *M. schreibersii* 3) or a small number of squares (*P. pipistrellus* 4, *T. teniotis* 5, *R. euryale* 7, *R. ferrumequinum* 7, *R. hipposideros* 13, *E. serotinus* 26).is The Atlas also provides the first assessment of the status of species in the Republic (IUCN categories): *R. euryale* VU, *R. ferrumequinum* VU, *R. hipposideros* VU, *M. nattereri* VU, *M. emarginatus* VU *M. bechsteinii* DD, *M. daubentonii* VU, *M. myotis* VU, *M. blythii* VU, *P. pipistrellus* LC, *P. kuhlii* LC, *H. savii* LC, *E. serotinus* LC, *P. auritus* DD, *P. austriacus* VU, *M. schreibersii* VU, *T. teniotis* VU.

BAT ACTIVITY IN A WELL PRESERVED HIGH ALPINE FOREST [O]

DINO SCARAVELLI[1,2], PAMELA PRIORI[2]**, GIANNI PAVAN[3],
**pamela.priori@gmail.com
[1]Department of Veterinary Medical Science, University of Bologna, Via Tolara di Sopra 50, 40064 Ozzano dell'Emilia, Bologna, Italy;
[2]ST.E.R.N.A. and Ornithological Museum F. Foschi, via Pedriali 12, 47121 Forlì, Italy;
[3]Interdisciplinary Center for Bioacoustics and Environmental Research, Department of Earth and Environment Sciences, University of Pavia, Via Taramelli 24, 27100 Pavia, Italy.

Despite bats being considered a tropical and equatorial based group of mammals, there is also actually much evidence of a powerful adaptation of some species to cold high elevation habitats. The Alpine ecosystem is one of the most interesting areas to study the evolution of adaptation of these bats thanks to the mosaic of ecosystems, different altitudes and sharp seasonal changes. Thanks to the possibility to record high quality echolocation and social calls of bats in remote locations as part of the collection of sounds for the project SABIOD (Scaled Acoustic Biodiversity) of Pavia and Toulon Universities, we investigated the bats present in a high elevation (1850 m asl) pristine forest dominated by larches and Swiss stone pine aged more than 500 years, located in the Somadida Forest Reserve (46°30'12"N and 12°15'46"E). In this very rare habitat was installed a Wildlife Acoustics SM4BAT-FS and (ultra)sounds were recorded on-trigger every night during August and September 2016. Temperature was recorded every 10 minutes. A diverse community of bats, including species of considerable interest for their specialization in the boreal type environments, was recorded. Among others, a large sample of *Pipistrellus pipistrellus*, *Eptesicus nilssonii*, *Nyctalus leisleri* and the rare *Myotis bechsteinii*, were recorded. The large collection of sounds also provides information on phenology of movements of the different species, the number and timing of feeding buzzes, and the increase of social calls in the middle of September. The long-term collection of sounds in remote areas provides a good potential instrument to identify and investigate the phenology of these elusive species in the last well-preserved areas in the Alps, helping to evaluate the changes that have occurred in the past from man-made transformations and to document possible modification due to global change.

MONITORING URBAN BAT POPULATIONS [O]

MARCEL J. SCHILLEMANS[1]**, LISA HÖCKER[2], ERIC A. JANSEN[1],
VITA J.A. HOMMERSEN[1], HERMAN J.G.A. LIMPENS[1],
**marcel.schillemans@zoogdiervereniging.nl
[1]*Dutch Mammal Society/Zoogdiervereniging, Nijmegen, the Netherlands;*
[2]*Institut für Tierökologie und Naturbilding, University of Vienna, currently ecologist at Institut für Tierökologie und Naturbilding, University of Vienna.*

Bats provide useful ecosystem services and are protected by the European Habitats Directive. A requirement of countries is to be able to report on the Favourable Conservation Status (FCS) of bat species. The FCS of the bat species in cities or urbanized municipalities is currently not or hardly monitored for populations that depend on the cities for roosting and (partly) foraging. As urbanization worldwide and in Europe is increasing, it is to be expected that it becomes more important to be able to assess the FCS of populations depending on the urban habitat. Furthermore, due to legal obligations, assessment at a legal entity level, such as a municipality, is preferred. The Dutch Mammal Society (DMS) has investigated and trialled the setup of such a monitoring scheme. Target species are common pipistrelle (*Pipistrellus pipistrellus*), Nathusius's pipistrelle (*Pipistrellus nathusii*) and serotine (*Eptesicus serotinus*). Commonly used monitoring methods do not work well or are less applicable in the urban environment, mainly due to the ecology of these species within this environment. Acoustic methods targeting activity appear to be more suitable than various types of roost counts. Three acoustic methods are discussed in more detail: transect counts, point counts and transect-point counts, done either on foot or by car or bicycle. Plotting and executing transects should adhere to some rules and preconditions as transects are stratified towards serotine and the (part of the) population that is mostly residing in the urban environment or municipality. Furthermore data management and sustainability are important factors for the applicability of any monitoring scheme. In two cities, pilots of transect counts by bicycle have been carried out by volunteers. The results of the pilots are analysed in more detail with emphasis on variability of measurements, detection probabilities, setup of the monitoring scheme including data management and ease and satisfaction of execution by voluteers.

OPTIMIZATION OF AUTOMATIC BAT IDENTIFICATION TOOLS FOR LONG TERM ACOUSTIC MONITORING SCHEMES [O]

BRUNO SILVA[1,2]**, SÍLVIA BARREIRO[1,2], PEDRO ALVES[3], ANTÓNIO MIRA[1,2], JOÃO TIAGO MARQUES[1,2], JOSÉ HERRERA[1,2], **bsilva@uevora.pt
[1]UBC- Conservation Biology Lab, Department of Biology, University of Évora, Évora, Portugal;
[2]CIBIO/InBIO-UE – Research Center in Biodiversity and Genetic Resources. Pole of Évora, Évora, Portugal; PLECOTUS – Estudos Ambientais, Portugal.

Automatic tools for the identification of bats are evolving quickly, but their call libraries are often designed for large geographic areas (multiple regions or countries) leading to inadequate call libraries for a particular region. This mismatch increases the probability of both other sound sources being classified as bat calls and bat species misclassification. We hypothesized that it is possible to develop a regionally-specific bat identification tool by fine-tuning a country wide call library. Our baseline library contains 1500 recordings from several locations across Portugal (16,000 individual calls) of 24 bat species (>90% of the known bat species) and 27,000 other sound recordings (particularly of insects). The identification tool consists of a classification tree with three sequential nodes, each composed of multiple machine learning classifiers: the first node separates bat calls from other ultra-sounds or noise; the second node classifies bat calls into broad species groups that have similar echolocation calls; and the third node refines the classification of bat calls into species or species-complexes. The tool is designed to enable updating by adding new labelled recordings. To test the performance along time we conducted a one month field trial. The library was continuously updated with expert labelled recordings from bat species and noise in order to incorporate local variability and fine-tune the machine learning models. During the trial we observed a continuous improvement in the classification results: the detection of bat calls increased while the number of noise recordings classified as bats and misclassifications decreased, particularly for the most abundant species. Our results show that classification tools benefit greatly from incorporating regional and local soundscape variability and we expect that during a continuous acoustic sampling, human supervision will become less demanding over time, due to the improvement of classification models.

DOES PHENOLOGY INFLUENCE POTENTIAL DISTRIBUTION OF EUROPEAN BATS? A CAUTIONARY NOTE FOR THE DEVELOPMENT OF SPECIES DISTRIBUTION MODELS [P*]

SONIA SMERALDO[1]**, MIRKO DI FEBBRARO[2], LUCIANO BOSSO[1], CARLES FLAQUER[3], DAVID GUIXÉ[4], FULGENCIO LISÓN[5], ANGELIKA MESCHEDE[6], JULIA PRUGER[7], DANILO RUSSO[1,8], **sonia5.6.89@hotmail.it

[1]Wildlife Research Unit, Dipartimento di Agraria, Università degli Studi di Napoli Federico II, Portici (NA), Italy;
[2]EnvixLab, Dipartimento Bioscienze e Territorio, Università del Molise, Pesche, Italy;
[3]Bat Research Group, Granollers Museum of Natural Sciences, Granollers, Catalonia, Spain;
[4]Forest Sciences Centre of Catalonia, Ctra. de Sant Llorenç de Morunys, Solsona, Spain;
[5]Department of Ecology and Hydrology, Faculty of Biology, University of Murcia, Murcia, Spain;
[6]Institute of Zoology II, University of Erlangen-Nuremberg, Erlangen, Germany;
[7]Interessengemeinschaft für Fledermausschutz und -forschung in Thüringen e.V., Schweina, Germany;
[8]School of Biological Sciences, University of Bristol, Bristol, U.K.

Phenology is a key feature to describe species niches due to its major importance in capturing seasonality in resource use and climate requirements . This is all the more true for temperate bats, whose ecological needs differ markedly across seasons, especially between hibernation and reproduction. Species distribution models (SDMs) are widespread tools to evaluate a species' potential distribution and identify its large scale habitat preferences. Modelling studies have experienced a recent boost thanks to the increasing amount of data available to implement SDMs: however, despite the chief importance of data phenology to describe a species' niche, the time of year data were collected is often neglected or not controlled for in the process.
In this study we tested the hypothesis that the output of SDMs developed for six European bat species will differ according to whether hibernation or reproductive occurrence data are used. We employed a dataset made of 470 occurrence records of bat hibernacula and 400 records of nursery roosts of selected species and developed both separate winter and summer models and mixed models for all of them. Our models were developed for the whole Europe so for our exercise, covering a large geographic scale, we only considered climatic variables. Seasonal and mixed potential ranges differed from each other and the direction of this difference was species specific. Overall, our work highlights the importance of considering data seasonality in species distribution models development in order to encompass all the different ecological requirements related to the species phenology in view of a more effective conservation strategy. We thank the Eurobats Advisory Committee for providing bat occurrence records for many of the countries within the Agreement range.

EFFECTS OF HOST ECOLOGY ON BAT FLY SPECIES RICHNESS IN EUROPEAN BATS [P]

TAMARA SZENTIVANYI[1,2], ORSOLYA VINCZE[3], OLIVIER GLAIZOT[1,2], PHILIPPE CHRISTE[1]

[1]Department of Ecology and Evolution, University of Lausanne, Switzerland;
[2]Museum of Zoology, Lausanne, Switzerland;
[3]Department of Evolutionary Zoology and Human Biology, University of Debrecen, MTA-DE "Lendület" Behavioural Ecology Research Group, Debrecen, H-4032, Hungary.

Host traits are known to explain parasite species richness in many vertebrate groups. Bats possess an extremely diverse and highly specific parasite fauna due to their ecology and evolutionary history. In the present meta-analysis based on literature data, we attempted to reveal the determinants of parasitic bat fly species richness in bats. We tested the effects of host distribution, body mass, brain size, colony size, IUCN threat status, longevity as well as roosting and migratory behaviour using phylogenetic correlation. We used the data from 43 European bat species and 17 bat fly species. Our results indicate that bat fly species show higher diversity towards the equator. Moreover, host species with more northerly distribution show less parasite diversity. In addition, hosts presented as Least Concern in the IUCN database harboured a higher number of bat fly species than hosts in the Vulnerable category. We did not find any effect on the other variables mentioned above.

THE LIFE PODKOWIEC+ PROJECT FOR CONSERVATION OF THE LESSER HORSESHOE AND SOME OTHER BAT SPECIES IN SOUTH POLAND [P]

RAFAŁ SZKUDLAREK[1], ROMAN GUZIAK[1]**, **podkowiecplus@wp.pl
[1]*Polskie Towarzystwo Przyjaciół Przyrody "pro Natura", Wroclaw, Poland.*

The poster presents activities of the EU LIFE funded project: Protection of the lesser horseshoe and other bat species in S Poland (PODKOWIEC+), which focuses on 3 out of 7 native bat species listed in the Habitats Directive: *Rhinolophus hipposideros*, *Myotis emarginatus* and *Myotis myotis*. The project implements conservation measures to prevent bat roost destruction, improve habitats in and around the roosts and flyways to the feeding areas, and to advance understanding of bat conservation in 29 Natura 2000 sites in South Poland. Project results and the status of bats are monitored in over 100 sites. In 2013-2016, deteriorated roof coverings were replaced in 8 summer roosts, and grilles mounted at 3 cave entrances. Habitat improvements were implemented in 37 roosts: measures to diversify thermal conditions, prevent draughts, reduce infiltration of light and access of predators. Platforms to collect bat guano were installed. Research on habitat use with detectors, counting frames, infrared cameras and photo-traps, revealed gaps in the lesser horseshoe bat flyways, which were filled near 7 roosts. Improper illumination was corrected in 2 sites. The concept of bat conservation use of the 'Land of the horseshoe bats' was promoted. The institutions and individuals engaged in bat conservation are recognised with 'The Land of the horseshoe' quality sign and 'The Golden horseshoe' medal. Training sessions for tourist guides as multipliers were provided. The 'Horseshoe Ambassador' competitions were organised to increase the interest of the multipliers. Other promotional activities were competitions, work with media, production of promotional material, organisation of events and information stands. The first of two study trips took place for land owners having bat colonies at their premises and persons whose occupation is related to the conservation of bats. The status of the lesser horseshoe bat in Poland changed from one known colony of 120 individuals in 1996 to c. 10,000 in 2015, partially due to conservation.

DISTRIBUTION AND SIZE OF SUMMER BAT COLONIES AROUND A LOWLAND WETLAND AREA – THE EXAMPLE OF 'DRU□NO LAKE' NATURE RESERVE, POLAND [O]

MARTA SZURLEJ[1]**, MATEUSZ CIECHANOWSKI[1], **marta.szurlej@wp.pl
[1]*Katedra Ekologii i Zoologii Kręgowców, Uniwersytet Gdański, ul. Wita Stwosza 59, 80-308 Gdańsk, Poland*.

Druzno Lake is a semi-natural, hypertrophic lake located on the Żuławy polders, near the delta of Vistula, Poland. This nature reserve is a protected, shallow eutrophic lake, with reedbeds and alder woodland, surrounded by open farmland. In the years 2008-2009 bioacoustic research was conducted in this site, analysis of the results showed its possibility to be an important foraging site for bats. We decided to investigate the bat roosting preference in this area, although nothing is known about bat ecology in this area. The aim of this study was to create an inventory of the summer bat colonies in the reserve and buildings adjacent to its borders. The study was carried out in June-July 2015-2016, based on observations of dawn swarming and counting individuals emerging at dusk. In several cases it was necessary to capture a few flying individuals to confirm the bat species. Roosts of 4 lactating females of *Plecotus auritus* were located using radiotracking during the day. Altogether, 23 breeding colonies of bats (*Pipistrellus nathusii*, *P. pipistrellus*, *P. pygmaeus*, *Nyctalus noctula*, *Eptesicus serotinus*, *Myotis daubentonii*, *Plecotus auritus*) were found in buildings and tree holes. Some features of buildings inhabited and uninhabited by bats were compared (age, roofing, wall materials, ventilation, illumination, window shutters, human activity, distance to trees, canals and open lakes.

THE IMPORTANCE OF TEMPORARY LAKES AND PONDS FOR BAT CONSERVATION IN NEOTROPICAL RAINFORESTS [O*]

LAURA TORRENT[1]**, ADRIÀ LÓPEZ-BAUCELLS[1,2,3], RICARDO ROCHA[1,3,4], PAULO E.D. BOBROWIEC[3], CHRISTOPH F.J. MEYER[3,5], **arual.torrent@gmail.com
[1]Granollers Museum of Natural Sciences, Catalonia, Spain;
[2]Centre for Ecology, Evolution and Environmental Changes, Faculty of Sciences, University of Lisbon, Lisbon, Portugal;
[3]Biological Dynamics of Forest Fragments Project, National Institute for Amazonian Research and Smithsonian Tropical Research Institute, Manaus, Brazil;
[4]Faculty of Life Sciences, University of Madeira, Funchal, Portugal;
[5]School of Environment and Life Sciences, Ecosystems and Environment Research Centre, University of Salford, Salford M5 4WT, U.K.

Recent studies predict a future decrease in precipitation across the Amazon rainforest, likely causing significant droughts, and thus a diminution of freshwater biomes, in particular temporary waterbodies. The immediate consequences for terrestrial fauna associated with tropical temporary lakes are mostly unknown, as the vast majority of studies comes from temperate regions. Amongst studies on bats conducted in the Neotropics, few have focused on aerial insectivorous species. Here, we studied the importance of temporary lakes surrounded by primary rainforest in the Central Brazilian Amazon for aerial insectivorous bats during both dry and rainy season. We compared patterns of richness and activity between temporary lakes and adjacent primary rainforest at ensemble and species level. Generalized Linear Mixed Model results indicated that 18 of 21 species were significantly more active over temporary ponds than in rainforest. Moreover, richness and activity of five species were significantly higher during the rainy season. Richness and total activity were positively correlated with lake size. Lake size influence on bat activity was species-specific, with activity levels being generally higher over larger lakes. Most bat families had the highest activity peak during the first hours of the night, with the exception of mormoopid bats, whose activity peaked around midnight. Our results suggest that all aerial insectivorous bats, even cluttered-space specialists, make heavy use of temporary lakes for foraging and drinking. Additionally, molossids and vespertilionids were more active over waterbodies than in rainforest. Droughts induced by climate change are likely to reduce the amount of temporary waterbodies across Amazonia and thus may negatively affect bats. More studies focusing on tropical temporary lakes are clearly needed to gauge their importance as habitat for aerial insectivorous bats in general and to obtain ecological information about the more elusive species.

GUANO SCENT AS A CUE FOR ROOST-FINDING IN VAMPIRE BATS [P]

NIA TOSHKOVA[1 2]**, GERALD CARTER[1], **niyatoshkova@gmail.com
[1]*Smithsonian Tropical Research Institute, Gamboa, Panama;*
[2]*National Museum of Natural History, Sofia, Bulgaria.*

Several studies show that bats can use echolocation and social calls to find new roosts. A few studies further show that bats can use scent to recognize roostmates and to select roosts. However these studies have focused on odors from glands (e.g. scent-marking) as a chemical cue to roost location, but bat roosts are also marked by guano and urine stains. Vampire bat roosts are particularly pungent, noticeable to humans from several meters away. We tested whether the common vampire bat, *Desmodus rotundus,* uses guano scent as a cue for selecting roosting locations. In a series of 4 experiments, we tested whether captive common vampire bats selected roost locations scented with guano and urine from their colony over unscented control locations. All experiments provided evidence that vampire bats preferred roosting in the scented locations. Our results are consistent with the hypothesis that bats might use guano and urine deposits at roosts as an additional cue.

LANDSCAPE POPULATION GENETICS OF THE GREATER HORSESHOE BAT (*RHINOLOPHUS FERRUMEQUINUM*) IN WESTERN FRANCE [O*]

ORIANNE TOURNAYRE[1]**, ANNE LOISEAU[1], MAXIME GALAN[1], JEAN-BAPTISTE PONS[2,3], MAXIME LEUCHTMANN[4], RAPHAËL LEBLOIS[1], DOMINIQUE PONTIER[2,3], NATHALIE CHARBONNEL[1], **nathalie.charbonnel@inra.fr
[1]*INRA, UMR CBGP, F-34988 Montferrier-sur-Lez, France;*
[2]*Univ Lyon, Université Lyon 1, CNRS, Laboratoire de Biométrie et Biologie Evolutive UMR5558, F-69622 Villeurbanne, France;*
[3]*Univ Lyon, LabEx ECOFECT Ecoevolutionary Dynamics of Infectious Diseases, Villeurbanne, F-69365 Lyon, France;*
[4]*Poitou-Charentes Nature, Jean Moulin 14, 86240 Fontaine-le-Comte, France.*

The greater horseshoe bat (*Rhinolophus ferrumequinum*) is among the most widespread bat species in Europe but its populations have experienced severe population declines during the last century. The primary known causes are the direct and indirect actions of humans, including landscape-use changes (intensification of agriculture, deforestation, etc.), destruction of natural habitats, pesticide poisoning and chemical pollution. In France, some populations of the greater horseshoe bat are still declining despite strengthening conservation efforts. In this study, we aim to understand the link between landscape and the decline of French populations of *R. ferrumequinum*. We focus on a fine spatial scale in western France. We genotyped 536 individuals at 17 microsatellites and analyzed the spatial genetic structure within and among 11 maternity colonies. We infer eco-demographic processes, including population size changes and gene flow, to examine the impact of landscape on this genetic structure. We expect that habitat fragmentation may lead to isolation of colonies and disrupted gene flow, inbreeding, increased drift and increased differentiation between nearby colonies, which could in turn result in increasing local risk of extinction. We find a weak genetic structure, both intra- and inter colonies, suggesting that important gene flow occurs between colonies despite potential landscape barriers. Altogether, our study, combined with ecological data relative to bat diet and ecotoxicological pressure, should enable improvement in the design of conservation strategies for the greater horseshoe bat in France.

PREY PARTITIONING IN BATS OF DIFFERENT FORAGING BEHAVIOUR: THE CASE OF *PLECOTUS AUSTRIACUS* AND *HYPSUGO SAVII* [P*]

NEREA VALLEJO[1]**, CARLOS IBAÑEZ[2], JESÚS NOGUERAS[2],
AITOR ARRIZABALAGA-ESCUDERO[1], INAZIO GARIN[1], **nvallejo004@ikasle.ehu.eus
[1]*Zoology and Animal Cell Biology Department, UPV/EHU, Sarriena z/g, 48940 Leioa, The Basque Country;*
[2]*Estación Biológica de Doñana, CSIC, Americo Vespucio 26, Isla de la Cartuja, 41092 Sevilla, Spain.*

When resources are limiting, their partitioning is vital for the coexistence of sympatric species. Differences in ecomorphological traits, such as wing morphology and echolocation, allow bats to exploit diverse habitats and resources. We analysed the diet of two bat species from different populations in Andalucia (Southern Spain): *Plecotus austriacus*, which is adapted to forage in cluttered spaces, and *Hypsugo savii*, which prefers open spaces. Using next-generation sequencing, we were able to identify prey items to species level. In total, 33 taxa were identified in the diet of *P. austriacus*, and 46 in the diet of *H. savii*, the majority being Lepidoptera. Only four prey items were identified in both species, resulting in low niche overlap between the two species. The diet of *H. savii* appeared to be more diverse within each population and between populations. The diet of *P. austriacus* varied less between populations and was dominated by *Thaumetopoea pityocampa*. *P. austriacus* appeared to feed on larger Lepidoptera than *H. savii*. Prey items associated with woodland habitats appeared mostly in the diet of *P. austriacus*, suggesting that differences in habitat use play a role in resource partitioning. The results, overall, show that morphological and behavioural differences facilitate resource partitioning between these two bat species, allowing their coexistence in sympatry.

CALCULATING BAT TRENDS BASED ON CAR-TRANSECT MONITORING DATA [O]

TON VAN DER MEIJ[1]**, ARNO. VAN STRIEN[1], LEO L. SOLDAAT[1],
ERIC A. JANSEN[2], HERMAN J.G.A. LIMPENS[2], MARCEL J. SCHILLEMANS[2],
**tvdmeij@xs4all.nl
[1]*Statistics Netherlands, The Netherlands;*
[2]*Dutch Mammal Society, Nijmegen, The Netherlands.*

Four years ago the Netherlands started a new bat survey program based on automatic recording of bat sounds with real-time recorders (batlogger-M) along car-routes. The purpose of this survey is to gain population trend data for four common species not covered in other monitoring schemes. These species are: *Pipistrellus pipistrellus*, *P. nathusii*, *Eptesicus serotinus* and *Nyctalus noctula*. At the same time it is also gaining distribution data for a few more species. The monitoring design includes repeated surveys within the season in order to gain information on the detection probabilities of species. The survey is a cooperative project of the Dutch Mammal Society (execution and volunteer management) and Statistics Netherlands (analyses and quality control) and is funded by the Ministry of Economic Affairs as part of the Dutch Network Ecological Monitoring. Calculating population trends for the four common species based on the information of this survey was a challenge, because first an optimal geographical subdivision of routes into transects or count units had to be found. Secondly, the use of dependent data had to be prevented. Thirdly, potential bias factors (traffic jam, incidental road blocks, weather conditions etc.) had to be assessed and dealt with. And last but not least, suitable statistical methods for detecting trends in abundance and distribution had to be found. Statistics Netherland uses several methods for calculating trends from different kinds of count and survey data. A few of those were tested on the data of this car-route survey project. We show the first results on the first four years of data.

PURPOSE-BUILT BAT HIBERNACULA AS A MITIGATION MEASURE [P]

BEN VAN DER WIJDEN[1]**, RALF GYSELINGS[2], LUC DE BRUYN[2],
**ben.van.der.wijden2@telenet.be
[1]*Brussels Environment, Brussels, Belgium;*
[2]*Research Institute for Nature and Forest (INBO), Brussels, Belgium.*

A total of 5 purpose-built bat hibernacula were constructed in the Brussels Capital region (Belgium) in the last decade. The designs and materials used for the construction of these structures are briefly discussed. The purpose-built bat hibernacula were intensively monitored to assess their use by bats. Hibernating bats were censused every winter. Three out of five hibernacula succeeded in attracting a maximum of 30 hibernating bats of two species. A preliminary acoustic survey with automatic recording devices demonstrates that swarming activity does indeed occur at the hibernacula that are used in winter. A preliminary survey with dataloggers in two hibernacula characterizes the thermal regime of the structure. The possibility to monitor 5 purpose-built hibernacula with similar characteristics, of which 3 are successful and 2 are not, is a unique opportunity to help understand how to construct successful bat hibernacula in the framework of mitigation/ compensation schemes. Future research options are suggested and good practice in terms of creation of bat hibernacula are discussed.

DIET COMPOSITION OF THE SCHREIBERS'S BENT-WING BAT (*MINIOPTERUS SCHREIBERSII*) IN THE IBERIAN PENINSULA [O*]

GERMAN VELAYOS-GAINZA[1]**, JESÚS NOGUERAS[2], CARLOS IBÁÑEZ[2], JOXERRA AIHARTZA[1], AITOR ARRIZABALAGA-ESCUDERO[1], INAZIO GARIN[1],
**germanvelayos@gmail.com
[1]*Zoology and Animal Cell Biology Dpt., University of The Basque Country UPV/EHU, Sarriena z/g, 48940 Leioa, The Basque Country;*
[2]*Estación Biológica de Doñana (CSIC), Americo Vespucio 26, Isla de la Cartuja, 41092 Sevilla, Spain.*

We aim to determine the factors affecting diet composition and variability of *Miniopterus schreibersii* (Kuhl, 1817), a cave dwelling bat species with long-range movements that is widespread throughout the Iberian Peninsula. Factors like climate of the area, location of the roost and individual sex were taken into account. Eight colonies of bats were sampled during July of 2012 and 2014: three from the north and five from the south of the Iberian Peninsula. By means of DNA extraction, amplification of a fragment of the COI gene (157bp) and sequencing, we inferred moth species present in faeces collected individually from 115 bats. Multivariate analysis (NMDS) and rarefaction curves based on species richness and Shannon diversity were estimated to compare dietary composition. The results showed that dietary composition was similar within the same climate or colony, but not when sexes were compared. Shannon diversity from northern colonies (oceanic climate) was higher. In addition, the lowest diet diversity was found in a colony with poor habitat diversity around the roost (almost entirely made of crops). Indeed, the northern caves were surrounded by mosaic-like landscapes.

VARIATION IN MORPHOLOGICAL AND CRANIAL CHARACTERS IN *HIPPOSIDEROS POMONA ANDERSEN*, 1918 (CHIROPTERA: HIPPOSIDERIDAE) AND ITS TAXONOMIC IMPLICATIONS [P*]

PARVATHY VENUGOPAL[1]**, PAUL BATES[2], GARETH JONES[1],
**pv14888@bristol.ac.uk
[1]*School of Biological Sciences, University of Bristol, Bristol, U.K.;*
[2]*Harrison Institute, Bowerwood House, St Botolph's Road, Sevenoaks, Kent, U.K.*

Bats are promising candidates for studying morphometric responses to geographical isolation. The present study tries to understand the morphometric and cranial variations and its taxonomic importance in *Hipposideros pomona* which is known from India, Myanmar, Thailand, Laos, Vietnam, Malaysia and southern China. Studies suggested that H. pomona might be a composite of at least two species: *H. pomona* which is restricted to peninsular India with a second species, comprising specimens currently referred to *H. p. gentilis* and *H. p. sinensis*, extending from NE India and into SE Asia. There might be a chance of occurrence of allopatric species in *H. pomona* due to this distant distribution. In order to verify this, we examined the crania of 84 *H. pomona* specimen from The Natural History Museum (London, UK), Harrison Zoological Museum (UK), Bombay Natural History Museum (India), and Zoological Survey of India. 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. The results showed that the first three principal components, PC1, PC2 and PC3, explained 56.97%, 29.73% and 3.34% 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. pomona* was derived from a cluster dendrogram, which identified at least two major groupings. Similarly, plotting PC1 vs. PC2 showed *H. pomona* skull samples clustering into two groups. This can be explained as: 1) The two groups might be two cryptic species, and they might show clinal variation explaining the gradient in PC values within each cluster. 2) *H. pomona* can be easily mistaken with two other species, *Hipposideros fulvus* and *Hipposideros ater*. One of the clusters might be composed of individuals misidentified before advanced identification guides were available.

DO WE NEED TO INCLUDE THE AEROSPHERE IN OUR CONSERVATION EFFORTS? [O]

CHRISTIAN C. VOIGT[1]**, **voigt@izw-berlin.de
[1]*Leibniz Institute for Zoo and Wildlife Research, Berlin, Germany.*

Our planet is currently facing the sixth mass extinction with yet unforeseen consequences for ecosystems, ecosystem services and ultimately the livelihood of humans. Previous conservation efforts proclaim the value of protected areas for rare plants, animals or whole communities. These areas have so far been realized on both land and sea. Here, I argue that protection of land areas and water bodies may largely neglect an important habitat used by a multitude of species worldwide, the aerosphere. The aerosphere is defined as the body of air around the earth. Recent advances in the tracking of animals, such as radar and GPS technologies have highlighted the fact that many animals depend heavily on the aerosphere. Yet, the aerosphere is threatened by various anthropogenic factors such as air pollution, artificial light at night and aerial traffic, including planes and aerial robot vehicles (e.g. optocopters). Last but not least, the aerosphere is also increasingly used for energy production by wind turbines. Thus, aeroconservation has recently emerged as a promising discipline. Bats, as the only mammalian taxon capable of powered flight, use the aerosphere for foraging, commuting, migrating and all these behaviours also include social interactions. In my conceptual perspective on this topic, I will evaluate the necessity for protecting certain aerospheres for animals in general and bats in particular.

SRY, NOT SRY - SEX DETERMINATION USING NON-INVASIVE MOLECULAR METHODS [P]

CONOR V. WHELAN[1]**, NICOLE M. FOLEY[1], EMMA C. TEELING[1],
**conor.whelan@ucd.ie
[1]*School of Biology and Environmental Science, Science Centre West, University College Dublin, Belfield, Dublin 4, Ireland.*

Data regarding sex biases, distribution, and numbers in a population is crucial for studies focused on determining relative roles of maternal or paternal effects, population pedigree constructions, and conservation genetics. In recent years, particularly amongst researchers studying protected or endangered species such as bats, there has been a preferential move towards non-invasive sampling. As such, it is now possible to obtain a wealth of information about an individual or population simply by sampling faeces, hair, and even saliva that is deposited by an animal. However, as these samples are often obtained opportunistically, accurate sex data is usually lacking. To address this, PCR primers were designed to amplify a portion of the sex-determining region of the Y-chromosome (SRY) using 18 mammals, including 4 bat species. Nine primer pairs were designed and tested using 6 male and 6 female positive controls. Primers were optimised using the cosmopolitan bat species *Myotis myotis* as a pilot study. Here we describe a cost effective and simple visual-based method to distinguish males and females using PCR and gel electrophoresis. These primers have the potential to be used across numerous bat species, and could also be used within genotyping multiplexes.

DO BATS OBEY RENSCH'S RULE? [O*]

ZUZANNA WIKAR[1]**, MATEUSZ CIECHANOWSKI[1], **zuzanna.wikar@gmail.com
[1]*Department of Vertebrate Ecology and Zoology, Faculty of Biology, University of Gdańsk, ul. Wita Stwosza 59, 80-308 Gdańsk, Poland.*

Rensch's rule describes the relationship between the extent of sexual size dimorphism (SSD) and general body size. Across a taxon, SSD increases when males are larger than females and decreases when female sex is larger. Occurrence, magnitude and direction of SSD depend on various factors, e.g. number of offspring, mating behaviour or living conditions. Chiroptera is a species-rich order, among which females are larger in the majority of species. However, the only few tests of Rensch's rule in bats either referred to intraspecific variation or based on a short series of species, exclusively with larger females and none of them confirmed that chiropterans followed the rule. In our study, we investigated whether longer series of species with bigger females will show compatibility with Rensch's rule and, for the first time, if the rule applies to species with larger males. In our analysis we used both published and unpublished data for 165 species from 13 families. Support for Rensch's rule was mixed, depending on chosen method of testing. When plotting male vs. female forearm length (n=136), we obtained a regression slope that did not differ from 1.0, suggesting no SSD scaling with body size, thus rejecting the rule. In a second method, we chose mean forearm length for both sexes as a body size indicator and calculated sexual dimorphism by simply subtracting mean forearm length of smaller sex from the other one. We revealed that 117 species with larger females do not follow the Rensch's rule (Pearson's correlation r=0.06, p=0.5). It confirms results of former studies and suggest that sexual dimorphism in these species is mostly associated with the number of offspring, which can be explained by Big-Mother hypothesis, or other factors. On the other hand, we found highly significant correlation between body size and magnitude of sexual dimorphism (r=0.48, p=0,001) in 46 species with bigger males, providing the first evidence that these bats do obey Rensch's rule.

POPULATION GENETIC STRUCTURE OF BECHSTEIN'S BATS (*MYOTIS BECHSTEINII*) ACROSS EUROPE AND BRITAIN: HAS BREXIT ALREADY HAPPENED? [O*]

PATRICK WRIGHT[1]**, PATRICK HAMILTON[1], HENRY SCHOFIELD[2], FIONA MATHEWS[1], **pw339@exeter.ac.uk
[1]*University of Exeter, U.K.;*
[2]*Vincent Wildlife Trust, U.K.*

The Bechstein's bat is a rare species across Europe and remains extremely challenging to study. Acoustic methods are unable to distinguish the species reliably and roosts are also particularly hard to monitor. Molecular approaches offer the potential to better inform conservation management by evaluating the fitness and viability of elusive species. We have collected data on 328 individual Bechstein's bats from eight sites in Britain and seven sites from elsewhere in Europe. The analysis of 747 bp of mitochondrial DNA and 14 species-specific microsatellites indicated high levels of diversity across Europe and Britain. Geographic barriers, such as the English Channel and the Alps, explained most of the genetic structure in Europe. Although the British population showed no particular evidence of inbreeding, important genetic structuring was observed between the northern and southern part of the country. Further landscape genetics analysis identified land cover as the main variable explaining genetic distance and emphasised the importance of woodlands in maintaining high connectivity between populations.

THE USE OF HIGH-RESOLUTION MOBILE RADAR AND ULTRASOUND DETECTORS FOR TRACKING FORAGING ACTIVITY OF BATS OVER A WATER RESERVOIR IN EASTERN POLAND [P]

MARCIN ZEGAREK[1], ZUZANNA HAŁAT[1], KRZYSZTOF GAJKO[2], JACEK KSEPKO[2], MAAREK KSEPKO[2], IRENEUSZ RUCZYŃSKI[1]**, **iruczyns@ibs.bialowieza.pl
[1]Mammal Research Institute, Polish Academy of Sciences, Białowieża, Poland; [2]3Bird Radar System, 3Gsc, Białystok, Poland.

Radar allows tracking single objects such as birds and bats. Correct identification and classification of object size is difficult and burdened with errors. In this study we tested whether the combination of data collected with the use of bat detectors and radar can provide relevant ecological data on density, changes in temporal and spatial activity and distribution of bats at open foraging sites. The study was conducted on the shallow, large, eutrophic Siemianówka water reservoir located near Białowieża Forest in eastern Poland, with a water surface of 32.5 km^2. Flying objects were tracked and recorded by mobile horizontal and vertical radar (Fruno, Model SN-36AF and Model XN-24AF) placed on a large dike crossing the Siemianówka reservoir. The survey covered 3.7 km^2. We registered GPS coordinates of the objects, their size and the speed of movement, we also assessed their height of flight. Three detectors on a floating platform recorded vocal activity of bats at the same time. Recordings reveals that *Nyctalus noctula*, *Pipistrellus nathusii* and *Pipistrellus pygmaeus* constituted most of the bat calls (87 %). Since wingspan and body mass of *Nyctalus noctula* and *Pipistrellus* spp. are clearly different, we divided the flying objects into two size classes: large and small bats. The only member of the first group was *N. noctula*. The second group included mainly the two *Pipistrellus* species. Preliminary analysis indicated that the combination of radar and detector methods can successfully be used for measuring density, distribution and temporal and spatial activity of bats. However, this method is limited to open areas, such as water reservoirs with low species richness. The project was funded by the Polish National Science Centre on the basis of decision number DEC-2013/10/E/NZ8/00725

ARE AGGRESSIVE VOCALIZATIONS THE HONEST SIGNALS OF BODY SIZE AND QUALITY IN FEMALE ASIAN PARTI-COLOURED BAT (*VESPERTILIO SINENSIS*)? [O*]

XIN ZHAO[1]**, TINGLEI JIANG[1], JIANG FENG[2], YING LIU[1],
**zhaox111@nenu.edu.cn
[1]*Northeast Normal University, China;*
[2]*Jilin Agricultural University, China.*

Animals need information about the callers to make decisions that affect survival and reproduction. However, there is much unreliable information in some communication. Generally, the honesty signal is costly to produce or is controlled by physical or physiological constraints that cannot be faked. Aggressive calls meet the above two points at the same time. In the Asian parti-coloured bat, *Vespertilio sinensis*, aggressive displays and vocalizations were produced when an intruding bat crawled over the native bats for a roost position. Thus, we examined whether the aggressive calls of female Asian parti-coloured bats encode reliable information about the body size and quality of the callers. In syllables, different syllable parameters were associated with different body size and quality indices in different syllable types. Frequency-related parameters were negatively correlated with the bats' body mass and immune response, and other syllable parameters were positively correlated with the bats' body mass and immune response. Forearm length and bite force were all positively correlated with syllable parameters. In calls, heavier bats produced shorter mean inter-syllable silence and shorter mean inter-syllable silence predicted better immune response. A positive relationship between immune response and vocal complexity was observed. These data demonstrate that female Asian parti-coloured bat aggressive calls are honest signals of body size and quality of callers.

DIVERSITY OF THREE BAT ASSEMBLAGES OF CENTRAL BRAZIL [P]

MARLON ZORTÉA[1]**, FAGNER CORREIA D'ARC[2], **mzortea@uol.com.br
[1]UAE Ciências Biológicas, Universidade Federal de Goiás, Regional Jataí, Br. 364 km 195, 75801-615 Jataí, GO, Brazil;
[2]Instituto Federal Goiano, Campus Urutaí, Rodovia Geraldo Silva Nascimento, km 2,5, Zona rural, Urutaí, GO, Brazil.

The state of Goiás is located in the central portion of Brazil and is covered mainly by Cerrado (Brazilian savanna). Its bat fauna is diverse, but poorly known, as in most areas of the state bats have not been sampled. In the present study, we made inventories of the bat communities in three sites in the mid-northern region of Goiás, Brazil, from 2009 to 2015. We used mist nets to capture bats, and set up the nets from sunset until four to six hours later, in a total sampling effort of 79,659 m^2h. We captured 977 bats of 32 species. Phyllostomidae was the predominant family in terms of abundance and richness. *Carollia perspicillata* was the most abundant species in all sites. The diversity profiles showed that only richness differed among sites, which supports that the three bat assemblages are structurally similar. However, the rarefaction curves showed similar richness among sites when we removed differences in sampling effort. In general, the largest difference among communities was species composition, as species turnover was high. We made five new records for the state of Goiás, some of them also new for mid-western Brazil (*Pteronotus personatus*, *Lophostoma silvicola*, *Tonatia saurophila*, *Noctilio albiventris*, and *Eptesicus diminutus*). We sampled many cave species. This result suggests that there might be several caves in São Patrício Valley, which may have contributed to the high richness observed. The recorded richness represents one third of the known species in the whole Cerrado.

CHECK LIST OF BAT ECTOPARASITES IN CROATIA [P]

VIDA ZRNČIĆ[1]**, **v.zrncic@gmail.com
[1]*Geonatura Ltd, Croatia.*

In order to better understand the ecology of bats, thus helping their protection, it is necessary to examine their ectoparasites as one of the potential carriers of diseases among bats. The aim of this study was to compile a basic list of ectoparasites from 34 bat species found in Croatia. During the period from 2008 to 2011, ectoparasites were collected from 21 bat species, from a total of 161 individuals. Sampling was conducted during 11 different projects, at more than 15 locations in Croatia. A total of 274 samples of Acari, Diptera and Siphonaptera were sampled during this period. This is the first checklist of bat ectoparasites in Croatia, since, until now, only sporadic data has been published.

CAVE VRLOVKA IN CROATIA AND TOURISM - YES OR NO? - RECOMMENDATIONS BASED ON BAT FAUNA RESEARCH [P]

PETRA ŽVORC[1], MARINA KIPSON[1], DANIELA HAMIDOVIĆ[1]**,
**daniela.hamidovic@dzzp.hr
[1]*Croatian Biospeleological Society (CBSS), Demetrova 1, 10000 Zagreb, Croatia.*

Vrlovka cave in Kamanje, Croatia, was proclaimed as a geomorphological nature monument in 1962. After entering the EU in 2013, the site "Područje oko špilje Vrlovka" became a part of the EU Natura 2000 Ecological Network with nursery colonies and hibernacula of *Rhinolophus euryale* and *Rh. ferrumequinum* listed as conservation targets. It is also listed as one of 55 UNEP/EUROBATS internationally important underground sites in Croatia, hosting 7 bat species throughout the year: *Eptesicus serotinus*, *Myotis capaccinii*, *Myotis daubentonii*, *Myotis emarginatus*, *Rhinolophus euryale*, *Rhinolophus ferrumequinum*, *Rhinolophus hipposideros*. The cave was recognized during the 1950s as an important bat site, thanks to the research of the late Prof. Đulić. Since the cave was opened for tourists in 1928 and again in 1982, the bat fauna dropped significantly both in numbers of species and individuals. From 1998 until 2015 the bat fauna in the cave was surveyed sporadically. In 2015, through Natura 2000 NIP Integration Project of the Ministry responsible for nature protection, the electrical and lights installation in the cave were reconstructed and bat-friendly gates were built at the main entrance. Our study of the bat fauna took place from August 2015 to October 2016 for the possible touristic exploitation recommendation. The cave was surveyed once per month and the bat fauna was recorded. Data loggers measuring temperature and relative humidity were placed on the roof of cave walls at 5 important bat sites with 5 minute recording intervals. The research was heavily compromised since at least 2 unauthorized visits were recorded, and a concert took place in September 2016 with more than 75 people present in the cave. The main results of the study are: the cave is inhabited by bats during whole year; the maximum number of bats recorded was 300 and 400 individuals in July and August respectively; it is not possible to avoid visitors interrupting bats while visiting the cave; the light reflectors were not installed properly according to known important bat places in the cave, and the number of bats dropped significantly (to 15-20 individuals from the expected number) in June and September as a consequence of unauthorized visits. The recommendations given to the authorities and Public Institution responsible for the cave management were to not open cave Vrlovka for tourism in order to safeguard the bat populations, bearing in mind all the ecological requirements of bat species inhabiting the cave. The acceptance of these recommendations is yet to be realised.

All the bioacoustic tools you need for bat research.

Kaleidoscope Pro
Analysis Software

NEW Echo Meter Touch 2 PRO
Handheld Bat Detector

Song Meter SM4BAT FS and ZC
Ultrasonic Recorders

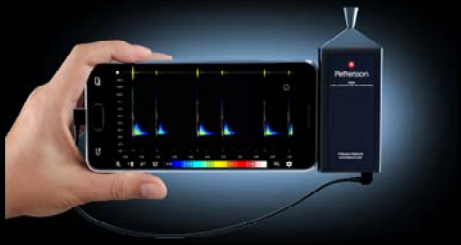
wildlife ACOUSTICS
BIOACOUSTICS MONITORING SYSTEMS

wildlifeacoustics.com

Pettersson
established 1983

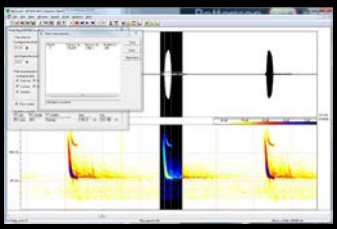
When quality matters

www.batsound.com



M500-384 USB microphone with
Android phone/Bat Recorder app

D1000X - the ultimate,
professional bat detector



BatSound - the easy to use
analysis software

M500 USB microphone with
BatSound Touch software

BATLOGGER

Your devices for static monitoring,

BATLOGGER A

for up to 3 nights recording time

BATLOGGER A+

for up to 5 nights recording time

BATLOGGER C

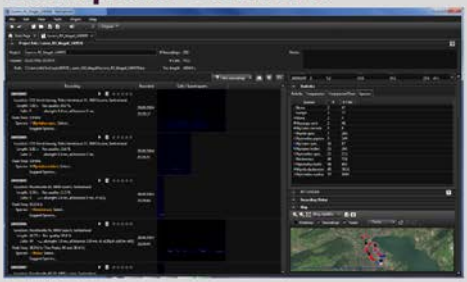
non stop recording with external power

mobile monitoring and data analysis

BATLOGGER M

The ideal companion for transects with its GPS function and highly sensitive recording system.

BatExplorer Software



Free software to analyse and organise your bat recordings

BATLOGGER.COM

Avisoft Bioacoustics

Hardware and Software for Investigating Animal Acoustic Communication

- Active bat monitoring with hand-held & PC-based recording devices
- Passive bat monitoring (an advanced Bat Call Trigger Filter option can efficiently reject unwanted noise)
- Acoustically luring bats into mistnets or newly installed bat houses

- Versatile software for detecting and classifying bat calls

Avisoft Bioacoustics

Visit **www.avisoft.com/app_bats.htm** for details.

avisoft.com

ANABAT SWIFT

World's most efficient compact passive bat detector

A full spectrum bat detector as easy to deploy as the *Anabat Express*

Full Spectrum
Records in Full Spectrum or Zero Crossing

Microphones
Omnidirectional and directional microphone options, to suit your recording environment

Power
Longest deployment times using only AA batteries: Up to 1000 hours recording time

Storage
Supports two SD Cards, allowing you to save more bat calls than ever

High Quality Recordings
Samples up to 500ksps

GPS
Built-in GPS, not an expensive accessory. Perfect for automatic night and transect mode

GET IN TOUCH
Titley Scientific – Andrew Dobson
16/17 Arkwright Suite
Coppull Enterprise Centre
Mill Lane, Coppull
Lancashire, ENGLAND PR75BW
P: 07818756965
E: uk@titley-scientific.com

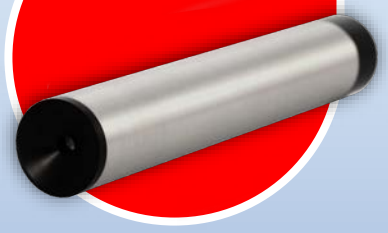
TITLEY SCIENTIFIC

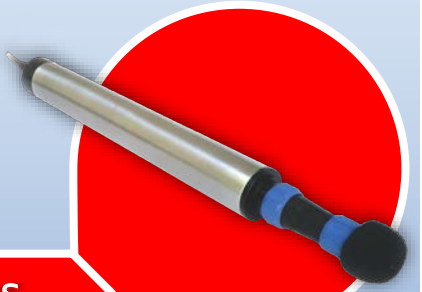
www.titley-scientific.com

DODOTRONIC

Audio and Ultrasonic devices

USB ULTRASONIC MICROPHONES





ULTRASONIC RECORDERS

ULTRASONIC ANOLOG MICROPHONES

PARABOLIC MICROPHONES

www.dodotronic.com

info@dodotronic.com

SERVICE

APODEMUS
field equipment

Solutions for bat research

THE APODEMUS SERVICE

- Free loan of replacement device, if defect within 3 years.
- All products in stock.
- No shipping fees (within Europe).
- Fast shipping.
- Payment through Paypal or invoice.

Biotope,
your partner for surveying bats in Europe

Our 20+ years of experience in the survey of bats in Europe has allowed us to identify the best technical solutions that we are proud to offer to you today to make your surveys successful.

Equipment

Biotope is an official dealer for several manufacturers of observation, listening and recording equipment (Wildlife Acoustics, Petterson, Titley, etc.). We also designed several solutions able to meet particular needs such as long-term recordings on wind masts (protection case and electricity supply from solar panel), etc.

Analysis

Our team has developed Sonochiro®, a software allowing automatic processing of bats recordings. An invaluable time-saving tool (processing time reduced to up to 90%) designed to suggest species ID, count bat passes, highlight social behaviours, etc.

SonoChiro®
Software

ultrasound recording | automated analysis | list of species recorded

31 European species + 80 neotropical species covered

Publishing / Communication

Biotope has published several books about bats, including the best-seller by Michel Barataud,
Acoustic Ecology of European Bats
describing the acoustic identification method developed by the author.

Find out more about our products and skills on ***www.leclub-biotope.com***

biotope

List of participants

Eve Afonso
eve.afonso@univ-fcomte.fr

Joxerra Aihartza
joxerra.aihartza@ehu.eus

Ostaizka Aizpurua
ostaizka.aizpurua@snm.ku.dk

Antton Alberdi
antton.alberdi@snm.ku.dk

Juan Tomás Alcalde
jtalcalde@gmail.com

Miren Aldasoro
maldasoro005@ikasle.ehu.eus

Benjamin Allegrini

Pedro Alonso Alonso

Pedro Jorge Alves
pjalves@plecotus.com

Sybill Amelon
batworldozarks@gmail.com

Francisco Amorim
fnlamorim@gmail.com

Leonardo Ancillotto
leonardoancillotto86@gmail.com

Arnold Andreasson
arnold@mellifica.se

Maggie Andrews
mmandrews37@gmail.com

Tommy Andriollo
tommy.andriollo@gmail.com

Bruno Antunes Silva
bsilva@uevora.pt

Grzegorz Apoznanski
apoznanski.grzegorz@gmail.com

Francisco Arcos
farcos@arcea.net

Aitor Arrizabalaga
arrizabalaga.aitor@gmail.com

Manuel Arzúa Piñeiro

Tina Aughney
info@batconservationireland.org

Stéphane Aulagnier
stephane.aulagnier@inra.fr

Hans J Baagøe
hjbaagoe@snm.ku.dk

Petra Bach
petrabach@bach-freilandforschung.de

Elias Bader
elias.bader@zoo.ch

Unai Baroja
ubaroja001@gmail.com

Silvia Barreiro
silviapereirabarreiro@gmail.com

Tomas Bartonicka
bartonic@sci.muni.cz

Yves Bas
yves.bas@mnhn.fr

Anna Bator
mystacinaa@gmail.com

İbrahim Raşit Bilgin
rasit.bilgin@boun.edu.tr

Anna Blomberg

Frank Bonaccorso
fbonaccorso@usgs.gov

Fabio Bontadina
fabio.bontadina@swild.ch

Kristine Boohman
kbohmann@snm.ku.dk

Filip Borms

Emma Boston
esmboston@hotmail.com

Elizabeth Bradshaw
ebradshaw71@icloud.com

Pedro Branco Leote
pedroleote@valetua.pt

Ilze Brila

Szilárd-Lehel Bücs
contact@lilieci.ro

Ivana Budinski
ivana.budinski@ibiss.bg.ac.rs

Ane Caro
ane.caro@ehu.eus

Andrew Carr
andrew.carr@bristol.ac.uk

Ana Belén Casais

M. Jesus Celaya

Oana Mirela Chachula
oana_chachula@yahoo.com

Nathalie Charbonnel
nathalie.charbonnel@inra.fr

Gloriana Chaverri
gchaverri@upacificosur.org

Jan Cichocki

Mateusz Ciechanowski
matciech@kki.net.pl

Fabien Claireau
fabien.claireau@mnhn.fr

Yuval Cohen
uvicohen@gmail.com

Irene Conenna
irene.conenna@gmail.com

Alexandra Corduneanu
alexandra.corduneanu@usamvcluj.ro

Alba Coronado Gomis

Gabor Csorba
csorba.gabor@nhmus.hu

Julie Dahl Møller

Luc De Bruyn
luc.debruyn@inbo.be

Carmelina De Conno
deconnoca@gmail.com

Dina Dechmann
ddechmann@orn.mpg.de

Jasja Dekker
jasjad@gmail.com

Stanimira Deleva
stanimira.deleva@gmail.com

Chloe Delgery
chloe.delgery@atkinsglobal.com

Jan Demjanovic
jan.demjanovic@seznam.cz

Anabel Díaz Suárez

Andrew Dobson

Mona Doss
mona@wildlifeacoustics.com

Marie-José Dubourg Savage
chirosavage@gmail.com

Heliana Dundarova
h.vulgaris@gmail.com

Sven Eisenbiegler

Katrine Eldegard

Morten Elmeros
elm@bios.au.dk

Simon Engelberger

Amaiur Esnaola Illarreta
amaiur.esnaola@ehu.eus

Nicolas Fasel
fasel.nicolas@gmai.com

Daniel Fernández Alonso
danielfernandezalonso@gmail.com

Ondine Filippi-Codaccioni
seise.ofc@gmail.com

Domhnall Finch
d.finch@exeter.ac.uk

Nicola M. Fischer
fischer.nicola@yahoo.com

Carles Flaquer
carlesflaquer@gmail.com

Jeremy Froidevaux
jeremy.froidevaux@bristol.ac.uk

Elisa Fuentes-Montemayor
ef12@stir.ac.uk

Lionel Gaches

Maxime Galan

Inazio Garin Atorrasagasti
inazio.garin@ehu.eus

Suren Gazaryan
s.gazaryan@gmail.com

Giada Giacomini
giada.giacomini19@gmail.com

Anita Glover
anitaglover@vwt.org.uk

Lena Godlevska
lgodlevska@gmail.com

Urtzi Goiti
urtzigoiti@yahoo.com

Colin Green

Kanat Gürün
kanatgurun@yahoo.com

Roman Guziak
podkowiecplus@wp.pl

Ralf Gyselings
ralf.gyselings@inbo.be

Alexandre Hacquart
ahaquart@biotope.fr

John Haddow
john.haddow1@btinternet.com

Tanja Halczok
Halczokt@uni-greifswald.de

Daniela Hamidovic
daniela.hamidovic@dzzp.hr

Andrew Harrington
andrew.harrington@postgrad.wit.ie

Elizabeth Hemond
lizhemond@gmail.com

Julia P. S. Hoeh
jhoeh@sycamores.indstate.edu

Vita Hommersen
vita.hommersen@zoogdiervereniging.nl

Sarah Hooper
hoopers@missouri.edu

Ivan Horacek
horacek@natur.cuni.cz

Paul Howden-Leach

Tony Hudson

Senta Huemer

Kjell Isaksen
kjell.isaksen@online.no

Angel Ivanov
angelivanov@bfu.bg

Klara Janikova

Eric Jansen
eric.jansen@zoogdiervereniging.nl

Maria Jerabek

Lide Jimenez
lide.jimenez@ehu.eus

Alison Johnston

Bob Jonge Poerink
bob@fieldworkcompany.nl

Marlotte Jonker Jonker

Jean-Francois Julien

Javier Juste Ballesta
juste@ebd.csic.es

Kubra Karaman
krmn.kubra@gmail.com

Goc Katarzyna

Brian Keeley

Andrzej Kepel
andrzej@salamandra.org.pl

Chirstian Kerbiriou
christian.kerbiriou@mnhn.fr

Lucinda Kirkpatrick
lucinda.kirkpatrick@uantwerpen.be

Tomasz Kokurewicz
tkokur@gmail.com
tomasz.kokurewicz@upwr.edu.pl

Brigitte Komposch
b.komposch@oekoteam.at

Sarah Koschnicke

Klemen Koselj
koselj@orn.mpg.de

Jasmina Kotnik
jasmina.kotnik89@gmail.com

Marcin Kowalczyk

Frauke Krüger

Sergei Kruskop
kruskop@zmmu.msu.ru

Karl Kugelschafter
karl.kugelschafter@chirotec.de

Eeva-Maria Kyheröinen
eeva-maria.kyheroinen@helsinki.fi

Yves Laurent
ylaurent@naturalsciences.be

Isabelle Le Viol
ileviol@mnhn.fr

Thomas Lilley
tmlill@liverpool.ac.uk

Herman Limpens
herman.limpens@zoogdiervereniging.nl

Peter Lina
phclina@telfort.nl

Tong Liu
liut035@nenu.edu.cn

Adria Lopez Baucells
adria.baucells@gmail.com

Hibat-Ellah Loumassine
loumassine_bouz@hotmail.fr

Helen Lucking

Julie Marmet
jmarmet@mnhn.fr

Ferdia Marnell
Ferdia.Marnell@ahg.gov.ie

Garazi Martin Bideguren
garazimartin025@gmail.com

Maria Mas Navarro
maria.cat12@gmail.com

Vanessa Mata
vanessamata@hotmail.com

Fiona Mathews
f.mathews@exeter.ac.uk

Edita Maxinová
edita.maxinova@gmail.com

Gary McCracken
gmccrack@utk.edu

Angelica Menchaca
am14886@bristol.ac.uk

Clare Marie Mifsud
cmifsud2@gmail.com

Ara Monadjem
aramonadjem@gmail.com

Susanne Morgenroth

Valentina Nardone
valentina.nardone@unina.it

Ioseb Natradze
ioseb.natradze@iliauni.edu.ge

Mads Nedergaard Olsen
madsolsen@biology.sdu.dk

Roberto Novella
r.novella-fernandez@soton.ac.uk

Ebbe Nyfors

Denise O'Meara
domeara@wit.ie

Martin Obrist
martin.obrist@wsl.ch

Kirsty Park
k.j.park@stir.ac.uk

Diana Parra Corbacho
dianacorbacho@gmail.com

Julie Pauwels
julie.pauwels@edu.mnhn.fr

Gunārs Pētersons
Gunars.Petersons@llu.lv

Lars Pettersson
info@batsound.com

Corinna Pinzari

Dominique Pontier

Pamela Priori
pamela.priori@gmail.com

Sebastien Puechmaille
s.puechmaille@gmail.com

Xavier Puig-Montserrat
xavierpuigm@gmail.com

Alek Rachwald
a.rachwald@ibles.waw.pl

Ana Rainho
amrainho@fc.ul.pt

Roger David Ransome
rogerransome@hotmail.com

Orly Razgour
orly.razgour@soton.ac.uk

Hugo Rebelo
hugo.rebelo@cibio.up.pt

Johannes Regelink

Ingrid Regina Reinkind

Guido Reiter
guido.reiter@fledermausschutz.at

Marco Riccucci
marco.riccucci@gmail.com

María Cristina Rios-Blanco
makris88@gmail.com

Niamh Roche
niamhr@batconservationireland.org

Javier Rodriguez

Charlotte Roemer
croemer@biotope.fr

Elizabeth Rowse
liz.rowse@bristol.ac.uk

Ireneusz Ruczynski
iruczyns@ibs.bialowieza.pl

Danilo Russo
danrusso@unina.it

Jens Rydell
jens.rydell@telia.com

Sonia Sanchez

Attila D. Sándor
adsandor@gmail.com

Dino Scaravelli
dino.scaravelli@unibo.it

Marcel Schillemans
marcel.schillemans@zoogdiervereniging.nl

Henry Schofield

Paul Scott

Caroline Shiel

Elena Sitnikova
sitnikovae@yandex.ru

Sonia Smeraldo
sonia.smeraldo@unina.it
sonia5.6.89@hotmail.it

Mariska Snijder-Nieuwenhuijsen

Friederike Spitzenberger
friederike.spitzenberger@aon.at
office@batlife.at

Ana Stamatescu
ana.stamatescu@gmail.com

Sylvia Stephan

Knut Åge Storstad
knutsto@hotmail.com

Valérie Strubel

Per Ole Syvertsen
posy@helgelandmuseum.no

Tamara Szentivànyi

Marta Szurlej
marta.szurlej@wp.pl

Emma Teeling
emma.teeling@ucd.ie

Elena Tena
etenalopez@gmail.com

Laura Torrent Alsina
arual.torrent@gmail.com

Àngel Torrent Iglesias

Nia Toshkova Luybenova
niyatoshkova@gmail.com

Orianne Tournayre
orianne.tournayre@supagro.fr

Peter Twisk

Hernan Ullon

Nicolas Valet
nicolas.valet@auddice.com

Nerea Vallejo
nvallejo004@ikasle.ehu.eus

Thomas van der Meij
tvdmeij@xs4all.nl

Ben Van der Wijden
ben.van.der.wijden2@telenet.be

Ville Vasko

German Velayos-Gainza
germanvelayos@gmail.com

Parvathy Venugopal
pv14888@bristol.ac.uk

Viesturs Vintulis

Christian Voigt
voigt@izw-berlin.de

Sean Walls
sean@biotrack.co.uk

Manon Warringa

Conor Whelan
conor.whelan@ucd.ie

Cecilia Wide

Zuzanna Wikar
zuzanna.wikar@gmail.com

Caroline Williams (Bat Cons. Trust)
cwilliams@bats.org.uk

Patrick Wright
pw339@exeter.ac.uk

Maja Zagmajster
maja.zagmajster@bf.uni-lj.si

Andreas Zahn
andreas.zahn@iiv.de

Xin Zhao
zhaox111@nenu.edu.cn

Marlon Zortea
mzortea@uol.com.br

Vida Zrnčić
v.zrncic@gmail.com

Universidad del Pais Vasco
Euskal Herriko Unibertsitatea

upna Universidad Pública de Navarra
Nafarroako Unibertsitate Publikoa

NATURAL HISTORY MUSEUM OF DENMARK
UNIVERSITY OF COPENHAGEN

ueu udako euskal unibertsitatea

EUSKO JAURLARITZA
GOBIERNO VASCO