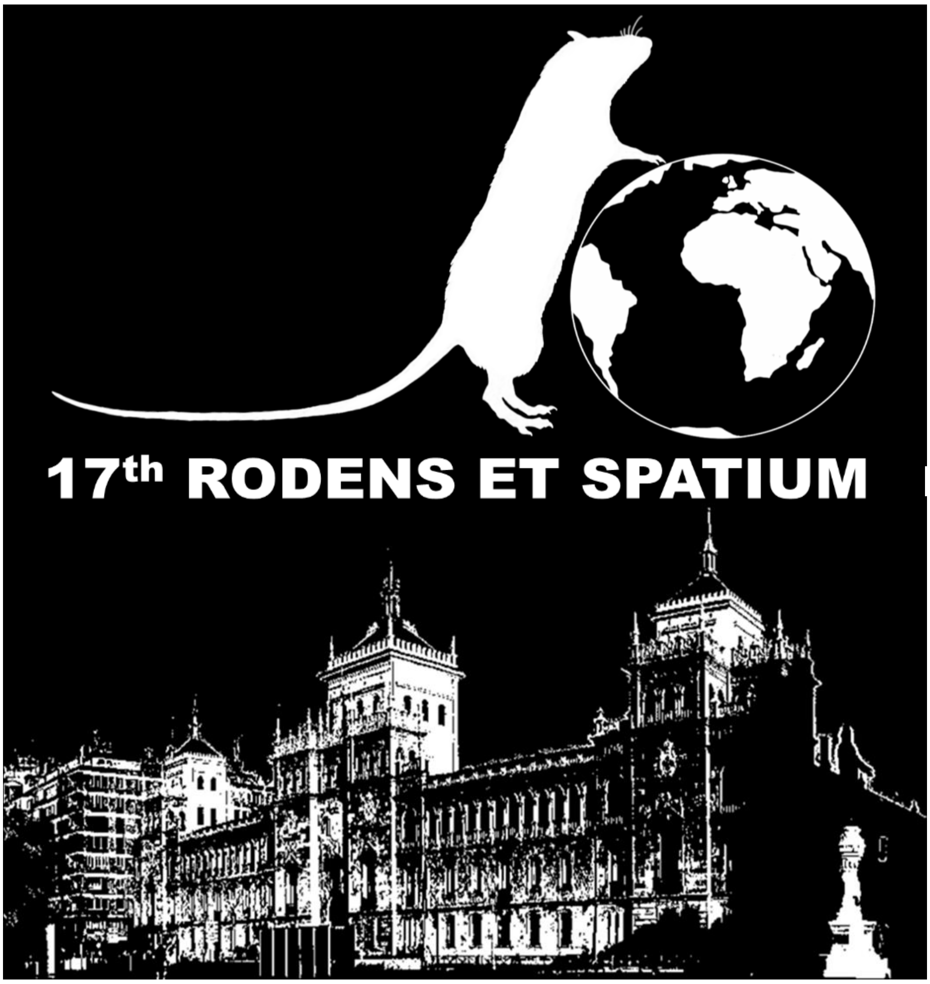

Book of Abstracts

Silvia Herrero-Cófreces and Juan José Luque-Larena, Editors

Departamento de Ciencias Agroforestales, Escuela Técnica Superior de Ingenierías Agrarias

Universidad de Valladolid

May 22nd – 26th, 2023 - Valladolid, Spain

Palacio de Congresos Conde Ansúrez, Real de Burgos s/n, 47011, Valladolid

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FOREWORD

Dear colleagues,

After two extensions imposed by a constantly shifting world, we are finally able to welcome you to the 17th RODENS ET SPATIUM international conference. The 17th RODENS ET SPATIUM conference was originally scheduled to take place in September 2020, but due to the global COVID-19 pandemic, we elected to suspend it. Due to the prolonged duration of the pandemic, as well as the “sister” rodent conference (ICRBM) in Tanzania taking place in 2022, the steering committee considered that 2023 was the perfect year to hold the 17th RODENS ET SPATIUM in Spain.

One of the positive things to come out of the pandemic has been the possibility and wide-spread acceptance of remote (e.g., online) participation at scientific conferences, which has proven both convenient for those who are unable to travel long distances and in helping to mitigate the risks posed by large gathering to public health in general. When we planned the conference in the aftermath of the pandemic, we imagined that most participants would choose the online mode. However, this has not been the case, and while some valued colleagues have chosen to participate remotely (enabling greater inclusion), it is never-the-less gratifying to see that many participants have chosen the in-person option. Despite the pandemic, there remains a desire to meet, see each other, discuss, and share science. Holding the 17th RODENS ET SPATIUM conference in Spain will provide a wonderful backdrop for us to do so, with Rodents as the real protagonists of the event.

We would like to thank Professor Heikki Henttonen, Chairman of the Steering Committee of RODENS ET SPATIUM, as well as the rest of the members of the committee, for supporting our proposal to hold the event in Valladolid. We would also like to thank the Fundación General de la Universidad de Valladolid (FUNGE) for their support and help in the technical organisation of the event, especially to Amaya Gaisán and Alfonso Zaloña. Likewise, we are immensely grateful for the support of Daniel Herrera in assisting with the technical organisation, especially with regards to the various digital requirements. Finally, we would like to thank the various entities and institutions that have supported the conference, including the Diputación de Valladolid, the Valladolid City Council, the University of Valladolid (UVA), the Agricultural Technology Institute of Castilla y León (ITACyL), and the Agricultural and Agri-Food Technology Centre (ITAGRA) and its wildlife management technical service FERUS.

Regarding the content of our conference, it is worth highlighting the quality and relevance of the speakers presenting the five plenary talks. We have the pleasure of several of the most internationally renowned and experienced rodent scientists presenting plenaries, not to mention a suite of the most promising young scientists who are currently developing attractive and cutting-edge research. We are convinced that the level of the plenary speakers will define the quality of the conference that is about to start. We hope that you will all enjoy the program on offer. Beyond the plenary sessions, participants' contributions will be divided into six symposia: (1) Ecology; (2) Taxonomy, genetics & conservation; (3) Biology & Evolution; (4) Diseases; (5) Conflicts & management; and (6) Methods & applied science. There will be just over one hundred participants at this conference. Notably, with regards to the gender of the participants, the majority (55%) are women. This should be celebrated, as it exemplifies both gender equality and increasing role women play in leading our field. Noteworthy, we will have participants from more than 40 different countries, which reflects the important diversity and international scope of the RODENS ET SPATIUM conference series. We declare that this conference is in line with the Universal Declaration of Human Rights adopted by the UN General Assembly, and that they are inherent to every human being without distinction of sex, national or ethnic origin, colour, religion, language or any other status (https://standup4humanrights.org).

We would especially like to thank those participants who will act as Chairs in the various symposia sessions, thus helping us to efficiently and smoothly implement the program presented. We would also like to thank the European agricultural rodent experts who will participate in the ITACyL round table planned in the middle of the conference week, as this will enable important contributions to the transfer of scientific knowledge to the local society interested and affected by problems associated with wild rodents.

We further announce that during the conference the steering committee of RODENS ET SPATIUM will meet to formalise the change of our Chairman, where Professor Heikki Henttonen will step down as Chairman with Professor Herwig Leirs taking over. We welcome our new Chairman and thank Professor Henttonen for his fantastic work and dedication in organising the RODENS ET SPATIUM conferences, both past and present, and wish him a well-deserved and happy retirement.

Finally, we can only wish all participants a rewarding and productive stay in Spain during the week which promises to be another successful celebration of a RODENS ET SPATIUM conference. We hope that the wonders of Valladolid can only help us to generate the best possible scientific climate amongst this valued collection of scientific colleagues.

Thanks to all.

Juan José Luque-Larena & Silvia Herrero-Cófreces

COMMITTEES

Local Committee

Juan José Luque-Larena, Universidad de Valladolid

Silvia Herrero-Cófreces, Universidad de Valladolid

Daniel Herrera Rodríguez, Universidad de Castilla-La Mancha

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THE RODENTS

Rodents are an outstanding group of living organisms. One of every three known mammal species is a rodent. They account for the largest fraction of mammalian diversity on Earth, and their relevance to ecosystems and human interests is practically unparalleled. Rodents have adapted to live in ecosystems all around the globe and, at the same time, they have a huge influence on those environments playing keystone roles as plant consumers, seed dispersers and prey to secondary consumers. Some species act as ecosystem engineers, truly modifying habitats and landscapes. Rodents can also be of nuisance to human interests, often causing significant damage to building structures and crop yields. They are also the most significant mammalian host group for numerous arthropod vectors and diseases of risk to public health. On the other hand, rodents constitute the key animal model for research worldwide. Hundreds of millions of lab rodents are annually breed and used to improve scientific knowledge and, ultimately, our life quality. The interest in progressing on rodent biology is thus global, and Rodens et Spatium international conference represents the best framework to update such knowledge.


FOTO: Eloy Revilla

Rodens et Spatium conferences started in France in 1987, under the name 'Le rongeur et l'espace'. In 1993, at its 4th edition held in Poland, the conference became international. Ever since the conference has been organized, almost biannually, in: Morocco (5th 1995), Israel (6th 1998), Czech Republic (7th 2000), Belgium (8th 2002), Poland (9th 2004), Italy (10th 2006), Russia (11th 2008), Turkey (12th 2010), Finland (13th 2012), Portugal (14th 2014), Czech Republic (15th 2016) and Germany (16th 2018). The next edition of the conference (17th) will take place, for the first time, in Spain. The conference will be held in the city of Valladolid between the 22nd and the 26th of May. Valladolid is the capital city of the astonishing northwest region of Castilla-y-León, the largest autonomous administrative region in Spain.


Foto: Eloy Revilla

Significantly, during the last three decades Castilla-y-León has experienced periodic and large rodent (common vole, *Microtus arvalis*) outbreaks across intensified farming landscapes, triggering significant plant damage and zoonotic spill-over episodes of socio-economic and public health concern. The appearance of a novel, abundant and cyclic prey on Castilla-y-León farmland has also had significant impact on local trophic webs, periodically attracting large numbers of predators, including long-distance migratory raptors of conservation concern. Therefore, and in order to promote an effective and integrative knowledge transfer from Rodens et Spatium to local stakeholders and rodent managers, an ad-hoc round table entitled "*Rodent-human conflicts in the XXI century: crop protection and public health*" and coordinated by ITACyL (Castilla-y-León Agriculture Technology Institute), will be organized during the conference. The round table will count with the presence of some European leaders on the topic.


Foto: Jacinto Roman

Noteworthy, the hosting region of the next Rodens et Spatium conference treasures magnificent historical heritage as well as unrivalled biodiversity, including emblematic and/or endemic species such as Spanish imperial eagle, Eurasian black vulture, great bustard, black stork, Cabrera's vole, Iberian desman, Iberian wolf or brown bear. Valladolid's weather and local food (tapas) and wineries (Ribera de Duero) will undoubtedly be a plus to encourage scientific debate on a friendly environment after the conference symposia. The social program for accompanying-persons will also provide a fantastic opportunity to get familiarized with historical and current Castilian tradition.

We are looking forward to seeing you in Valladolid!

SCHEDULE

	MONDAY	TUESDAY	WEDNESDAY	THURSDAY	FRIDAY
9:00	*- Entrance hall -* ***Registration***	*- Main conference room -* **PLENARY: Sandra Telfer**	*- Main conference room -* **PLENARY: Patrick Giraudoux**	*- Main conference room -* **PLENARY: Nigel Bennett**	*- Main conference room -* **PLENARY: Ricardo Pita**
10:00		Coffee break	Coffee break	Coffee break	Coffee break
10:30		*- Room A -* **DISEASES** **(I)** *- Room B -* **CONFLICTS** **&** **MANAGEMENT** **(I)**	*- Main conference room -* **"ITACYL" ROUND TABLE:** ***Rodent-human conflicts in the XXI century: crop protection and public health***	*- Room A -* **TAXONOMY, GENETICS & CONSERVATION** **(I)** *- Room B -* **BIOLOGY** **&** **EVOLUTION** **(II)**	*- Room A -* **ECOLOGY** **(IV)** *- Room B -* **TAXONOMY, GENETICS & CONSERVATION** **(II)**
11:00	*- Main conference room –* **Opening event** *- Main conference room -* **PLENARY: Herwig Leirs**				
11:30					*- Posters & coffee room -* **Closing event & farewell drink**
12:30			**MID CONFERENCE TOUR** local winery and castle (lunch included)		
13:00	LUNCH	LUNCH		LUNCH	
15:00	*- Room A -* **ECOLOGY** **(I)** *- Room B -* **METHODS** **&** **APPLIED SCIENCE** **(I)**	*- Room A -* **ECOLOGY** **(III)** *- Room B -* **CONFLICTS** **&** **MANAGEMENT** **(I)**		*- Room A -* **DISEASES** **(II)** *- Room B -* **METHODS** **&** **APPLIED SCIENCE** **(II)**	
16:30	Posters' opening & coffee break	Poster session & coffee break		Poster session & coffee break	
17:30	*- Room A -* **ECOLOGY** **(II)** *- Room B -* **BIOLOGY** **&** **EVOLUTION** **(I)**			Rodens et Spatium Steering Committee Meeting	
	WELCOME COCKTAIL	CITY TOUR		BANQUET	

PROGRAMME

Monday, May 22nd 2023

09:00–11:00 **REGISTRATION**

OPENING CEREMONY

11:00 Presentation by Academic and local authorities – press release

11:30 Scientific opening by Local and Steering Committees

11:45–12:45 **PLENARY LECTURE**

Herwig Leirs: ***"The multimammate mouse*** **Mastomys natalensis*****: from pest to model"***

13:00–14:30 **LUNCH**

15:00–16:15 Symposia talks

ROOM A: ECOLOGY (I)

Chairperson: **Paola Correa Cuadros**

15:00 **Ana Maria Benedek**: *Habitat selection patterns reveal competition between two forest rodents and suggest recent elevational expansion of* Apodemus flavicollis

15:15 **Deon Roos**: *The partial synchronisation of population cycles through travelling waves*

15:30 **Valentina Tagliapietra**: *Linking climatic variables to wild rodent population dynamics as predictors for zoonotic disease transmission*

15:45 **Ricardo Pita**: *Spatially explicit capture-recapture modelling and parentage analysis of Cabrera voles in high population density patches*

16:00 online@ **Helena Sabino-Marques**: *Context-dependent species associations: environmental and seasonal effects on local co-occurrence patterns of two Mediterranean voles*

ROOM B: METHODS & APPLIED SCIENCE (I)

Chairperson: **Aurelio Malo**

15:00 **Miriam Maas**: *One conjugate doesn't fit all: choosing the right conjugate for your serological assay in small mammal research*

15:15 **Tuomas Aivelo**: *Entering the rat world: secondary school students collecting reliable data on urban near-environment species*

15:30 **Constantino Caminero-Saldaña**: *New technologies and old allies: can common kestrel GPS-tracking help in detecting common vole during low density phases?*

15:45 **Bram Vanden Broecke**: *Can animal personalities save human lives? Evidence for repeatable differences in activity and anxiety in African giant pouched rats* (Cricetomys ansorgei)

16:00 **Jens Jacob**: *Establishing an early warning system for human Puumala Hantavirus infections in Germany*

16:30–17:30 **Posters' opening** & coffee break

17:30–18:45 Symposia talks

ROOM A: ECOLOGY (II)

Chairperson: **Wendy Ruscoe**

17:30 **Paola Correa Cuadros**: *Gradual and eruptive dynamics of rodent pests: outbreaks in house mice in Australia and common voles in Spain*

17:45 **Heikki Henttonen**: *Ecology of sympatric bank and red voles,* Myodes glareolus *and* M. rutilus*, in Northern Finland*

18:00 **Marie Bouilloud**: *Impacts of forest anthropization on the relationships between small mammal communities and their gut microbiota*

18:15 **František Vejmělka**: *Community composition of non-volant mammals along a complete elevational gradient in New Guinea: fieldwork, musea, genetics, and ecology*

18:30 **Constantino Caminero-Saldaña**: *Prospecting the effects of the landscape structure on the spatio-temporal evolution of the abundance of the common vole in Castilla y León, Spain*

ROOM B: BIOLOGY & EVOLUTION (I)

Chairperson: **Alena Fornuskova**

17:30 **Maílis Carrilho**: *Physiological and behavioural habituation of wild wood mice,* Apodemus sylvaticus*, to laboratory conditions*

17:45 **Chevret Pascale**: *Evolution of zona pellucida genes in rodents*

18:00 **Aurelio Malo***: Androgenization effects on endoparasite loads on males from two contracting European woodland rodent populations*

18:15 **Sabrina Renaud**: *Morphological diversification along the invasion of Senegal by the house mouse*

19:30 **WELCOME COCKTAIL**

Tuesday, May 23rd 2023

09:00–10:00 **PLENARY LECTURE**

Sandra Telfer: ***Rodent-borne disease: risk, epidemiology and control***

10:00–10:30 Coffee break

10:30–12:15 Symposia talks

ROOM A: RODENT-BORNE DISEASES (I)

Chairperson: **Xavier Lambin**

10:30 **Daniel Herrera Rodríguez**: *Infestation patterns and zoonotic bacteria prevalence in ticks collected from small mammals inhabiting the intensive farmland of Northwest Spain*

10:45 **Alena Fornuskova**: *Diversity of trypanosomes in rodents and marsupials from New Guinea*

11:00 **Marieke de Cock**: *Increased rat abundance and zoonotic disease hazard in urban green: smart urban greening required?*

11:15 **Vincent Sluydts**: *Are associations between zoonotic pathogens driven by host community diversity, gut microbiome and environmental indicators in forests and urban parks throughout Europe?*

11:30 **Lucas Wauters**: *Invading species and their parasites: spillover of an alien nematode affects personality and reduces survival in a native species*

11:45 **Bram Vanden Broecke**: *Drivers behind co-occurrence patterns between pathogenic bacteria, protozoa, and helminths in populations of the multimammate mouse,* Mastomys natalensis

12:00 online@ **Christian Imhold**: *Pathogen traits determine landscape persistance during climate extremes*

ROOM B: CONFLICTS & MANAGEMENT (I)

Chairperson: **Peter Brown**

10:30 **Aaron Shiels**: *Overcoming barriers of poor zinc phosphide bait efficacy for reducing vole damage to grass seed fields in Oregon, USA*

10:45 **Wendy Ruscoe**: *Effects of cropping practices on habitat use by pest house mice (*Mus musculus*): implications for management*

11:00 **Miriam Báscones**: *Biological control of common vole (*Microtus arvalis *Pallas) through the provision of artificial nesting boxes for birds of prey in intensified cropping areas of Castilla y Leon, Spain*

11:15 **Andrea Bonacchi**: *An insight into the ecology of an invasive rodent on small Mediterranean islands: a first step for management*

11:30 **Azucena Bermejo-Nogales**: *Analysis of single nucleotide polymorphisms of the VKORC1 gene in the brown rat* (Rattus norvegicus) *population of the urban sewage system of Leganés*

11:45 **Nyo Me Htwe**: *Are long-term population and damage patterns of rodents in Southeast Asian rice agroecosystem different from European field rodents'?*

12:00 **Mohamad Thaqit Mohd Khairuddin**: *Development and evaluation of unmanned aerial vehicle rodenticide applicator (R-Drop Drone) for rodenticide application in oil palm plantation*

13:00–14:30 **LUNCH**

15:00–16:15 Symposia talks

ROOM A: ECOLOGY (III)

Chairperson: **Maria da Luz Mathias**

15:00 **Tiago Filipe Crispim-Mendes**: *Local drivers of post-colonization demogenetics of the Cabrera vole in ephemeral patches*

15:15 **Xavier Lambin**: *Demographic drivers of vole population cycles.*

15:30 **Santtu Pentikäinen**: *Exploring spatiotemporal variation in urban rat population through pest management data*

15:45 **Dominique Fauteux**: *Lemming cycles in the Canadian high arctic: new insights about the extended low abundance phase*

ROOM B: CONFLICTS & MANAGEMENT (II)

Chairperson: **Jens Jacob**

15:00 **Sofia Gabriel**: "*What doesn't kill you makes you stronger": anticoagulant rodenticide resistance in insular and continental house mice*

15:15 **Constantino Caminero Saldaña**: *Can population structure derived variables be useful for predictive modelling of demographic fluctuations of common voles?*

15:30 **Daniel Dornan**: *Understanding spatial-temporal patterns of* Rattus rattus *abundance in rural Madagascar to inform control strategies.*

15:45 **Peter Brown**: *Background food influences efficacy of the rodenticide, zinc phosphide, in wild house mice – an enclosure study*

16:30–17:30 **Poster session** & coffee break

18:00 **FREE CITY TOUR** – Historic Valladolid

Wednesday, May 24th 2023

09:00–10:00 **PLENARY LECTURE**

Patrick Giraudoux: *Rodent pest management in multifactorial socio-ecosystems: a practical application at the Jura massif*

10:00–10:30 Coffee break

10:30–12:30 **"ITACyL" ROUND TABLE & DISCUSSION**– Free access to invited public

Rodent-human conflicts in the XXI century: crop protection and public health

Chairs: Constantino Caminero Saldaña and Juan José Luque Larena

Co-chairs: François Mougeot, Jens Jacob and Patrick Giraudoux

10:30 **Part 1:** Rodent integrated management across Europe: southern (Spain), central (France) and northern (Germany) regions.

11:30 **Part 2:** Open debate on future strategies and milestones.

12:45 **MID CONFERENCE TOUR**

14:00 Lunch (El Barco Restaurant – Peñafiel town, Valladolid province)

16:30 Peñafiel Castle & Wine Museum (Peñafiel town, Valladolid province)

18:30 Winery visit & wine tasting (**PROTOS** ®, Peñafiel-Valladolid) D.O./Certificate of Origin "*Ribera del Duero*"

Thursday, May 25th 2023

09:00–10:00 **PLENARY LECTURE**

Nigel Bennett: ***Social induced infertility in highly social mole-rats: a tale of two mechanisms of reproductive suppression***

10:00–10:30 Coffee break

10:30–12:15 Symposia talks

ROOM A: TAXONOMY, GENETICS & CONSERVATION (I)

Chairperson: **Josef Bryja**

10:30 **Jelena Blagojevic**: *B chromosomes in urban populations of yellow-necked wood mice,* Apodemus flavicolis *(Mammalia, Rodentia)*

10:45 **Gerald Heckel**: *The genomic legacy of 5000 years of complete isolation in Orkney voles*

11:00 **Emilie Hardouin**: *Insight into the population genetic and evolution of an endemic species:* Mus cypriacus

11:15 **Michaela Uhrová**: *Are there more species of the naked mole-rat* (Heterocephalus glaber)*? Species delimitation using phylogenomics*

11:30 online@ **Getachew Mulualem Muche**: *Taxonomic revision and evolutionary history of the Ethiopian clade of climbing mice* (Dendromus) *- the role of elevation and geographical barriers in the speciation processes*

11:45 online@ **Frederico Mestre**: Infering the biogeographic history of the Cabrera vole by integrating niche modelling, genomic and fossil data

12:00 **Josef Bryja**: *Fifty shades of grey: phylogenomics helps to delimit species in African thicket rats (*Grammomys*)*

ROOM B: BIOLOGY & EVOLUTION (II)

Chairperson: **Azucena Bermejo-Nogales**

10:30 **Sabrina Renaud**: *Wild vs lab house mice: does captive breeding affect inner ear morphology?*

10:45 **Elizandra Cardoso**: *Response to urban exposure to heavy metals in two synanthropic rat species: a multi-marker evaluation*

11:00 **Irene Espinosa Manjón**: *Physiological drivers of home-range size in a woodland rodent*

11:15 **Guilherme Aparício**: *Influence of traffic noise on the behaviour and physiology of two small mammal*

11:30 **Ryoko Koizumi**: *Cercadian activity pattern of rats living in livestock farm*

11:45 **Barbora Pavlíčková**: *Factors affecting the quantity of mitochondria in African small rodents*

12:00 **Vladimir Kupriyanov**: *Grooming stereotypes of the common hamster (*Cricetus cricetus*) in the context of individual and social behavior*

13:00–14:30 **LUNCH**

15:00–16:15 Symposia talks

ROOM A: RODENT-BORNE DISEASES (II)

Chairperson: **Ruth Rodríguez-Pastor**

15:00 **Hadas Hawlena**: *The mystery of* Bartonella*'s pervasive nature in rodent communities*

15:15 **Lovisa Hoekby**: *The potential role of beavers and associated landscape wetness for* Francisella tularensis *infection in Swedish hares*

15:30 **Andrew McManus**: Myodes glareolus*; a longitudinal investigation of an invasive species and it's pathogens.*

15:45 **Joanna Nowicka** *The role of ground beetles as intermediate hosts for* Mastophorus muris

16:00 online@ **Calvin Mehl**: *Two lineages of Lymphocytic Choriomeningitis Mammarenavirus in a German zoo*

ROOM B: METHODS & APPLIED SCIENCE (II)

Chairperson: **António Ferreira**

15:00 **Carlos Cuéllar**: *A preliminary view of the relationship between common vole population abundance and the diet of barn owl in biological control research areas in Palencia y Valladolid provinces, Spain*

15:15 **Franziska Höhn**: *Voles in forest regeneration in Germany - impression from the KUSAMWET project*

15:30 **Nathaniel Mull**: *A framework for understanding and predicting Orthohantavirus functional traits using rodent host ecology*

15:45 **Francois Mougeot**: *Using short-eared owl tracking and sightings to study and predict rodent outbreak*

16:00 **Aaron Shiels**: *Effectiveness and future utility of goodnature A24 self-resetting rat traps for multiple rodent species*

16:30–17:30 **Poster session** & coffee break

17:30–18:30 Rodens et Spatium Steering Committee meeting

20:30 **BANQUET** (Club 1844, Valladolid)

Friday, May 26th 2023

09:00–10:00 **PLENARY LECTURE**

Ricardo Pita: ***Ecology and conservation of threatened Iberian voles in Mediterranean farmland***

10:00–10:30 Coffee

10:30–11:30 Symposia talks

ROOM A: ECOLOGY (IV)

Chairperson: **Francois Mougeot**

10:30 **Zbigniew Borowski**: *Recovery of small mammals after large-scale grassland wildfire*

10:45 **Rita Monarca**: *The stressed life of island invasive rodent species*

11:00 **Paola Correa Cuadros**: *Long-term rodent data in north-central Chile: could megadrought and European rabbit impact the rodent population*

11:15 online@ **Chie Murano**: *Unique population dynamics of Japanese field vole: winter breeding and summer population declineline*

ROOM B: TAXONOMY, GENETICS & CONSERVATION (II)

Chairperson: **Gerald Heckel**

10:30 **Maria Kachamakova**: *Could the genetic monitoring predict the conservation translocation's output: case study of the European ground squirrel*

10:45 **António Ferreira**: *Land-use effects on the gene flow of a threatened small mammal in fragmented Mediterranean farmland*

11:00 **Veronika Chalupova**: *Genetic structure of the central European* Apodemus agrarius *populations*

11:30–12:30 **CLOSING EVENT & FAREWELL DRINK**

PLENARY TALKS

17th RODENS ET SPATIUM
Valladolid, Spain 2023

Socially induced infertility in highly social mole-rats: a tale of two mechanisms of reproductive suppression

Bennett, Nigel

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African mole-rats display a wide array of social organization ranging from strictly solitary living species through to truly social or eusocial species. The naked and Damaraland mole-rats are colonial living subterranean mammals which exhibit an extreme reproductive skew. Only a single female, called the queen, produces offspring with the most dominant males of the group. Non-reproductive females of both species are physiologically suppressed by the presence of the queen. Physiologically suppressed animals have low concentrations of luteinising hormone (LH) released from the pituitary and also have a reduced responsiveness of the pituitary to stimulation with gonadotropin releasing hormone. Removal of the queen from the colony reverses these effects and leads to endocrine profiles comparable to those of the reproductively active female. In males, reproductive suppression is different between the two species. Non reproductive male Damaraland mole-rats have basal LH concentrations and elevated LH concentrations in response to a GnRH challenge similar to those of the reproductive male, but in non-reproductive male naked mole-rats the basal LH concentrations are low and there is a muted response to a GnRH challenge. In the naked mole-rat the queen shows aggressive actions towards the subordinates to maintain her reproductive supremacy, whereas no such action arises in the queen Damaraland mole-rat where the colony is quite harmonious. This renders these two species ideal models to unravel the physiological, behavioural and neuroendocrine mechanisms regulating the hypothalamic-pituitary-gonadal axis. The recently discovered neuropeptides kisspeptin and RFamide-related peptide-3 are likely candidates that play a critical role in the regulation of reproductive functions in these two fascinating mole-rat species.

Keywords: Bathyergidae; hormones; physiology; neuroendocrine; reproduction

Rodent pest management in multifactorial socio-ecosystems: a practical application to the Jura massif

Giraudoux, Patrick

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For nearly a hundred years, a mass of attempts has been made to understand the causes of multi-annual fluctuations of rodents. Approaches that seek to isolate one factor among possibly dozens have all led to a long list of conclusions, all correct, about "what does not explain…". Approaches assuming multifactor explanations face the major difficulty of considering the complexity of systems where the importance of each of the multiple factors can vary in space and time. They need to be evaluated by long-term and large-scale observations and experimental manipulations, options that hardly get long-term human involvement and financial support. Meanwhile, some rodent populations can still have a devastating impact on agriculture, food, health and other species and little has been provided from ecological sciences to improve control operations. This leaves the field open to intensive usage of rodenticides, often too late or for too long and with adverse effects, and farmers poorly armed to protect their crop.

The montane water vole, *Arvicola amphibius* and the common vole, *Microtus arvalis*, can reach densities of several thousand per hectare, in the grasslands of mid-altitude mountains of Europe. The multiannual fluctuations of those species, studied since the late 1970s in the Jura massif, are the results of a shift in farming practices in the 1960s, themselves determined by socio-economic constraints. The importance of specific drivers on each scale (from local to regional) has been evidenced by multidisciplinary and multisectoral partnerships. Regional partnerships with agricultural organizations in particular have made it possible to set up long-term monitoring operations (voles, predators, pathogens, etc.) and quasi-experiments to measure the effects of habitat modifications and interventions at low population density in parallel with more basic works carried out by researchers. This led to design a toolbox making farmers able to control small mammal populations at a lesser environmental cost and to better understand the drivers of small mammal populations dynamics in such socio-ecosystems. The context which allows such consortia and the way it worked will be discussed.

Keywords: vole control; agroecology; population dynamics; landscape; socio-ecosystem

The multimammate mouse *Mastomys natalensis*: from pest to model

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Mastomys natalensis is a species of rodents, found throughout sub-Saharan Africa. Its natural habitat is disturbed grassland, but it is also common in agricultural fields and human settlements. In Tanzania, it was estimated that it causes 5-15% harvest loss annually in maize fields, but during population outbreaks this may increase to over 80%. It is the natural reservoir of Lassa virus in West Africa and is also known to carry plague bacteria and other pathogens. It is no wonder that this species is considered one of the most important pest species in Africa, affecting livelihoods of millions of people. Studies to document its role as an agricultural pest or carrier of disease and to consequently support management strategies, have yielded a number of interesting insights in the species' biology. It has an impressive reproductive capacity, with up to 24 young in one litter and more than 5 litters per year. On the other hand, animals rarely become older than one year. Its population dynamics show strong seasonal fluctuations, linked to rainfall and vegetation growth. Unusual rainfall pattern may lead to population explosions with up to 1000 animals per hectare. The large changes in densities linked to weather events make it an interesting species to study the effects of climate change, and this can be compared between areas in Africa with very different climate conditions. Obviously, it also allows to experimentally study social relations under diverse density conditions and, for example, the effects of density on space use, contacts and pathogen transmission. Several geographically separate mitochondrial lineages can be recognized within *M.natalensis,* many of these associated with a separate arenavirus. This makes it a very interesting model to study host-pathogen evolution and ecology. Over the past decades years we have collected numerous data on this species in Morogoro, Tanzania, including a 30 years time series (still ongoing) of monthly capture-recapture data which we make available to anybody who is interested.

Keywords: population dynamics; social structure; host parasite evolution; transmission ecology

Ecology and conservation of threatened Iberian voles in Mediterranean farmland

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Despite their crucial role in ecosystem functioning and dynamics, voles (together with other small mammal species) are still largely neglected in wildlife ecology and conservation research when compared to other mammal groups. Attention to vole ecology usually arises when populations are overabundant, causing serious farming and public health problems. However, voles also provide crucial opportunities to applied conservation science, due to several key traits that make them highly responsive to environmental change at relatively fine temporal and spatial scales. Moreover, because voles often occur in large and complex communities, they also provide opportunities to test ecological theory for instance related to species interactions across environmental gradients. In the European context, the Iberian Peninsula comprises a relatively high diversity of vole species (11 sp), and thus a variety of ecological questions related to the conservation and coexistence of those species that occur at low numbers. Among these, the Iberian endemic Cabrera vole (Microtus cabrerae) and the southern water vole (Arvicola sapidus) have been consistently classified as being in unfavourable conservation status in biodiversity assessments, both at national and global scales. Here, I will present and summarise the research carried out over the past decade on the ecology and conservation of these species in Mediterranean farmland. In particular, I will share some of the key insights regarding species distribution, abundance, population dynamics, abiotic tolerances and interspecific interactions across multiple spatial and temporal scales, based on a combination of multiple methodological approaches and survey techniques. In view of the increasing human disturbance in Mediterranean farmland, I will argue the need for future research contributing for building expertise and overcome knowledge gaps on the ecology of threatened Iberian voles (including those less studied such as M. rozianus and M. lavernedii), so as to better identify species monitoring and conservation approaches across the Iberian Peninsula.

Keywords: biodiversity assessment; environmental change; Iberian Peninsula; population ecology; species interactions

Rodent-borne disease: risk, epidemiology, and control

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Rodents carry a wide range of diseases that can be transmitted to people. Ecological, environmental and socioeconomic factors can all influence the risk from rodent-borne zoonoses (RBZ). Climate, habitat and landscape can influence transmission dynamics within rodent populations through impacts on the abundance of rodents, vectors and/or free-living infectious particles, as well as through impacts on rodent movement. Socio-economic factors can influence individual and community exposure risks. To develop management strategies to reduce the risk from RBZ we need to understand spatio-temporal disease dynamics within rodent populations, including the relationship between rodent abundance and infection prevalence, as well as how rodent management may impact the abundance of infected individuals. Using studies conducted on pathogens with different transmission routes (*Leptospira* spp., *Rickettsia* spp., *Yersinia pestis*, hantavirus) in various landscape contexts within Madagascar, we explore drivers of infection probability in rodent populations. Key drivers of infection probabilities in rodent populations differ between pathogens, with different associations with habitat type and contrasting relationships between infection prevalence and measures of host abundance and host diversity. We also report the preliminary results from a project trialling intensive rodent control inside houses, reflecting on the impact of control on rodent and vector abundance and potential consequences for disease risk.

Keywords: disease; parasites; pathogens; management

ORAL PRESENTATIONS

17th RODENS ET SPATIUM
Valladolid, Spain 2023

Entering the rat world: secondary school students collecting reliable data on urban near-environment species

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Rats are considered as one of the most disliked and disgust-evoking animals in urban landscape. Thus, they are a great focal species in a citizen science project looking at the presence of; attitudes towards; and potential of learning with unloved animals. We studied secondary school students' participation in Helsinki Urban Rat Project and collected data on rat occurrence in their own near-environment by using track plates. In total, over 3 000 students have participated; 778 students have answered questionnaire; 29 students were interviewed and 9 student groups were video and audio recorded during their participation. Based on the interviews; we found that students valued experientiality; involvement; meaningfulness; and freedom to choose in the project; which suggests that data collection in itself can be participatory. This contrasts to a common criticism towards data collection-centered citizen science projects where this kind of project is criticized as shallow. Students described a wide range of factual; conceptual; procedural; and metacognitive knowledge that they acquired during their participation. In general; older students had more negative attitudes towards rats. Interestingly, those students who had higher disgust sensitivity also had more positive attitude toward rats. We compared students' assessment of rat track abundance in the plates to expert scientists' assessment and found that students provide largely reliable data, independent of their attitudes. More fundamentally; the students attuned to the rat atmospheres during participation: paying attention to rats' habitats and behaviour disrupted nature/culture binary and called in to question the functionality and materiality of the research material; i.e; track plate. Our results suggest that even quite straightforward participation in authentic research can provide meaningful experiences for the participants. Furthermore, citizen science can foster attentiveness to multispecies worlds entangled within our own living environment.

Keywords: citizen science; science education; population dynamics; attitudes; disgust

Symposium: METHODS & APPLIED SCIENCE

Influence of traffic noise on the behaviour and physiology of two small mammals

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Urbanization has been growing at alarming rates, thus increasing the pressure on wildlife. Many animal species are now forced to live and adapt to the challenges imposed by urban environments. Urban environments are the source of different types of pollution and disturbances (e.g., human settlements, roads and train tracks) that may impact species presence and survival. Detailed and specific information about how animals adapt in urban habitats is key to wildlife conservation. The main objective of this study was to assess the impact of traffic noise on the behaviour and physiology of small mammals. More specifically, we compared how locations with different noise levels affected the proactive behaviour and the stress levels of two species: the rodent Algerian mouse (*Mus spretus*) and the insectivorous greater white-toothed shrew (*Crocidura russula*). We hypothesized that noisier places would induce higher levels of proactivity and of stress levels in both species. To test our predictions, we captured individuals from both species in sites with different noise levels and assessed their behaviour and stress levels in the field. We performed a behavioural test (bag or bucket test) to measure the proactivity of the individuals and analysed faecal corticosterone from samples collected upon capture to assess stress. Our results suggest that road noise does not affect the general behaviour of the studied species, but it seems to affect the behavioural variability of the individuals. Animals in sites with higher noise levels react more differently among each other than those in sites with less noise. Noise levels did not explain the differences between corticosterone levels in the sampling sites.

Keywords: urbanization; noise level; proactive behaviour; stress; faecal corticosterone

Symposium: BIOLOGY & EVOLUTION

Prospecting the effects of the landscape structure on the spatio-temporal evolution of the abundance of the common vole in Castilla y León, Spain

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In agricultural production systems, common vole (*Microtus arvalis* Pallas) cyclical outbreaks are associated with risk situations for crops. However, the final affectation is dependent on varying parameters such as the duration of the phenomenon until population collapse, reached abundances, dispersion and colonization from the reservoir areas to cultivated plots, crop type and phenological stage, etc. In turn, each of these parameters is modulated by other intrinsic and extrinsic factors of the common vole population itself. There is no scientific consensus on the ultimate explanation underlying this complex system, and the discussion on what factors affect it and what relationships can be established with the evolution of population abundance and damage to crops is still an open issue. In this study we prospect for the possible influence of factors linked to the landscape structure, identified through land use/land cover (LU/LC) maps retrieved by satellite images. The covariates referring to the distribution of reservoirs areas, wooded areas of feasible ecological compensation, dispersal corridors and surfaces linked to different groups of crops and use (i.e., rainfed/irrigated) were obtained and related to an over a decade database of the common vole abundance monitoring in Castilla-y-León (a region covering more than 3 million hectares of arable land). Results show that the spatial distribution of these surfaces may have an impact on the spatio-temporal differential expression of common vole abundance, both in reservoirs and in cultivated plots. In the light of these results, future research might be conducted on their consideration for predictive modelling or on zonal characterization of potential risk for crops, both aspects of undoubted interest in their application for the integrated management of this agricultural problem in Castilla-y-León.

Keywords: *Microtus arvalis*; land use/land cover maps; satellite images; integrated management

Symposium: ECOLOGY

Biological control of common vole (*Microtus arvalis* pallas) through the provision of artificial nesting boxes for birds of prey in intensified cropping areas of Castilla y Leon, Spain

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The Central Plateau of Castilla y León has large extensions of cereal steppe (>3 million hectares of arable land) in which cyclical demographic outbreaks of common vole (*Microtus arvalis* Pallas) related with significant crop damage have been detected during last decades. As part of the integrated management strategy for this agricultural problem in Castilla-y-León, a catalogue of good management practices has been defined, to be considered by both farmers and other agents with interests and competencies in the agricultural territory. Some of these practices are based on the ecological imbalance existing in the predator-prey relationship in these strongly intensified agrarian landscape areas. Within this, promoting the presence of highly specialized in rodent hunting native birds of prey, by installing artificial nesting boxes, is one of the tools to be consider in risk areas. In this contribution, we present an overview of the results in the main experimental zones distributed in Castilla-y-León for common vole biological control research. The types of boxes used are designed to provide substrate for shelter, nesting and reproduction for barn owl (*Tyto alba*), common kestrel (*Falco tinnunculus*) and, more recently, little owl (*Athene noctua*). Since 2010, hundreds of nest boxes have been yearly monitored during the raptors breeding season, recording occupancy and reproduction data. In parallel, the abundance of common vole populations in the different study areas has been monitored. The observed fluctuations in the number of raptor breeding pairs and their reproductive success in the different zones are shown and discussed, relating them to the potential availability of food, more specifically to the observed demographic fluctuations of the common vole. Results show the interest of the installation of nest boxes as an environmentally friendly pest management tool, with applications both in the regeneration of the predator-prey balance and in monitoring demographic fluctuations of common vole programs.

Keywords: integrated pest management; *Tyto alba*; *Falco tinnunculus*; *Athene noctua*; predator-prey balance

Symposium: CONFLICTS & MANAGEMENT

Habitat selection patterns reveal competition between two forest rodents and suggest recent elevational expansion of *Apodemus flavicollis*

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Numerous mammal species exhibit dynamic habitat use and selection, choosing the more preferred habitats at low densities when these are more readily available. Habitat selection may also vary along elevation and in relation to other populations' densities, with habitat segregation usually considered as a result of past competition. However, little is known about these effects combined. Therefore, we aimed to evaluate the differential habitat selection by dominant rodents in relation to intra- and interspecific density along an elevational gradient. We used trapping data collected over seven years (2002-2008) in forests of the Romanian Carpathian Mountains. *Apodemus flavicollis* (yellow-necked mouse) and *Clethrionomys glareolus* (bank vole) dominated the small mammal communities, having significantly lower densities in odd years. We hypothesized that 1. habitat selection varies with elevation and 2. population density, 3. habitat segregation facilitates coexistence of the two dominant rodents, 4. the "ghost of competition past" is weaker at high elevations, 5. abundance and intensity of habitat selection by *C. glareolus* are affected by the dominance of *A. flavicollis*, known to be more competitive. As predicted, habitat selection by *C. glareolus* was less intense at high elevations and in odd years, but for *A. flavicollis* results were not significant. The two rodents showed significant opposite responses to most habitat characteristics, invoking past competition. As expected, the dissimilarity between their responses was smaller at high elevations, as a possible result of the recent elevational expansion of *A. flavicollis* favoured by climate warming. Contrary to expectations, the intensity of habitat selection by this species increased with the dominance of *C. glareolus*, showing lower abilities to cope with habitat variability where its competitor was dominant. Our study provides insight into the interactions between *C. glareolus* and *A. flavicollis* in forests along the elevational gradient, suggesting asymmetrical competition and recent elevational expansion of the latter.

Keywords: elevational gradient; intra- and interspecific density; the ghost of competition past; yellow-necked mouse; bank vole

Symposium: ECOLOGY

Analysis of single nucleotide polymorphisms of the VKORC1 gene in the brown rat (*Rattus norvegicus*) population of the urban sewage system of Leganés

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Urban and agrarian ecosystems are habitats where brown rats (*Rattus norvegicus*) are commonly found and catalogued as pest. Authorities must control the populations in order to avoid health and economic issues. Nowadays, the main method of control in the urban ecosystem is the application of anticoagulant rodenticides (ARs) that inhibit the enzyme vitamin K 2,3-epoxide reductase (VKORC1), responsible for reducing vitamin K. The inhibition of VKORC1 prevents the activation of the coagulation factors resulting in animal death by internal bleeding. Resistance to AR is associated to mutations in the vkorc1 gene and have been found worldwide. This work aims to study the presence of single nucleotide polymorphisms (SNPs) in rodents captured in the sewer system of the city of Leganés. According to the design of a systematic sampling, the municipality was divided into grids of 500 x 500 m to ensure the collection of a sufficient number of samples that encompass the largest number of rat colonies. The sampling design in the sewer system of the two hydrographic basins (Butarque and Culebro streams) included the selection of sites of at least one segment of the practicable for at least 100 m long and high sewage collection-nodes. The pest control service of Leganés sent us 80 samples of rat tails distributed throughout the sewage network. We identified the rodent species analysing the cytochrome b gene. Mutation frequency was done in exon2 and exon 3 of the vkorc1 gene as a marker of possible ARs resistance. We identified three genetic variants (E155K and two haplotypes) with different spatial distribution. The E155K mutation is the most frequent in rat populations of two neighbourhoods with higher use of ARs. Monitoring of anticoagulant resistance evolution over time and space by the use of genetics of vkorc1 gene in rodent populations would improve management strategies. Acknowledgement - This research was funded by a charge of the Ministry for Ecological Transition to INIA (EG17-017) and the project PID2019-108053RJ-I00/AEI/10.13039/501100011033 funded by AEI.

Keywords: rodents; *Rattus norvegicus*; SNP; resistance; anticoagulant rodenticides; VKORC1

Symposium: CONFLICTS & MANAGEMENT

B chromosomes in urban populations of yellow-necked wood mice, *Apodemus flavicolis* (Mammalia, Rodentia)

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B chromosomes (Bs), or supernumerary chromosomes, are highly polymorphic special chromosome group. Among rodents, 37 species harbour individuals with Bs in their populations. Genus *Apodemus* is specific, with even six species having Bs. Furthermore, long-term studies in natural populations of the yellow-necked wood mouse *Apodemus flavicollis* showed that one-third of individuals carry Bs on average. In more than 40 natural populations we analysed in Serbia, the frequency of animals with Bs ranged from 0.11 to 0.63 and correlated negatively with average temperature and positively with attitude. In general, non-Mendelian transmission and frequent heterochromatic composition are characteristics that have classified Bs as selfish genetic elements in the past. However, there are increasing confirmations of active genes in them, which opens the discussion on their adaptive significance. We aim to investigate how urbanisation influences the frequency of Bs in this species. Urbanisation is rapidly changing natural habitats and affecting animal community composition, genetic diversity, and the interrelationship between populations of native species. Habitat fragmentation is the leading course of genetic diversity loss. We analysed the frequency of animals with Bs in four managed city forests on the territory of Belgrade, the capital of Serbia, characterised by different sizes and degrees of isolation. Our study revealed that the frequency of animals with Bs varies significantly among studied sites, from 0.04 to 0.50. We assume that, besides other factors, genetic drift plays a significant role in obtained differences.

Keywords: B chromosomes; *Apodemus flavicollis*; urbanisation; habitat fragmentations

Symposium: TAXONOMY, GENETICS &CONSERVATION

An insight into the ecology of an invasive rodent on small Mediterranean islands: a first step for management

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Invasive rodent species are a great threat to island ecosystems, thus often requiring their control or eradication. Such practices must be optimized based on the demography and spatial behaviour of the species. Currently, relatively little information on these aspects is available on the house mouse *Mus domesticus* on small islands, although this species is known to severely impact these fragile ecosystems. Using spatially-explicit capture-recapture (SECR) analysis, we estimated population density, capture probability and home range size of house mouse on three small islands in the Tavolara Punta Coda Cavallo marine protected area (Sardinia, Italy). Islands are characterized by the same vegetation type and free of mouse competitors and terrestrial predators. Capture sessions were carried out in April and September 2022, for an average of 6 consecutive trap-days. Out of 705 total captures, we trapped 258 individuals on Isola Piana, 39 on Spalmatore di Terra and 100 on Isolotto Rosso. Mouse densities greatly differed between the three sampling sites. With mean values around 100 and 125 individuals per hectare respectively, densities on Isola Piana and Isolotto Rosso were more than 10 times higher than on Spalmatore di Terra. Capture probability was lower and animal movements shorter on Isolotto Rosso compared to Spalmatore di Terra and Isola Piana. In particular, estimated sigma values ranged from 9 m (Isolotto Rosso) to 23 m (Spalmatore di Terra), reflecting different home range sizes among islands. Our research provides new insight into insular house mouse populations, evidencing the need to calibrate management protocols at local scale, even on small islands in close proximity.

Keywords: *Mus musculus*; density; home range; spatially-explicit analysis; capture-mark-recapture

Symposium: CONFLICTS & MANAGEMENT

Recovery of small mammals after large-scale grassland wildfire - population dynamics, survival and behaviour

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Wildfires, significant factors in spatio-temporal changes in terrestrial ecosystems, have become more frequent due to climate change. The mechanisms by which post-fire recovery proceeds are influenced by the abundance and distribution of survivors. Therefore, characterising early post-fire ecological and evolutionary processes seems critical to understanding ecosystems' demographic and community responses to fire. The large-scale grassland fire of April 2020 burned an area of about 5500 ha in Biebrza National Park, Poland. We quantified the effects of this wildfire on species diversity, sex ratio, and body mass of the small mammal community in the sedge meadow. We also measured energetics and behaviour in a dominant small mammal species - the root vole (Microtus oeconomus). We hypothesised that voles colonising the post-fire area should differ significantly in these individual traits from those living in unburned grassland. Results indicate that small mammals' recolonisation of burned areas began two months after the fire, and their communities were more diverse than those of the unburnt ones. The number of voles increased between spring and autumn, but population density was always the highest in the unburnt meadow. Body mass and energetics of root voles that colonised burnt areas did not differ from individuals captured at unburnt sites. However, voles inhabiting post-fire meadows were less exploratory than individuals from unburned sites. Additionally, it was observed that vole survival was lower in burned habitats. Summarising, the presented study shows that the natural regeneration process of small mammals after large-scale wildfires in grassland habitats was fast; however, the small mammal community structure in the first year of recolonisation deviated significantly from unburned areas. Furthermore, likely due to the change in habitat structure and increased predation, vole survival on burned sites was lower, which suggests that observed voles' behaviour differences result from higher selective pressure at post-fire habitats.

Keywords: disturbance; fire; recolonisation; animal personality; root vole

Symposium: ECOLOGY

Impacts of forest anthropization on the relationships between small mammal communities and their gut microbiota

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Anthropization affects wild communities by favoring species that can adapt to rapid changes associated with human pressures. The gut microbiota could participate in such adaptation, by rapidly modulating host phenotype. Conversely, the microbial composition of some species could be disrupted under human pressures, resulting in dysbiosis and negative impacts on host fitness. The links between anthropization, host communities and gut microbiota have only been scarcely explored. Here we address this question by studying small terrestrial mammals sampled along a gradient of forest anthropization (from rural forests to urban parks) in fall 2020. The gut was collected and bacteria were described using a 16S metabarcoding approach. We estimated the alpha and beta diversity of gut microbiota and we described potential functions of the metagenome. We tested whether anthropization lead to changes in small mammal communities and in the diversity and composition of the gut microbiota, and we investigated the mechanisms underlying these changes. We revealed that anthropization was associated with important changes in the composition (species) and structure (relative abundance) of small mammal communities. We found that the response of the microbiota to anthropization differed between host species. For generalist species, anthropization had an impact on the diversity of the microbiota but only weakly influenced its composition. The microbiota was therefore resistant / resilient to anthropization, what may be explained by functional redundancy. For the specialist urban species, we found a lower diversity and a different composition of the gut microbiota, compared to the generalist species. Their gut microbiota assembly was governed by stochastic effects, what could indicate dysbiosis. However, we also found new functions in these urban species, that could be associated with adaptation to anthropogenic environments. In conclusion, this study shows that anthropization can have complex and contrasting effects on the links between small mammal communities and their microbiota.

Keywords: community; gut microbiota; metabarcoding; small mammals; urban ecology

Symposium: ECOLOGY

Background food influences efficacy of the rodenticide, zinc phosphide, in wild house mice – An enclosure study

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Introduced wild house mice (*Mus musculus* L.) cause infrequent but significant damage to grain crops in Australia. Historically, mouse plagues occur every 3-5 years and cause around $100 million of damage each event. This leaves growers either re-sowing crops and managing some of the mouse damage by applying rodenticide baits or suffering significant yield losses. In Australia, zinc phosphide (ZnP)-coated wheat bait is the only registered in-crop rodenticide for the management of mouse damage. However, the efficacy of ZnP baits in a field setting can be highly variable and could be related to several factors including the amount of toxin on baits, the acceptability of the bait substrate, mouse behaviour (bait shyness), and competition with background food. The competition of ZnP baits with background food has received scarce research effort and could be a critical component in understanding the efficacy of field application of rodenticides. It is often assumed that abundant alternative food will reduce rodenticide efficacy, but it is rarely measured. The aim of this research was to understand the role of background food quantity on the efficacy of ZnP baits. Background food quantity was manipulated using a gradient design in mouse-specific enclosures. When small quantities of background food were provided, mouse survival was low, but when background food was abundant, survival was high. Our results confirm that background food influences the efficacy of ZnP in an enclosure setting. These findings have significant implications for the development of robust recommendations for farmers. The challenge will be to reduce mouse food supply in cropping systems so that control actions conducted by farmers can be effective.

Keywords: control; gradient design; management; *Mus musculus*; survival

Symposium: CONFLICTS & MANAGEMENT

Fifty shades of grey: phylogenomics helps to delimit species in African thicket rats (*Grammomys*)

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Thicket rats of the genus *Grammomys* are partly arboreal rodents distributed in large part of sub-Saharan Africa (except central Congolian forests and deserts). Our previous work based on two mitochondrial and one nuclear DNA fragments showed that highest evolutionary diversity is found in forests and woodlands of Eastern Africa and that the evolutionary history of the genus roughly mirrors the evolution of African forests from the end of Miocene. At the same time, we found that the taxonomy of the genus is not sufficiently solved and currently delimited species (names) do not correspond to major genetic clades. Here we employed thousands of single nucleotide polymorphisms (SNPs) developed by ddRAD approach to perform phylogenomic analysis and to delimit genomic pools (i.e. candidate biological species). The revealed molecular operational taxonomic units (MOTUs) were then compared with all other available data (distribution, ecological requirements, mitochondrial DNA variability, morphology, sequences from the type material, etc.) and used for an integrative taxonomic solution of the genus. In the presentation we will show the African thicket rats as a classical example of challenging problems in current integrative taxonomy. Nowadays it is relatively easy to obtain genomic data and delimit candidate species, but it is much more complicated to give them species names using the valid rules of zoological nomenclature.

Keywords: integrative taxonomy; Africa; Murinae; phylogenomics; diversity

Symposium: TAXONOMY, GENETICS & CONSERVATION

The integrated management strategy to reduce risks linked to the presence of common vole in Castilla y León, Spain

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The common vole (*Microtus arvalis* Pallas) undergoes cyclical population outbreaks during which it colonizes any space providing shelter and food, including crop plots. In addition to the agronomic losses caused, it can carry zoonotic diseases, constituting an environmental amplifier of health risks. Consequently, its presence in agricultural ecosystems causes important conflicts with and between the different stakeholders with interests in the agricultural territory. Due to the successive population outbreaks episodes detected in Castilla-y-León, the Ministry of Agriculture, Livestock and Rural Development of the Government of Castilla-y-León, through the Order AYG/96/2019, has developed an Integrated Management Strategy against the risks derived from the endemic presence of the common vole in the region. This strategy aims to integrate the characteristics of the agroecosystem, productive needs and respect for the environment, defining an integrated management model with an eminently preventive, permanent and timeless nature, based on continuous management of the territory and involving the entire network of agents with interests or competencies in the target areas. In general, the actions described in the strategy can be grouped as follows: Development of a program to monitor the evolution of the populations and the associated risks; implementation of an information system between the agents involved; definition of a training plan on the vole problem, its effects on agricultural ecosystems and the management to be considered; promotion of research on management tools applicable to the integrated management; establishment of a good management practices catalogue to minimize risks to crops; definition of specific actions that could be exceptionally considered when detecting a risk for crops situation. In this contribution we will expose the history of coexistence in Castilla y León with this agricultural problem up to the definition of the integral management strategy that we present here, as well as some of the results and discussion about its implementation.

Keywords: *Microtus arvalis*, agricultural pest, stakeholders relationships.

Presented in the "ITACyL" ROUND TABLE

Can population structure derived variables be useful for predictive modelling of demographic fluctuations of common voles?

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The common vole (*Microtus arvalis* Pallas) experiences natural phenomena of demographic increases, during which it can multiply its population size by several hundred in a very short period of time. When its presence is linked to agricultural environments, the occurrence of these phenomena can give rise to risk scenarios for crops and conflicts with farming productive interests. The integrated management of the problems derived from these situations requires the conception of actions that allow minimizing the damage to the crops that could potentially be caused. But once a population outbreak has been triggered, the control of this species becomes very complicated, making possible control measures ineffective or difficult to apply. In this way, in order to achieve an adequate and effective strategy for the integrated management of the common vole, the development of predictive models that allow early detection of the possible occurrence of these population phenomena is recommended. In this contribution, we explore a ten-year database of seasonal assessments in Castilla y León, including characterization of individuals caught by trapping and estimates of population abundance. Temporal covariates related to population structure parameters have been derived, based on the frequency distribution of weights, sex, reproductive status, and their combinations. Preliminary insights on the coevolution of these covariates with population abundance and its subsequent variations are shown, discussing their potential interest in predictive modelling of demographic fluctuations of the common vole.

Keywords: *Microtus arvalis*; agricultural pest; integrated management; monitoring; covariate coevolution

Symposium: CONFLICTS & MANAGEMENT

Response to urban exposure to heavy metals in two synanthropic rat species: a multi-marker evaluation

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Synanthropic black rats (*Rattus rattus*) and brown rats (*Rattus norvegicus*) are putative bioindicators for the evaluation of contaminants in an urban environment due to their close relationship with humans. Even at low concentrations, several mutagens can have deleterious effects, and their detection in the environment is a challenge. In this study, we evaluated the exposure to heavy metals of two populations of black and brown rats inhabiting two port cities in Portugal with distinct levels of urbanization, Lisbon (higher) and Ponta Delgada (lower). A total of 144 animals were live-trapped within a 10 km radius from the city ports. Heavy metal concentrations were evaluated in the liver (Cr, Ni, Cu, Zn, As, Pb and Cd) as well as several response biomarkers. The frequency of micronucleated cells (MN) and of sperm abnormalities were investigated. Results showed a higher accumulation of As in Lisbon for both species, and Cu, but only in *R. rattus*. Regarding micronuclei and sperm abnormalities, these were significantly increased in Lisbon, for both species. A moderate positive correlation was detected for *R. rattus* between micronuclei and As accumulated and micronuclei and Cr. Biomarkers responses showed increased lipid peroxidation (LPO) in Lisbon for *R. norvegicus* and in Ponta Delgada for *R. rattus*. Overall, we showed that species respond differently to heavy metal contamination, suggesting the activation of different detoxification mechanisms, most likely due to the exploration of distinct resources.

Keywords: *Rattus norvegicus*; *Rattus rattus*; urban ecosystems; contamination; heavy metals

Symposium: BIOLOGY & EVOLUTION

Physiological and behavioural habituation of wild wood mice, *Apodemus sylvaticus*, to laboratory conditions

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Habituation is often defined as the change of locomotor and exploratory behaviour along time. In a captive environment, animals are exposed to novel stimuli, which can result in changes regarding stress levels and behaviour. As such, it is important to consider changes associated to the habituation of wild animals to captivity. The aim of our study was to assess the physiological and behavioural habituation of wild-caught wood mice (*Apodemus sylvaticus*) to laboratory conditions. Wood mice are a good model to test habituation to captivity since the species is one of the most commonly used wild small mammals in experimental research, being widely distributed and abundant across Europe and not-threatened. The main hypothesis formulated for this study is that wild wood mice adjust both physiologically and behaviourally to laboratory conditions. The mice were maintained in captivity for four weeks and their behaviour tested once per week. For each individual, five faecal samples for corticosterone analysis were obtained, one from the field and one from each of the weeks of captivity. Our results showed a decrease of corticosterone levels over time in captivity, particularly between the field and the last week of a captivity. Similarly, the animals' activity in a behavioural test decreased over time, being most pronounced between the first and the last week. The body mass increased slightly between the field and last week of captivity. Other parameters measured, such as the presence of stereotypic behaviour and the nestbuilding behaviour, did not show any changes over time. The information obtained in present study can help researchers which intend to use wild animals in experimental research to understand the influence of the laboratory environment on the natural behaviour and physiology and plan their experimental timeline accordingly.

Keywords: stress; faecal corticosterone; personality; repeatability; stereotypic behavior

Symposium: BIOLOGY & EVOLUTION

Genetic structure of the central European *Apodemus agrarius* populations

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Striped field mouse (*Apodemus agrarius*) is a small murid rodent widespread in most of the Palearctic region. The species originated in Eastern Asia from where it colonized most of Eurasia. Expansion in Central Europe occurred probably during late Quaternary reflecting the climatic and habitat changes. As a result of relatively recent spread event, genetic variation over Europe is not pronounced and thus cannot reveal its population and expansion history. Here, we use substantial number of single nucleotide polymorphism (SNP) data over the whole genome using ddRAD sequencing technique to overcome problem of relatively shallow genetic differentiation. Totally, we obtained genetic information from 96 individuals from 30 localities over seven Central-European countries. Our results indicate that for the first time any genetic data can be used to recover population structure in recently expanded *A. agrarius* in Europe, showing a clear structure that reflects the potential spread pathways from the east and potential geomorphological features encountered. Three main population units includes the Pannonian Plain, northern part of the Central Europe (from the northern Czech and Slovak Republics northwards) and at least one intermediate population between them (Moravia region of the Czech Republic); with other more detailed substructure. These main populations might reflect supposed northern and southern colonization routes around the Carpathians. Documentation of the recent contact between the northern and the Pannonian *A. agrarius* populations brings other questions of its admixture and the impact on other spread potential. Additional more comprehensive and focused sampling from new localities will provide more complex insight into evolutionary history of these *A. agrarius* populations and contribute to our general understanding of processes playing role at an animal distribution edge and its fluctuation. The research was funded by Grant Agency of Masaryk University (project MUNI/C/0090/2022) and Scientific Grant Agency of the Ministry of Education of the Slovak Republic VEGA 1/0277/19.

Keywords: striped field mouse, ddRAD sequencing, expansion, population history, SNP

Symposium: TAXONOMY, GENETICS & CONSERVATION

Evolution of zona pellucida genes in rodents

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Mammalian eggs are surrounded by an extracellular matrix called the zona pellucida (ZP). This envelope participates in processes such as acrosome reaction induction, sperm binding, protection of the oviductal embryo, and may be involved in speciation. In eutherian mammals, this coat is formed of three or four glycoproteins (ZP1–ZP4). While the house mouse (*Mus musculus)* has been used as a model to study the ZP for more than 35 years, surprisingly, it is one of the few eutherian species in which the ZP is formed of three glycoproteins (ZP1, ZP2 and ZP3), Zp4 being a pseudogene. Zp4 was lost in the *Mus* lineage after it diverged from *Rattus*, although it was not known when precisely this loss occurred. In this work, ZP proteins were studied in rodents by phylogenetic, molecular, and proteomic analyses. Additionally, assays of cross in vitro fertilization between three and four ZP rodents were performed to test the effect of the presence of ZP4 and its possible involvement in reproductive isolation. Our results showed that Zp4 pseudogenization is restricted to the murine subgenus *Mus*, which diverged around 6 Mya from the other *Mus* subgenera. Heterologous in vitro fertilization assays demonstrate that a ZP formed of four glycoproteins is not a barrier for the spermatozoa of species with a ZP formed of three glycoproteins. This study identifies the existence of several rodent species with four ZPs that can be considered suitable for use as an experimental animal model to understand the structural and functional roles of the four ZP proteins in other species, including human.

Keywords: molecular evolution; phylogeny; pseudogenization; proteomic; oocyte

Symposium: BIOLOGY & EVOLUTION

Long-term rodent data in north-central Chile: could megadrought and European rabbit impact the rodent population

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Phyllotis darwini and *Abrothrix olivaceus* are native Chilean rodents in semiarid ecosystems, mainly in north-central Chile. They are granivorous-herbivorous, and their breeding season is in the rainy period when vegetal biomass increases. Darwin's leaf-eared and olive grass mouse are one of the main prey of Chilean predators, essential in the food webs and predator's conservation. Thus, the population dynamics of these rodents are necessary to understand drivers such as rainfall anomalies and invasive species impact, which could have a role in the population size of these rodents. Using long-term data of rodents in Las Chinchillas National Reserve and dynamic population models were performed to understand the increases and collapse of rodents. We obtained that the likelihood of survival is higher in males than females when the population is analyzed annually, where survival decreases in The Niña years (drought) and after the megadrought began in north-central Chile 15 years ago. Also, we analyzed the population according to the breeding and non-breeding seasons, showing that the probability of survival is according to seasonality, being higher in the breeding season. Results evidenced two possible regime changes, first in 1995 when rodent size decreased slightly for the Niña year, but remained constant over time, perhaps due to the appearance of the European rabbit in the consumption of native predators, releasing the predation pressure over rodents. Second, the megadrought since 2003, where the population diminished gradually and constantly. These results are relevant to evidence of the decrease in the survival and population size of these native rodents suitable for conserving and understanding the invasive species' role in semiarid ecosystems.

Keywords: native Chilean rodent; conservation; population dynamics; drought; invasive species; lagomorphs

Symposium: ECOLOGY

Gradual and eruptive dynamics of rodent pests: outbreaks in house mice in Australia and common voles in Spain

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Pest mammals damage most crops, and the solution is to attack them using agrochemicals or other types of controls, but often without success. It is generally forgotten that crops are an ecosystem regulated by interactions and feedback between climate, crops, pests, and biological agents. Understanding the relationships and identifying the drivers causing the pest makes it possible to predict them. Population dynamics allows studying pest population changes to understand the increase, collapse, and relationships with the environment, food, and interactions. House mice in Australia and the common vole in Spain have been causing damage to crops, consuming plant cover. The causal mechanisms that trigger their explosions are still unknown. Seasonal and annual mathematical models were used to identify the factors that explain and predict their population dynamics to predict their outbreaks. These models used abundance data, climatic variables, competitors (small rodents) and predators (birds and mammals). The increase in pest populations is better explained by low evaporation, high humidity, and accumulated rainfall due to their effects on the soil to dig their burrows and on the increase in food, as well as the decrease in small rodents as competitors for food resources. Likewise, predators play an important role since the percentage of consumption has been increasing over time. Pest abundance explains the population collapse in the outbreak phase and the abundance of predators. These results are useful for predicting future outbreaks and reducing their economic impact on crops.

Keywords: pest mammals; population dynamic; mathematical models; weather; predators

Symposium: ECOLOGY

Local drivers of post-colonization demogenetics of the Cabrera vole in ephemeral patches

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Metapopulation models examining the effects of patch size, quality, and connectivity on local abundance and rates of extinction and (re)colonization have been well studied. However, the relative contributions of these attributes to key demographic and genetic parameters that determine local population viability are still largely unknown. This is particularly true for species occurring mostly as small populations in ephemeral patches, hence being highly vulnerable to stochastic demographic and genetic factors. Here we developed and implemented individual-based stochastic simulation modelling to assess the extent to which patch size, connectivity, and quality affect demographic and genetic (demogenetic) dynamics in small local populations inhabiting ephemeral patches, using the Cabrera vole as model. Based on known information regarding species life-history traits and genetic diversity in natural populations, we used a pattern-oriented modelling strategy to simulate the impact of patch size, quality, and connectivity on post-colonization population demogenetics (e.g., density, local recruitment, migration rates, genetic diversity, relatedness, inbreeding) within habitat patches with short lifespan (up to two years). Global sensitivity analyses were implemented to estimate the strength of linear associations between demogenetic responses and each patch attribute, as well as to distinguish and quantify the main and interaction effects among patch attributes over time. Results indicated that patch size was the most important patch attribute driving demogenetic processes shortly after colonization, but the interaction among patch size, quality, and connectivity had an overriding influence when patches persist for over one year post-colonization. Overall, our study highlights the need to consider both single and complex interaction effects among patch size, quality, and connectivity to better understand the demogenetic dynamics of small local populations in ephemeral patches, which is crucial to assess the viability of 'whole' metapopulations in disturbed environments.

Keywords: demography; genetics; individual-based-model; local populations; sensitive analysis

Symposium: ECOLOGY

Increased rat abundance and zoonotic disease hazard in urban green: smart urban greening required?

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Urban greening has become an increasingly popular strategy to improve urban life and human health. However, there are indications that the presence and extent of urban green may increase the abundance of wild rats and the risk for rat-borne zoonotic pathogens. Therefore, we performed a field study in which we investigated which environmental, socio-economic and climatic factors are associated with rat abundance, with a special focus on factors related to urban green. Furthermore, we tested all captured rats (n=412) for 18 different zoonotic pathogens (bacteria, viruses and parasites) to investigate the relation between the amount of urban green and pathogen prevalence and diversity. We observed significant positive relations between rat abundance and both urban green and different proxies for food sources (restaurants, waste items and petting zoos). Additionally, we observed that the presence of ground-covering plants had a significant negative relation and the presence of mixed shrub forest and perennial plants had a significant positive relation with the relative abundance of rats. Furthermore, the infection rate of rats with *Bartonella* spp. and *Borrelia* spp. was significantly positively associated with urban green, and we also observed a positive trend between pathogen diversity and urban green. Our findings corroborate that urban green is associated with both a higher abundance of wild rats and an increased disease hazard of rat-borne zoonotic pathogens. This stresses the importance for policy makers and city planners to take actions to limit these negative effects, which requires smart urban greening. This study provides new insights on how to perform smart urban greening in which urban green is designed to optimize its beneficial effects, while structurally reducing both the carrying capacity for rats and the potential risks for public health.

Keywords: *Rattus norvegicus*; zoonoses; disease transmission; public health; disease ecology

Symposium: RODENT-BORNE DISEASES

Understanding spatial-temporal patterns of *Rattus rattus* abundance in rural Madagascar to inform control strategies

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Whilst eradication of invasive rodents may be possible on some smaller islands, rodent management in larger and more complex areas such as Madagascar is likely to be an ongoing commitment. It is therefore essential that the rodent management is both effective (at reducing the impact) and sustainable. Abundance can fluctuate spatially and temporally, with the key demographic rates of reproduction, survival, immigration, and emigration influenced by ecological and environmental factors (e.g., temporal variation in local resource availability, proximity to different habitats). Understanding how seasonal patterns of abundance depend on local habitat and landscape contexts is therefore crucial for management. In this study, we investigated how rat abundance is influenced by season, local habitat, and landscape features. We used data from two studies in different areas of central Madagascar and implemented multinomial N-mixture models separately for females, males, and sub-adults. These models allow uncertainty in the detection process to be accommodated. Our analysis reveals that abundance tends to peak after the main harvest season followed by rapid decline. However, seasonality varies depending on landscape characteristics e.g., areas with high proportion of irrigated rice tend to observe greater peaks in abundance as well as greater declines then other habitats. We discuss the relevance of our results for management strategies aimed at reducing rodent abundance and the risk from rodent-borne disease in the rural highlands of Madagascar.

Keywords: ecologically-based; management; zoonosis; invasive; N-mixture

Symposium: CONFLICTS & MANAGEMENT

Physiological drivers of home-range size in a woodland rodent

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Here we seek to better understand the factors that determine home-range size, a key population variable for many terrestrial vertebrates. Males with higher androgen levels (i.e., testosterone) are expected to show bolder and higher activity rates that can therefore lead to larger home ranges. Likewise, males with higher basal metabolic rates are expected to present larger home-range sizes to satisfy their energy maintenance demands. We tested first whether androgenization and basal metabolic rate are independent predictors of home-range size, and second, whether basal metabolic rate mediates the effect of androgenization on home-range size. This study was carried out in a long-term monitored wild wood mouse population from Silwood Park (Imperial College London, UK) during the summer season (July). Basal metabolic rate (bmr) was measured by respirometry method (in a non-breeding, postabsorptive and resting within a thermoneutral zone) to obtain the volume of carbon dioxide exhaled (vCO_2) per unit time. Androgen levels were calculated as anogenital distance corrected for body size (anogenital distance index; adgi). Finally, minimum convex polygon method (MCP) were used to calculate home-range size (hr) from a dataset constructed with rodent relocation data using 10 mobile data logger units. We ran linear models to test our hypothesis considering other potentially confounding variables, such as chamber temperature and body mass. Our results show how that the effect of androgen levels on home-range size is direct and not mediated by bmr. In addition, we also observed a significant relationship between androgen levels and basal metabolic rate. Both relationships showed positive trends, as expected. In contrast, basal metabolic rate was not correlated with home-range size. These results seem to confirm that males with higher androgen levels have higher basal metabolic rates which would permit larger home ranges as the increased-intake model suggests, thus refuting the opposite model based on the compensation hypothesis.

Keywords: androgenization; basal metabolic rate; space use; increased-intake model; *Apodemus sylvaticus*

Symposium: BIOLOGY & EVOLUTION

Lemming cycles in the Canadian high arctic: new insights about the extended low abundance phase

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The low abundance phase in Arctic lemming cycles is inherently data deficient and thus remains difficult to study and fully grasp the mechanisms responsible for it through empirical studies. However, as time series of seasonal abundances of lemmings of the Canadian High Arctic are being extended over time, we now start to see patterns among the rare, but accumulated data in years of low lemming abundance. Our recent work on Bylot Island (73°N, 80°W), Nunavut, has revealed new insights about how interactions among predators, including specialist predators such as ermines and snowy owls, may cause variations in the periodicity of cycles. Furthermore, over the course of the past 15 years of live-trapping lemmings, we captured much fewer females than males during the low abundance years, which contrasts with high abundance years where sex-ratios are close to 1:1. This biased sex-ratio may be a consequence of previous-season factors, and this will be discussed. For this presentation, I will present these new data in more details and present our most recent hypotheses that will be tested on Bylot Island, including the role of intraguild predation as a disruptive factor in the response of a specialist predator, and the role of differential vulnerability of male and female lemmings to predation in explaining the low phase.

Keywords: seasonality; demography; population dynamics; trophic interactions; specialist predator hypothesis

Symposium: ECOLOGY

Diversity of trypanosomes in rodents and marsupials from New Guinea

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The tropical island of New Guinea is a biodiversity hotspot. The composition of the local biota is diverse due to its geographical history. The island not only has marsupials that migrated in several waves from Australia, but also rodents that colonized New Guinea from Indonesia via Wallacea. These are rodents from the tribes Rattini and Hydromyini. The different evolutionary history of the two tribes has likely affected the composition of blood parasites. Investigating the diversity and prevalence the blood parasites of New Guinea's marsupials and rodents is an essential step toward discovering pathogens that could be of concern for the conservation of these endemic species. We analyzed samples from 974 individuals from over 35 different marsupial and rodent genera using nested polymerase chain reaction with primers targeting the 18S subunit of the rDNA gene. Infection was detected in 207 individuals (overall prevalence of 21,3 %). In addition to *Trypanosoma* samples we detected presence of kinetoplastid flagellates from the suborder Bodonina (genera *Bodo*, *Neobodo*, *Parabodo* and *Dimastigella)*. Bodonina include free-living, commensal and ecto- and endoparasitic species. The rodent genus with the highest prevalence of *Trypanosoma* was *Rattus:* Out of 514 tested samples of this genus, *Trypanosoma* was detected in 165 individuals, i.e. a prevalence of 32,1 % in *Rattus*. *Trypanosoma* from the *theileri* clade was observed mainly in endemic species of marsupials (families Burramyidae, Dasyuridae, Paramelidae, Petauridae, Phalangeridae and Pseudocheiridae) and rodents of the tribe Rattini. This clade includes trypanosomes endemic to Australia and Indonesia. *Trypanosoma* of the cosmopolitan clade *lewisi* occurred in both Hydromyini and Rattini tribes, but not in marsupials. Further research would help to elucidate the potential health impacts of infection with *T. theileri* and *T. lewisi* in endemic rodents and marsupials of New Guinea.

Keywords: blood parasites; biodiversity; mammals; Melanesia

Symposium: RODENT-BORNE DISEASES

"What doesn't kill you makes you stronger": anticoagulant rodenticide resistance in insular and continental house mice

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Resistance to anticoagulant rodenticides (ARs) is a major problem in controlling mouse populations and their negative effects. Over the last decade, numerous studies, particularly in Europe, have detected the presence of several mutations in the gene vitamin K epoxide reductase complex subunit1 (*Vkorc1*) associated with some level of resistance to different ARs in synanthropic rodents. Here, we characterized the status of genetic resistance to ARs within *Mus muscuslus domesticus* populations from mainland Portugal and southern Spain, the Madeira and Azores archipelagos. A total of 241 house mouse samples were genotyped for the 3 exons of the *Vkorc1* gene (45 from mainland Portugal and Spain, 149 from the Azores archipelago and 49 from the Madeira archipelago). Overall, eight mutations were identified in the *Vkorc1* gene, seven of which non-synonymous. Among these variations, two of the most geographically widespread mutations in mice, L128S and Y139C, were detected, particularly in the insular settings. Additionally, four substitutions in exon 1 and one substitution in exon 2, constituting the *Vkorc1*^{spr} genotype, were identified at high frequency in the mainland populations, a sequence variant resultant of an adaptive hybridization phenomenon between *Mus spretus* and *Mus musculus*. Both mutations, L128S and Y139C, as well as the *Vkorc1*^{spr} genotype are all associated with high levels of resistance to first generation anticoagulant rodenticides and some resistance to more potent second-generation rodenticides like bromadiolone and difenacoum. These findings are in agreement with the informal feedback from farmers from Madeira and Azores regarding the difficulties in controlling house mouse populations. These results highlight the need for adaptation of standard rodent management practices in order to prevent the inefficient use of ARs in resistant populations.

Keywords: Vkorc1; *Mus musculus domesticus*; Vkorc1^{spr} genotype; Y139C; L128S

Symposium: CONFLICTS & MANAGEMENT

Insight into the population genetic and evolution of an endemic species: *Mus cypriacus*

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Mus cypriacus is one of three small palaeoendemic mammals which have survived the anthropization of Mediterranean islands. Endemic to Cyprus, this species was described just in 2006 and is one of the last mammal species to have been discovered in Europe. It diverged from *M. macedonicus* 0.53 million years ago and it is mostly found in areas with vast cultivation at moderate altitudes (300-900 metres). Even though it has been assessed as 'Least Concern-LC' in the IUCN Red List, there is scarce data on its genetics, ecology and life history traits. Our study investigates the population genetic structure and genetic diversity of this rodent. Our analysis did not pinpoint low levels of genetic diversity, suggesting that indeed this species is not particularly threatened, despite its apparent rarity. No geographic structure was observed across Cyprus, a fact in relation with *M. cypriacus*' habitat preference, inferred using sample locations.

Keywords*: Mus cypriacus;* Muridae; Rodentia*;* palaeoendemic mammals*;* Cyprus

Symposium: TAXONOMY, GENETICS & CONSERVATION

The mystery of Bartonella*'s pervasive nature in rodent communities*

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Some pathogens cause only short-term infections due to their host immune responses, yet often these host populations support pervasive pathogen populations. We investigated this limited-term pathogens' puzzle in a model system of Bartonella bacteria and their three coexisting rodent species, which inhabit Israel's north-western Negev Desert. From the rodent perspective, we tested the hypothesis that at least some of the rodents exhibit a waning immune response, which allows reinfection. We inoculated rodents from all three species with the same Bartonella strain, and we quantified the bacterial dynamics and Bartonella-specific IgG antibody kinetics through 139 days after the primary inoculation and then for 60 days following re-inoculation with the same strain. Contrary to the waning immune response hypothesis, we found a strong, long-lasting IgG antibody response, with a protective immunological memory in all three rodent species. That response prevented re-infection upon exposure to the same Bartonella strain. From the Bartonella perspective, we tested the hypothesis that rapid evolution allows Bartonella to evade the specific antibodies of the rodents. To test this hypothesis, we conducted an evolution experiment in which we serially passaged a Negev desert Bartonella strain colony (designated as the ancestor strain) through 20 individual rodents and stored the resulting mutant (designated as evolved strain). We inoculated individual rodents from the three species with either the ancestor or the evolved strain and then re-inoculated them with the alternative strain (e.g., individuals that were first inoculated with the ancestor were reinoculated with the evolved strain). Only one of the three rodent species developed a secondary infection upon reinoculation with an alternative strain, partly supporting our immune-escape hypothesis. These results suggest that to solve the limited-term pathogens' puzzle, it is important to consider both host and pathogen perspectives, multiple host species, and the coevolution between pathogen and host traits.

Keywords: disease ecology; antigen evolution; experiment; host-parasite interactions; immune response

Symposium: RODENT-BORNE DISEASES

The genomic legacy of 5000 years of complete isolation in Orkney voles

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Human activities have led to the fragmentation of populations of many species and to the introduction of organisms to new, geographically-isolated areas. Theoretical predictions for the future of isolated populations are typically grim but empirical studies of the effects of long-term isolation under natural conditions are limited. Here we analyzed the genomic consequences of more than 5000 years of isolation experienced by common voles (*Microtus arvalis*), introduced to the Orkney archipelago off Northern Scotland by Neolithic settlers from continental Europe. We sequenced dozens of full genomes of common voles and a sibling species sampled throughout the distribution range including individuals from all inhabited Orkney islands. Our analyses show that Orkney voles derive from individuals originating at the northern coast of France or Belgium and have remained isolated since without detectable gene flow. Orkney vole colonization started on the biggest island and populations on other islands split off gradually, without signs of secondary admixture. Orkney vole genomes retained only 8-29% of the heterozygosity of continental conspecifics despite having large modern population sizes. Homozygosity of deleterious variation accumulated to a dramatic degree particularly in populations on smaller Orkney islands. This natural system shows that extremely long isolation is associated with the strong loss of genetic diversity and accumulation of homozygous deleterious alleles expected from population genetics theory. Yet the demographic success of these voles suggests that the potential negative effects of such a genomic background can be overcome even in complete isolation, and the particular life history of rodents is likely to play a crucial role in this success story.

Keywords: common vole; *Microtus arvalis*; evolutionary genomics; isolated populations; deleterious variation

Symposium: TAXONOMY, GENETICS & CONSERVATION

Ecology of sympatric bank and red voles, *Myodes glareolus* and *M. Rutilus*, in Northern Finland

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In Europe, bank vole, Myodes glareolus, is widely spread while red vole, Myodes rutilus, is a northern species. In the northern part of the taiga both species occur in sympatry; this overlap zone is 100 – 150 km north - south wide. These species are closely related, they can even hybridize, but ecologically they are quite different. The habitat selection is more restricted in rutilus, their food selection in winter is different, and the litter size of M. rutilus is higher than that in M. glareolus. I have monitored the population dynamics of these species in a sympatric multispecies arvicoline community (8 species) at Pallasjärvi, northern Finnish taiga since 1970. Population dynamics during this period have been characterized both by strong population cycles, but also by a long more stable “noncyclic” period. The multiannual dynamics of these two species are synchronous, depending on cyclicity factors. However, clear interspecific competition occurs between glareolus and rutilus. Breeding females of Myodes species have clear exclusive territories, and this territoriality occurs also between breeding females of different species. Neither the breeding males seem to overlap very much, even if they do not have totally exclusive territories, rather variable home ranges. Based on field experiments, M. glareolus dominates over M. rutilus. Removal of M. rutilus does not affect the density of M. glareolus, while removal of M. glareolus results in higher densities of M. rutilus. However, the nonbreeding, docile subadults seem to overlap extensively. Maturation of Myodes species is strongly density-dependent. In the glareolus-rutilus system it takes place at the whole community level. Therefore, summer maturation of young rutilus is regulated by total density of glareolus+rutilus. Disappearance of cycles has been discussed in recent years. Community level analyses (8 arvicoline species at Pallasjärvi) help to distinguish between species and community level regulating factors.

Keywords: multispecies vole communities; northern taiga; cycles; competition

Symposium: ECOLOGY

A preliminary view of the relationship between common vole population abundance and the diet of barn owl in biological control research areas in Palencia y Valladolid provinces, Spain

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The common vole (*Microtus arvalis* Pallas) cyclically causes conflicts with agricultural production systems in Castilla-y-León region (Spain). Within the research on possible tools to be considered for its integrated management, since 2009 a program related to its biological control is being carried out, mainly through the provision of artificial nesting substrates for its native predators. The main objective is to determine if these management options effectively contribute to reducing crop damaging through their potential impact on the common vole population dynamics. In this context, it is necessary to identify the relationships between the feeding habits of these predators with respect to the demographic fluctuations of potential prey in the target study areas. In this study we consider six biological control experimental areas with artificial nesting boxes in Palencia and Valladolid provinces (Castillla-y-León), monitored during 2021 and 2022. In each area, pellets linked to nest boxes with reproductive breeding pairs of Barn Owl (*Tyto alba*) was sampled, dissected and analysed during the study period. In parallel, common vole abundance in crop plots was monitored through indirect activity indices. In our preliminary results we show the relationship between the variations in the common vole abundance with the percentage of inclusion of this species in the barn owl diet, through the frequency of appearance of arvicoline skulls and mandibles in the pellets.

Keywords: *Microtus arvalis; Tyto alba*; trophic relationships; pellets; biological control

Symposium: METHODS & APPLIED SCIENCE

Infestation patterns and zoonotic bacteria prevalence in ticks collected from small mammals inhabiting the intensive farmland of Northwest Spain

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Rodents are important hosts for ticks, efficient vectors spreading zoonoses between wildlife, domestic animals and humans. We carried out a long-term survey (2009-2016) of ticks parasitizing the small mammal community (*Apodemus sylvaticus, Crocidura russula, Microtus arvalis* and *Mus spretus*) inhabiting the intensive farmland of NW Spain. We explored variation in tick prevalence according to host species, sex, and density, months and habitats. We also tested one pool of ticks per host for *Anaplasma spp., Borrelia spp., Coxiella spp., Francisella spp.,* and *Rickettsia spp.* using real-time PCR. Positives samples were sequenced to identify bacterial species. The tick community was dominated by *Rhipicephalus turanicus* (93%), followed by Hyalomma spp. (2.8%), Rhipicephalus spp. (2.6%), Dermacentor spp. (0.9%) and Rhipicephalus pusillus (0.7%). Hosts were infested by ticks only in July, with a prevalence of 9,4% (143/1515). *Crocidura russula* was the most frequently infested host, whereas *M. arvalis* had the lowest prevalence but the highest infestation intensity range. The lowest tick prevalence among *M. arvalis* occurred after a peak in vole abundance, with a significant female bias. We found a negative correlation between tick prevalence and mouse density. Ticks tested negative to all bacteria except for *Rickettsia*, which was detected in 56.1% of the pools (69/123). We identified four species of *Rickettsia*: *R. massiliae,* the commonest (92.7%), was detected in all hosts; *R. raoulti* (2.9%) detected only in ticks from *A. sylvaticus*; *R. slovaka* (2.9%) and *R. typhi* (1.4%) only in ticks from *M. arvalis*. Some animals were collected during a tularemia outbreak, but no positive ticks for *F. tularensis* were found. Ticks infesting small mammals may therefore not play an important role in the epidemiology of this disease in NW Spain. The zoonotic character of the bacteria detected is remarkable, standing out the positive for *R. typhi*, because this clinically relevant flea-borne disease is circulating in ticks of the study area.

Keywords: cyclic vole population; ectoparasite vectors; one health; *Rickettsia*; zoonosis.

Symposium: RODENT-BORNE DISEASES

The potential role of beavers and associated landscape wetness for *Francisella tularensis* infection in Swedish hares

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Tularemia is a zoonosis caused by the bacterium *Francisella tularensis*. Human infections have increased steadily in the last decades, not only in Sweden, but Europe-wide. The transmission cycle of tularemia is complicated as it depends on environmental persistence, vectors and different potential amplifying host species (e.g., beavers), which explains the still limited knowledge on this zoonosis. Here, we tested if landscape wetness is related to infection in hares and if the occurrence of the bacterium in water varies among wetland types. We analyzed landscape composition within buffer zones reflecting hare home ranges. The buffers were centered on the localities of hares found dead that tested positive (n = 115) and negative (n = 337), respectively, for *F. tularensis* in 2016-2021. The area of waterbodies and soil moisture were higher in the landscape buffers with hares that tested positive for *F. tularensis* than in buffers with hares that tested negative. We explored this result further, by testing for the occurrence of the bacterium in water samples from beaver-affected and non-affected wetlands. Out of 28 water samples, we found *F. tularensis* in three of them, all taken from beaver affected wetlands. Our results confirm an important role of landscape wetness for the presence of *F. tularensis* and we discuss our results in relation to potential direct (e.g., presence of beavers) and indirect (e.g., creation and presence of wetlands suitable for vectors of *F. tularensis* such as mosquitoes) drivers of tularemia outbreaks

Keywords: Tularemia; *Francisella tularensis holarctica*; beavers; hares; vector borne disease

Symposium: RODENT-BORNE DISEASES

Voles in forest regeneration in Germany - impressions from the KuSaMWET Project

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Climate change-driven forest damages caused by storms, droughts and bark beetle outbreaks have led to an increase of deforested areas in the federal state of Saxony in Germany. Sites that require reforestation are regularly covered with fast growing grass and herb species promoting the occurrence of vole species and thus increasing the feeding damage on forest regeneration. The complex temporal and spatial mosaic of such areas complicates the management of voles as potential forest pests. One of the biggest challenges with regard to voles in forestry is an early regulation of the population density. However, due to restrictions on the use of rodenticides since 2019, short-term control is increasingly difficult, which is why more attention has to be paid to precise monitoring procedures. In this context, the KuSaMWET research project at the Chair of Forest Protection at Technische Universität Dresden conducted a number of field experiments studying habitat conditions to predict the colonization probability of voles and show present deficits of currently applied methods in vole management.

Keywords: forest development types; vole damage; monitoring; snap trap; plant community

Symposium: METHODS & APPLIED SCIENCE

Are long-term population and damage patterns of rodents in Southeast Asian rice agroecosystem different from European field rodents'?

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The population abundance of several rodent species fluctuates within years (seasonal changes) and among years (multi-annual cycles or fluctuations with associated high amplitude outbreaks). There is evidence that the combination of food availability, predation, parasite load and other intrinsic factors shape multi-annual population dynamics of field and forest rodents. It is also generally believed that changes in long-term small mammal dynamics are related to weather and climatic conditions that act on a continent-wide spatial scale. The project is intended to assess long-term dynamics of commensal rodents in South East Asia. Available data were assessed for characteristic patterns (e.g., regularity of multi-annual outbreaks) and checked for correlation among natural environmental drivers of long-term dynamics. The population and damage patterns varied among locations and cropping season (wet and dry). Relevant indicators of long-term rodents abundance and higher damage is still analysing.

Keywords: commensal rodents; outbreaks; climate change; food security; rodent management

Symposium: CONFLICTS & MANAGEMENT

Pathogen traits determine landscape persistence during climate extremes

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Long-term climate change and accompanying climate extremes are projected to disturb host-pathogen dynamics in many ecosystems. This response likely varies among pathogens depending on traits like host-specificity or mode of transmission. An increased understanding of these processes will support climate-based early warning efforts in public health planning. Between 2017 and 2019 common voles (*Microtus arvalis*) were trapped at 21 sites in western Thuringia (eastern Germany) and investigated for Tula orthohantavirus (TULV) specific RNA as well as *Leptospira* spp. DNA. Trapping began prior to the 2018/2019 severe drought in central Europe. The aim of this study was to investigate the relative impact of host dynamics as well as drought and wetness indices on site occupancy and prevalence of both pathogens. The results indicate fundamentally different drivers of landscape persistence in both pathogens. TULV retained a strong association with host abundance independent of drought severity, while *Leptospira* spp. presence was independent of host abundance during severe droughts and was only associated with host abundance in wetter conditions. This study emphasizes, that pathogen-specific traits like host association or environmental stability can drastically alter the response to climate extremes, like droughts. With a projected increase in frequency of such events, policy makers need to incorporate an ecological understanding of zoonotic diseases into climate change mitigation efforts.

Keywords: climate; drought; Orthohantavirus; *Leptospira*; rodents

Symposium: RODENT-BORNE DISEASES

Could the genetic monitoring predict the conservation translocation's output: case study of the European ground squirrel

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The European ground squirrel, *Spermophilus citellus*, is a hibernating rodent, endemic for the open habitats of Central and Eastern Europe. It plays a key role in the grassland ecosystems and is included in Annex II of the Habitat Directive. Unfortunately, the range and the population numbers of the species have been progressively declining during the last decades mainly due to habitat destruction. In 2020 it was declared endangered by IUCN. The efforts to improve its conservation status resulted in multiple conservation translocations implemented throughout the its range with various success rate. However, the effects of reinforcement and reintroductions on the genetic diversity have not been studied until now. The bottleneck effect and the inbreeding depression, i.e., potential consequences of the limited number of translocated individuals, could hinder the long-term survival of these populations. Thus, determining the inbreeding levels and reproductive success of translocated individuals might help to predict the long-term survival of the population and to assess the need of further reinforcement. Here we present a 5-years genetic monitoring applied during and after a population reinforcement of *S. citellus* in south-eastern Bulgaria. Both translocated and resident individuals were sampled, as well as their offspring. The samples were processed through last generation sequencing methods (ddRAD, Illumina) that allow for maximal informativeness and standardisation. The study is part of the efforts for establishing the monitoring of the genetic diversity as a tool to plan conservation actions, as well as to assess and improve their results.

Keywords: conservation genetics, population reinforcement, SNPs, ddRAD sequencing

Symposium: TAXONOMY, GENETICS & CONSERVATION

Establishing an early warning system for human Puumala hantavirus infections in Germany

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The most common hantavirus in Europe is the Puumala orthohantavirus (PUUV) that is transmitted to humans by infected bank voles. Hantavirus disease has been notifiable in Germany since 2001. In the first six years until 2006, merely 1,044 human PUUV-infections were reported. Just in 2007, the reported cases increased to 1,625. Since then, there have been five years with > 1,000 annual cases, the latest in 2021 with 1,222 cases countrywide. We designed, developed, validated and tested a prediction model for the annual human PUUV-infection risk at the district level in Germany. This talk will summarize its development and report on its first implementation for 2023. Our model consists of a binary classifier based on Support Vector Machines that predicts whether there will be a local outbreak in each district in a specific year. Our pool of predictors included freely available weather parameters from the two previous years, which govern the growth of the bank vole populations. In addition, we used the beech flowering intensity from the previous year, which had the highest Pearson correlation coefficient with the classification target, equal to 0.59 (p-value $\ll 0.001$). A leave-one-year-out cross-validation of our method led to 83% mean annual accuracy in 16 years, with 12% overestimations and 5% underestimations. We will present the automatic data collection and prediction generation, and discuss the prediction for 2023, compared to the cases reported until early May. The annually updated prediction will be available on the homepage of the German Environment Agency. The publication will be accompanied by media to disseminate it among health offices, physicians and the public. This project was commissioned by the German Environment Agency and funded by the Federal Ministry for the Environment, Nature Conservation and Nuclear Safety within the departmental research plan - research code 3720 48 401 0.

Keywords: prediction; zoonoses; bank voles; outbreak; machine learning

Symposium: METHODS & APPLIED SCIENCE

Cercadian activity pattern of rats living in livestock farm

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It is widely accepted that brown rats (*Rattus norvegicus*) are predominant rats in North America and Europe. Black rats (*Rattus rattus*) are predominant rats in Japan; relatively few studies have investigated the ecology of them. We observed the circadian activity pattern and behavior repertories of black rats in a cow barn and pig house and compared them. This study was conducted on a cow barn and pig house in the same farm located in Ibaraki; Japan. Eleven and 13 camera-traps that had been set in a cow barn and pig house and recorded videos for a 60-second period from August to October 2021. Then; we analyzed the date and time of the videos black rats were taken and counted numbers of avoidance (changing the direction of rats); stretch attend posture (elongated body stationary); general exploration; communication (sniffing and/or touching other individuals); self-grooming; and lying. Circadian rhythm was assessed using the package "Overlap" of R-software. The behaviors between the livestock houses were compared using Fisher's exact test followed by multiple comparison with Bonferroni correction. Black rats were started to be recorded just after the sunset and most frequently during night in the cow barn. In contrast; black rats were started to be recorded in the mid-afternoon and most frequently recorded around the sunrise and sunset in the pig house. The overlap rate between them was Δ=0.58. Of behaviors; avoidance and exploration were the most observed and stretch attend posture was the least in the cow barn. On the other hand; social behavior was the most observed and stretch attend posture was the least in the pig house. The study suggests the ecology of black rats in the two livestock houses are different each other. The habitat environment is seemed to affect the ecological characters of black rats in livestock houses.

Keywords: black rat; behavior repertories; camera-trapping; habitat environment; biased distribution

Symposium: BIOLOGY & EVOLUTION

Grooming stereotypes of the common hamster (*Cricetus cricetus*) in the context of individual and social behavior

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The organized sequence of behavioral acts is a fundamental characteristic of behavior. Its syntax analysis allows the identification of behavioral complexes and stereotypes. This is important for determining the functional significance of certain behaviors as well as the possible phylogenetic behavior signal. Grooming is one of the oldest behaviors among mammals, and its main biological function is to maintain a fur quality, which is essential for proper thermoregulation and recovery from ectoparasites. However grooming patterns include various elements of social interactions: aggressive and sexual. This raises a question on similarity of grooming performed in different situations. For our study, we chose the common hamster *Cricetus cricetus*, which has well-developed specific skin glands and pronounced aggressive behavior towards conspecifics, that enables us to analyse behavioral responses within social context. We performed 3 series of laboratory experiments with males in fur wetting situations, and in social interactions with conspecific males and females. Using video recordings, we described specific behavioral patterns and their sequences. On the basis of probabilistic and quantitative analysis, we interpreted the relationship of specific grooming patterns and their stereotypes with the context of the experiment. Differences were found in the grooming orientation on a specific part of the body, for example, the location of specific skin glands. Some patterns and stereotypes were similar in all three series of experiments, but were also unique to each of them, suggesting their functions. This method can be applied to other forms of behavior, as well as for inter-species comparisons of behavior.

Keywords: behavioral sequences, grooming elements, video recording, gland stimulation, social interaction

Symposium: BIOLOGY & EVOLUTION

Demographic drivers of vole population cycles

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Achieving a demographic understanding of population cycles remains an enduring challenge to population ecology because cycles are instances where signal in population dynamics, periodicity and a degree of repeatability of population trajectories, exceeds noise in population dynamics. Using monthly capture-mark-recapture (CMR) data collected during 1996-2007 (~20,000 captures of ~10,000 voles), we studied demography of a cyclic field vole (*Microtus agrestis*) population in Kielder Forest, England. We estimated survival and recruitment rate, the number of new animals in the population at a sampling occasion per animal in the population at the previous sampling occasion. We evaluated models including standardised estimates of present and past autumn and past spring density, and cumulative number of voles present during the plant growing season and categorisation of cycle phase. Recruitment rate showed strongly seasonal (recruitment was high during early and mid-breeding season, and low at the crash and low phase) and phase specific (recruitment was high during increase and peak phase, and low in crash or low phase). Current population density negatively influenced recruitment rate during the mid-breeding or late-breeding/winter season, but not during the early breeding season. Population density during the previous autumn positively influenced recruitment, whereas that in spring negatively affected it. Although apparent survival showed a strong phase-specific variation during early breeding season (survival was high during increase and peak phase but low during crash or low phase), there was no obvious phase-specific pattern in survival. Survival was negatively influenced by current population density, and population density in the previous autumn; population density in the previous spring had small, positive influence on survival. Our results suggest that the pattern of direct and delayed density dependence is strongly seasonal and parameter-specific, and more complex than previously thought.

Keywords: survival; recruitment; population growth rate; seasonality; capture recapture

Symposium: ECOLOGY

One conjugate doesn’t fit all: choosing the right conjugate for your serological assay in small mammal research

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Serological assays are an important tool for diagnosing infectious pathogens. For animal species that are commonly studied, species-specific conjugates are available to be used in these serological assays. However, for many wild rodent species and insectivores, no species-specific conjugates are available. Often in these cases, immunoglobulin-binding proteins such as protein G or protein A are used, that have a broad binding range across species. Even so, we noticed in our work that for some rodent and insectivore species, the conjugate did not attach to the antibodies of our species tested. This triggered us to test a variety of conjugates, ranging from species- or family-specific secondary antibodies to protein G, on six rodent species and two insectivore species. An overview of the results will be presented. Our take home message: don’t assume that if a serological assay works for one rodent or insectivore species, it will also work for the other, but always test your conjugate beforehand.

Keywords: serology; species-specific; diagnostics; validation; rodents; insectivores

Symposium: METHODS & APPLIED SCIENCE

Androgenization effects on endoparasite loads on males from two contracting European woodland rodent populations

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In male vertebrates, androgens influence primary and secondary sexual traits, body condition as well as reproductive success associated behaviors. The immunocompetence handicap hypothesis states that high levels of testosterone should reduce immune function, potentially increasing parasite loads. In this communication, we used two intensively studied populations of European wood mouse (*Apodemus sylvaticus*) in England and Spain to test the effect of male androgenization on endoparasite loads. We do so accounting for the effects of individual home ranges and other confounding individual-level factors. Androgenization was recorded measuring the anogenital distance (AGD) controlling for body size (AGDI) during biweekly trapping sessions. We used coprological analysis to identify 34 species of endoparasites, including platyhelminthes, rotifers, nematodes and protozoa. We used space use dataloggers to calculate home-range sizes on pit-tagged rodents. The Iberian population showed, contrary to expectations, that highly androgenized males showed significantly lower endoparasite loads not supporting the immunosuppression handicap hypothesis, whilst no effects were observed in the British population. We finally discuss the ecological differences between populations and relationships between variables that explain these contrasting effects.

Keywords: androgenization, basal metabolic rate, space use, increased-intake model, *Apodemus sylvaticus*

Symposium: BIOLOGY & EVOLUTION

Myodes glareolus: a longitudinal investigation of an invasive species and its pathogens

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The non-native bank vole (*Myodes glaroelus*) was accidently introduced into western Ireland during the early 20th century. This invasion presents a unique opportunity to study parasite dynamics during a biological invasion and the potential effects on the native wood mouse (*Apodemus sylvaticus*) and as a model system for investigating disease ecology. The need to investigate pathogens in natural settings has been highlighted in the literature, however, few studies investigating disease using wild rodent populations have been published. Ireland has a depauperate mammal community, allowing for easy identification and quantification of the effects the bank vole invasion has had on the native wood mouse. Extensive work has taken place in the field and laboratory to identify the parasite communities present in these rodents, with over 1,200 rodents sampled across Ireland from 2016, 2017, 2021 and 2022. Our study using this model system has observed the invasion to change the prevalence, and parasite abundance, in a number of parasite species in both the invasive bank vole and the native wood mouse. These results on the bank vole invasion in Ireland demonstrates how it can be used as a model system for analysing disease dynamics during in a biological invasion.

Keywords: invasive species; pathogens; helminths; wildlife; disease

Symposium: RODENT-BORNE DISEASES

Two lineages of lymphocytic choriomeningitis mammarenavirus in a German zoo

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Lymphocytic choriomeningitis mammarenavirus (LCMV) is a globally distributed zoonotic pathogen spread by house mice (*Mus musculus*). Four lineages of LCMV are currently recognized, with lineages I and II being the most common found worldwide. Recently, a host-specific relationship was hypothesized such that lineage I and II being found in *M. m. domesticus* and *M. m. musculus*, respectively. Here, we report the re-emergence of LCMV in a German zoo in late 2021. A Golden lion tamarin (*Leontopithecus rosalia*) succumbed to illness, later confirmed to be infected by LCMV. To determine the role wild mice may have had in the dispersal of this pathogen, mice from routine pest management were screened for LCMV. Subsequently, LCMV RNA was found in ~55% of wild house mice from the zoo in 2021/2022, but not in mice from 2009. Full virus genome sequencing revealed the presence of both LCMV lineages I and II in these mice. Furthermore, sequences obtained from the mtDNA d-loop confirmed that all mice belonged to *M. m. domesticus*, inconsistent with hypothesized host species-specificity. Virus sequences from the tamarin were almost identical to that from a wild mouse, suggesting cross-species virus transmission.

Keywords: LCMV; Germany; re-emergence; house mouse

Symposium: RODENT-BORNE DISEASES

Drivers behind co-occurrence patterns between pathogenic bacteria, protozoa, and helminths in populations of the multimammate mouse, *Mastomys natalensis*

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Advances in experimental and theoretical work increasingly suggest that parasite interactions within a single host can affect the spread and severity of wildlife diseases. Yet empirical data to support predicted co-infection patterns are limited due to the practical challenges of gathering convincing data from animal populations and the stochastic nature of parasite transmission. Here, we investigated co-infection patterns between micro- (bacteria and protozoa) and macroparasites (gastro-intestinal helminths) in natural populations of the multimammate mouse (*Mastomys natalensis*). Fieldwork was performed in Morogoro (Tanzania), where we trapped 211 *M. natalensis* and tested their behaviour using a modified open-field arena. All animals were checked for the presence of helminths in their gastro-intestinal tract, three bacteria (*Anaplasma*, *Bartonella,* and *Borrelia*) and two protozoan genera (*Babesia* and *Hepatozoon*). Besides the presence of eight different helminth genera (reported earlier), we found that 21% of *M. natalensis* were positive for *Anaplasma,* 13% for *Bartonella,* and 2% for *Hepatozoon* species. Hierarchical modelling of species communities was used to investigate the effect of the different host-related factors on these parasites' infection probability and community structure. Our results show that the infection probability of *Bartonella* increased with the host's age, while the infection probability of *Anaplasma* peaked when individuals reached adulthood. We also observed that less explorative and stress- sensitive individuals had a higher infection probability with *Bartonella*. Finally, we found limited support for within-host interactions between micro-and macroparasites, as most co-infection patterns could be attributed to host exposure time.

Keywords: Tanzania; *Bartonella; Anaplasma*; Hepatozoon; helminths; co-infection

Symposium: RODENT-BORNE DISEASES

Inferring the biogeographic history of the Cabrera vole by integrating niche modelling, genomic and fossil data

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The reconstruction of species' glacial refugial history and demographic changes over time has generally been based on comparing inferences from single-method approaches, with no truly methodological integration. Here, we aimed to overcome this shortfall by integrating ecological, genomics and paleobiology methods while discussing each method's limitations and advantages. We evaluated the palaeodistribution of the Cabrera vole (*Microtus cabrerae*), integrating ecological niche modelling (ENM), genomics and fossil data. The species is currently distributed in Portugal and Spain, and extended to southern France in the past, according to the fossil record. After compiling and mapping the raw fossil data for the Last Glacial Maximum (LGM) and Mid-Holocene (MH), we calibrated an ENM relating occurrence with climatic variables and projected it to the LGM, YD and MH. As for genomic analyses, we used previously obtained Genotyping-by-Sequencing data to evaluate the demographic history and range expansion patterns of four Evolutionarily Significant Units, in an integrative framework. We found that fossil abundance was higher in southern and eastern Iberia and southern France from the LGM to the MH. ENM- and genomics-inferred refugial areas supported higher suitability in central-to-north Iberia during the LGM. Given the discordance of ENM and genomic results with the fossil record, we believe that this study system might highlight a frequently overlooked possibility that the fossil record may misrepresent the ancestral distribution of this species. This highlights the importance of cautiously considering fossils for ancestral distribution reconstruction, particularly due to potential biases associated with fossilization conditions. Therefore, our combined analysis of all three data types supports a northern glacial refugium for the Cabrera vole in the Iberian Peninsula during the LGM, highlighting the need for integrative approaches to accurately reconstruct a well-supported picture of species biogeographic history.

Keywords: demographic inference; fossilization; hindcasting; paleoclimate; paleo-distribution

Symposium: TAXONOMY, GENETICS & CONSERVATION

Development and evaluation of unmanned aerial vehicle rodenticide applicator (R-Drop Drone) for rodenticide application in oil palm plantation

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The traditional method of controlling rat populations and rat fresh fruit bunch damage in oil palm plantations is via rodenticides application using manual labour. Due to the COVID-19 pandemic and the resulting labour shortage, new methods for rodenticide application have been explored, including the use of unmanned aerial vehicles (UAVs). Recently, Sime Darby Plantation Research Sdn Bhd and a drone manufacturer, Poladrone Solutions Sdn Bhd (AONIC) have codeveloped a specialized Unmanned Aerial Vehicle (R-Drop Drone) for rodenticide application. The R-Drop Drone employs a mechanism that drops rodenticides onto the field and includes a spinner to regulate the application timing and rate. The R-Drop Drone can be used to apply rodenticides in difficult areas with poor accessibility, such as water-logged areas, hilly and steep areas as well as immature fields with thick legume cover crops. This new technology is capable to improve productivity and worker safety. A field trial was conducted using flocoumafen rodenticides applied via the R-Drop Drone to evaluate the efficacy, accuracy, productivity, and robustness of the new technology in an oil palm plantation estate in Johor, Malaysia. The trial was conducted at three (3) different age groups (immature, young mature and mature oil palm). Results showed that good accuracy of application in immature and young mature fields was achieved but the accuracy was lower in the mature plots. Nevertheless, significant fresh damage reduction and rat populations were significantly reduced in all treatment plots, with plots using multiple baits showing the highest reduction. Overall, the use of flocoumafen rodenticide via the R-Drop Drone application was effective in controlling rats in oil palm plantations. The R-Drop Drone also passed the robustness test with no major breakdowns occurring during the long period of operation hours in the trial.

Keywords: UAV; R-Drop Drone; rodenticide; rat baiting; fresh damage; the rat population

Symposium: CONFLICTS & MANAGEMENT

The stressed life of island invasive rodent species

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Rats have spread across the globe alongside humans, and successfully colonized a wide range of locations and habitats. The invasive success of rats in oceanic islands is due to a combination of factors, from lack of predators, to elevated availability of food and year-round breeding. We hypothesized that islands rats experience reduced environmental stress compared with continental locations, due to abundance of resources, reduced predation risk and lower levels of anthropogenic activity and associated hazards (*e.g.* chemical pollution, noise). In this study we compared populations of Black and Brown rats (*Rattus rattus* and *Rattus norvegicus*) from two locations, a continental city and an insular city. We assessed long term stress through the measurement of hair corticosterone levels and validated mechanism of stress response by assessing serum corticosterone levels, after a stressful event (capture and handling). Results suggest species specific response to environmental stress supporting niche-partition hypothesis between *R. rattus* and *R. norvegicus*. Corticosterone levels after a stressful event revealed an active mechanism of stress response, probably facilitated by continued exposure to environmental stress. Our results do not support the hypothesis of reduced environmental stress on islands, these species are likely to face challenges underestimated in this study. However, stress response mechanisms may help explain the success of invasive species, as they help animals on the necessary actions to respond to and protect themselves from the environmental demands.

Keywords: environmental stress; corticosterone; serum; hair; rats

Symposium: ECOLOGY

Using short-eared owl tracking and sightings to study and predict rodent outbreaks

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Rodent control interventions are most effective when implemented at the inception of an outbreak. This calls for early warning signals of rodent emergence to inform stakeholders when and where to initiate rodent management efforts. Specialized rodent predators, such as short-eared owls (SEOs), are very efficient at tracking where their preferred prey are abundant. They are highly mobile, roaming over entire continents to effectively track prey fluctuations in space and time. Their movements and increased occurrence could therefore be used for an early detection of rodent (re)emergence, and as a warning signal for timely rodent management action. To test this hypothesis, we fitted SEOs with high resolution GPS tracking devices during 2019-22. We studied their movements at different spatial scales in NW Spain, where common voles invaded 5 million ha of farmland during the 1990s and outbreaks have periodically occurred since, causing crop damages and public health impacts. We first show that SEO tracking allowed to identify not only areas, but also specific fields within a farmland mosaic with higher than average vole abundance. We further compiled available citizen science data (web-based platforms) at regional and local scales and show that SEO sighting rate not only allows to reconstruct past vole outbreaks, but also predicted spring vole population growth. Our results highlight the usefulness of tracking SEO invasions to predict vole emergence and identify rodent hotspot areas at different spatial scales.

Keywords: vole emergence; nomadic specialist predator; numerical response; pest management

Symposium: METHODS & APPLIED SCIENCE

A framework for understanding and predicting orthohantavirus functional traits using rodent host ecology

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Orthohantaviruses present a global public health threat; there are 58 distinct viruses currently recognized by the International Committee on Taxonomy of Viruses, with many more proposed, and case fatality of pathogenic orthohantaviruses ranges from <0.1% to 50%. All known human disease-causing orthohanatviruses are carried by rodents, and except for one potential exception of a localized outbreak of Andes virus, each human infection is the result of a novel spillover event from rodent to human. An Old World versus New World dichotomy is frequently applied to distinguish human diseases caused by orthohantaviruses. However, this geographic grouping masks the importance of phylogeny and rodent-virus ecology in shaping orthohantavirus traits, especially since related arvicoline rodents and their orthohantaviruses are found in both regions. We argue that orthohantaviruses can be separated into three phylogenetically based rodent host groups – murid-borne, arvicoline-borne, and non-arvicoline cricetid-borne – which display differences in key functional traits, namely human disease, transmission route, and virus-host fidelity. Murid-borne orthohantaviruses cause hemorrhagic fever with renal syndrome with moderate mortality, are primarily transmitted through aerosolized excreta, and generally have high host fidelity with occasional spillover; arvicoline-borne orthohantaviruses cause nephropathia epidemica with low mortality, are commonly transmitted through saliva and aerosolized excreta, and have high host fidelity; non-arvicoline cricetid-borne orthohantaviruses cause hantavirus cardiopulmonary syndrome with high mortality, are primarily transmitted through saliva, and have relatively low host fidelity. Our framework is generalizable and can help understand and predict traits of under-studied and newly discovered orthohantaviruses and guide public health and biosafety policy.

Keywords: HCPS; HFRS; host fidelity; transmission; zoonotic infection

Symposium: METHODS & APPLIED SCIENCE

Taxonomic revision and evolutionary history of the Ethiopian clade of climbing mice (*Dendromus*) - The role of elevation and geographical barriers in the speciation processes

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There is increasing evidence that the Ethiopian highlands functioned as a long-term refugium for many montane taxa and also served as a source of colonization for other mountain blocks during warm and humid Plio-Pleistocene episodes. The climbing mice (*Dendromus*, family Nesomyidae) are widely distributed in grassy habitats across most African mountain regions, making them a suitable model to investigate how climate and topography have impacted the evolution of diversity in the Eastern Afromontane Biodiversity hotspot. Recent phylogenetic study based on mitochondrial DNA sequences identified a monophyletic *Dendromus* clade grouping all but one Ethiopian taxon. The only exception is *Megadendromus nikolausi*, currently forming a separate endemic Ethiopian genus, plus two nearby lineages outside Ethiopia (= "the Ethiopian clade" hereafter). However, for taxa within this clade, the species limits, phylogenetic relationships, and ecological requirements remained unresolved. Here we analysed the genomic and morphological data of this group with the aim to delimit species and assess their distribution and evolutionary history. Genetic data included sequences of mitochondrial DNA and thousands of SNPs from ddRAD sequencing from all major lineages sampled across their known distribution ranges. Further, we examined their external and cranio-dental morphology (the latter by geometric morphometric approaches). Mitochondrial sequences provided a well-supported phylogeny, i.e., the presence of seven major clades corresponding to seven putative species, and this result is partly congruent with nuclear phylogenomic analysis revealed by ddRAD data. Some of the revealed gene pools are clearly morphologically distinguishable and will be described as new species. The most likely evolutionary scenario included the radiation in the Ethiopian highlands, followed by one "out-of-Ethiopia" dispersal event, leading to colonization of Imatong Mts. and Mt. Kilimanjaro. This study was supported by the CSF (project no. 20-07091J) and the RFBR (project no. 19–54-26003).

Keywords: climbing-mouse; ddRAD; Ethiopian highlands; morphometry; phylogeography

Symposium: TAXONOMY, GENETICS & CONSERVATION

Unique population dynamics of Japanese field vole: winter breeding and summer population decline line

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It is common knowledge that winter temperatures influence the life history of small mammals. Cold temperatures necessitate increased energy requirements for survival, and recent studies indicate that snow cover can have both negative and positive influences. With each new observation, we develop a more comprehensive understanding of the mechanisms that influence small mammal populations. Here we report on our recent study on Japanese field vole Alexandromys (*Microtus) montebelli*, which reaches its peak in population during the early spring and its low during the autumn. To understand the population dynamics of these voles, we conducted a capture-mark-recapture survey, then estimated the seasonal abundance, recruit, capture probabilities, and survival probabilities using the Bayesian hierarchical model. We also analysed the impact of mammalian generalist predator visits on the survival probabilities. Our data indicates that the early spring peak in population is due to intensive winter breeding and the highest survival probabilities during the periods of deep snow cover. When snow cover reaches a certain depth, the circumstances can combine to raise survival probability and favour breeding. During the breeding season in May and June, on the contrary, the survival probability reached its lowest, resulting in a decrease in population despite breeding. The low survival probability between spring and autumn could be attributed to the impact of generalist predators, and low vegetation may have amplified the effect. In summary, the deep snow cover and generalist predators were considered to be the key factors shaping this unique population dynamics in this orchard area.

Keywords: snow; generalist predator; *Alexandromys*; *Microtus*; vegetation management

Symposium: ECOLOGY

The role of ground beetles as intermediate hosts for *Mastophorus muris*

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Mastophorus muris known as cosmopolitan, gastric spiruid nematode requires an obligatory intermediate invertebrate host. Larvae can develop in stomach of Orthoptera, Dermaptera, Dictyoptera and Siphonaptera. Larvae of spirurid parasite may also develope in ground beetles (e.g. Geotrupidae). Bank voles are omnivorous rodents, especially herbivorous. However, their diet is occurred also with arthropodes and annelids. Natural sources of proteins from invertebrates are usually the most important during of breeding and lactation, when rodents have the greatest protein requirements. Beetles are considered to be reservoirs of infection for their occasional predators that include rodents. Our objectives were to monitor the prevalence of *M. muris* in the ground beetles species (*Anoplotrupes stercorosus*, *Trypocopris vernalis*) found in three separated locations – Pilchy, Tałty and Urwirałt and to assess the potential role of ground beetles as intermediate hosts for *M. muris*. Beetles were dissected and then any parasites present were counted, recorded, transferred to a glass slide, and examined under light microscope. Found larvae were stored in 70% ethanol for molecular analysis – Polymerase Chain Reaction (PCR). Products of PCR reaction were observed by electrophoresis method. We detected *M. muris* larvae in 18 from 240 dissected beetles, with an overall prevalence of 7,5% (23,8% for Pilchy, 40,0% for Tałty and 26,3% for Urwitałt). We provided sequencing of *M. muris* genome and obtained 10 various sequences. These results contribute to our understanding of the abundance of M. muris in ground beetles in Poland and confirm that *M. muris* circulates in *A. stercorosus* and *T. vernalis*. Therefore, they may potentially play a role as reservoirs of this parasite in the sylvatic environment. This research was funded through the 2018–2019 BiodivERsA joint call for research proposals under the BiodivERsA3 ERA-Net COFOUND programme. JN and MG were supported by the National Science Centre, Poland, under the BiodivERsA3 programme (2019/31/Z/NZ8/04028).

Keywords: nematodes; rodents; invertebrates; PCR assay; molecular biology

Symposium: RODENT-BORNE DISEASES

New technologies and old allies: can common kestrel GPS-tracking help in detecting common vole during low density phases?

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Common vole (*Microtus arvalis* Pallas) is considered to be one of the most aggressive agricultural pests in Europe: its demographic fluctuations are associated with cyclical periods of high population densities, during which they can cause extensive damage to crops. However, once a population outbreak has been triggered, efforts to control this species become extremely difficult, being ineffective on many occasions. Early detection of this species during low-density periods is essential to prevent its proliferation. The native predators of the common vole are considered as natural allies within the integrated management of this species. But, beyond its potential to reduce populations of this agricultural pest, its specialization in prey detection may be a concept to consider in its possible use for early detection of initial risk sources of common vole. In the present contribution, a preliminary approach on the feasibility of addressing this objective by monitoring the movements and routes of the common kestrel (*Falco tinnunculus*) is proposed. During a low vole population density phase, five common kestrel males from nest boxes placed on agricultural land were captured, tagged with solar-powered GPS transmitters, and released. Tracking was carried out for two months (May 12 to July 10, 2022), biweekly reviewing the spatio-temporal distribution of points reported by each kestrel during its periods of activity (frequency of transmission was up to one minute in the central hours of the day). Home range was defined, on which a raster (cell size = one hectare) referring to number of points observed/expected was generated, allowing the identification of the hot-spots most visited by kestrels. Subsequently, vole abundance indices were field monitored in the hotspots and in control cells with similar landscape and land use characteristics within the home-range. Our preliminary results show that the flight trend of the common kestrel could provide a signal related to the presence of voles during low-density situations, although further studies are needed because other factors not controlled in our study may be involved.

Keywords: *Microtus arvalis*; *Falco tinnunculus*; GIS; early detection; pest prevention

Symposium: METHODS & APPLIED SCIENCE

Factors affecting the quantity of mitochondria in African small rodents

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Mitochondria are cellular organelles responsible for the production of ATP. Environmental conditions and their changes can induce adaptive changes in mitochondrial structure or their quantity. Such changes can result in increased ATP production, which appears to be an advantage in adaptations to high altitudes. The purpose of this study was to investigate the factors affecting the inter- and intraspecific differences in quantity of mitochondria in small African rodents from genera Stenocephalemys and Lophuromys from Guassa and Choke mountain ranges in Ethiopian Highlands. The quantitative PCR was used to quantify the relative quantity (RQ) of mitochondria from liver and thigh muscle tissue in 81 individuals collected in various elevations. The expected effect of elevation on mitochondrial quantity was not confirmed, but the RQ of mitochondria differed significantly between tissue types and between genera. Results of this study showed that the long-term adaptation to high elevation is not through the increase of the quantity of mitochondria, despite the fact that the short-term increase in mitochondrial numbers has been observed in rodents. The study itself can be used as a pilot study for further research of adaptive evolution of mitochondria using the Ethiopian rodents inhabiting different elevations as a model system

Keywords: number of mitochondria; ecophysiology; Ethiopian Highlands; qPCR; long-term adaptation

Symposium: BIOLOGY & EVOLUTION

Exploring spatiotemporal variation in urban rat population through pest management data

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Brown rats (*Rattus norvegicus)* inhabit urban environments all over the globe. Despite of proximity to and interaction with humans, basic ecology of wild rats is not well known. Population dynamics of city rats is widely unexplored, especially in boreal areas with harsh winter conditions. I assess spatiotemporal population fluctuations of wild rats over 8-year period (2013-2021) in Helsinki, Finland, based on citywide rat trapping data from a pest management company, and model the dynamics using open access environmental data on the resolution of postal code areas. We find overall population growth during the years with ambiguous seasonal pattern. Human population density has a positive effect whereas socioeconomic status of humans, measured as median income, correlates negatively with rat population size. I further reflect on the possible biases in using trapping data to model spatiotemporal fluctuations in population size. We emphasize the importance of using multiple approaches and independent datasets, as population dynamics and trappability of rats depend on the environmental context and behaviour.

Keywords: population dynamics; wild rats; *Rattus norvegicus*; trapping data

Symposium: ECOLOGY

Spatially explicit capture-recapture modelling and parentage analysis of Cabrera voles in high population density patches

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Assessing animal population density and reproductive behaviours (e.g. mating tactics) is critical to understand population dynamics and improve conservation planning for target species. The Cabrera vole *Microtus cabrerae* is a near-threatened Iberian endemism with global declining trends, being largely restricted to small patches of herbaceous wetland. Reported density estimates of Cabrera vole populations vary largely, ranging from <20 to >100 individuals/ha. Although such differences may be, at least in part, related to differences in methodological and analytical procedures or assumptions, there might be considerable variation in population densities according to local ecological conditions. Variable population density often leads to changes in mating tactics. In low-density populations the Cabrera vole typically shows genetic monogamy, but this could potentially be altered in high-density patches given the increased likelihood of extra-pair mating, as suggested in other monogamous rodents. Here we addressed this issue by reporting density estimates and genetic mating pattern of the Cabrera vole in two habitat patches from Extremadura (central-western Spain), where the notably high abundance of vole signs was suggestive of high population density. Based on 167 genotyped faecal samples (10 microsatellite loci) collected in May-June 2021 from the two selected patches, we implemented spatially explicit capture-recapture models within a Bayesian framework to estimate local population density, while accounting for eventual gender differences in the detection process. Genetic mating pattern was assessed from parentage analysis using full-pedigree likelihood approach. Results indicated relatively high densities (point estimates of 73 and 137 ind/ha) compared to those obtained elsewhere using similar methods (17-29 ind/ha). Notably, genetic monogamy was the most supported mating pattern in the high-density patches studied. These results suggest relatively low plasticity (and hence limited adaptive potential) of Cabrera voles' reproductive behaviour across variable population densities, which may be linked to the remarkable low sperm competition observed in this species.

Keywords: density-independent; genetic monogamy; genetic non-invasive sampling; mating tactics; population density

Symposium: ECOLOGY

Land-use effects on the gene flow of a threatened small mammal in fragmented Mediterranean farmland

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Understanding the factors influencing animal movement and gene flow is crucial for developing effective landscape-level conservation management. Individual-based genetic data has been increasingly used to parameterize resistance surfaces and to test hypotheses about landscape characteristics affecting movement. Here we used genetic non-invasive sampling to assess how land-uses favour or hinder movements and gene flow of the threatened Cabrera vole in fragmented Mediterranean farmland, contributing to more informed conservation planning. We focused on the end of the wet season (February-March), when population size peaks and movement rates are expectedly higher. Based on 87 genotyped samples of vole faeces collected in a 462-ha farmland landscape from southwest Portugal, we estimated pairwise genetic distance among 78 identified individuals. We then used vector-based data of 18 land-uses identified in the field to derive 3 types of surfaces in raster format (10-m pixel resolution) based on: i) the presence-absence of each land- use; ii) the percentage cover of each land-use; and iii) the distance from each pixel to each land- use. Lastly, we assessed the relative support of all surfaces in explaining pairwise genetic distances, by using computer optimization to estimate resistance surfaces. We found that the distance to extensive pastures was the best-performing resistance surface, with lowest resistance to gene flow being in areas close to such pastures, although increasing rapidly and steeply further away. Although performing less well, the proximity to (and cover of) low-traffic dirt-roads were also predictors of lower gene flow resistance, most likely due to their association with relatively undisturbed grass verge habitats. Overall, these results are in line with the prediction that increasing functional connectivity for Cabrera voles in farmlands requires the maintenance of habitat matrices dominated by extensive pastures and the preservation of dirt-road verge habitats linking otherwise isolated sites.

Keywords: *Microtus*; dispersal; resistance; roads; genetic distance

Symposium: TAXONOMY, GENETICS & CONSERVATION

Wild vs lab house mice: Does captive breeding affect inner ear morphology?

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The semi-circular canals of the inner ear are involved in balance and velocity control. Being crucial to insure efficient mobility, their morphology display an evolutionary conservatism attributed to stabilizing selection. Release of selection in slow-moving animals as been argued to lead to morphological divergence and increased inter-individual variation. In its natural habitat, the house mouse *Mus musculus* is moving in a tridimensional space where efficient balance is required. In contrast, laboratory strains are bred since decades in small cages. This regime of mobility reduction should have released selection on the inner ear morphology, allowing to test for this effect in an experimental setting. Four groups were compared here: (1) several populations of wild mice trapped in commensal habitats in France; (2) their second-generation laboratory offspring, to assess plastic effects related to breeding conditions; (3) a standard laboratory strain (Swiss); (4) hybrids between wild offspring and Swiss mice. The morphology of the semi-circular canals was quantified using a set of 3D landmarks and semi-landmarks analyzed using geometric morphometric protocols. All wild mice shared a similar inner ear morphology, contrasting with the important divergence of the Swiss strain. The release of selection in the laboratory strain obviously allowed for an important drift of the otherwise conserved structure. Hybrids displayed a morphology close to the wild parents, suggesting an accumulation of recessive and presumably unfavorable alleles in the laboratory strain. Contrary to the expectation, however, wild mice displayed slightly higher levels of inter-individual variation compared to lab mice, possibly due to the higher levels of genetic variance within and among wild populations compared to the lab strain. Differential allometric response of the different canals was also documented; the wide age range documented in wild mice could also contribute to increased morphological variance.

Keywords: *Mus musculus*; geometric morphometrics; semi-circular canals; allometry; mobility reduction

Symposium: BIOLOGY & EVOLUTION

Morphological diversification along the invasion of Senegal by the house mouse

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The house mouse *Mus musculus domesticus* is a well-known commensal invasive species that expanded its range by taking advantage of human transport. In Senegal, house mice were established in colonial cities along the Atlantic coast since the middle of the 19th century. Following the construction of roads during the 20th century, mice started to progress further inland, are is still expanding nowadays. Genetic analyses suggested that this invasion started from one initial introduction event. The eastward subsequent spatial spread was associated with a decrease in genetic diversity, suggesting serial founder events during expansion. This invasion also exposed house mice to new environments, thus potentially challenging adaptive processes. The shape of the upper molar was thus studied as a potential marker of genetic divergence and adaptation to new food resources. The 2D molar outline was quantified using geometric morphometrics in populations along the Atlantic coast and the two main roads of the inland invasion, compared to populations from Mainland Europe, assumed as the initial source of colonization. Senegalese mice were differentiated from their European relatives. Within Senegal, a further differentiation is observed between the two main invasion roads. Molar shape variation was strongly related to the fine scale genetic structure, estimated by microsatellites. This suggested a predominant role of neutral processes underlying morphological differentiation. However, house mice from Senegal overall displayed a level of inter-individual morphological variance equal or even slightly higher than their European relatives. This is in apparent contradiction with the observed reduction of genetic diversity as a consequence of serial bottlenecks. The important disparity, together with the occurrence of unusual phenotypes, suggests that the invasion dynamics, promoting founder effects and evolution in small populations, triggered a decrease in canalization and/or the expression of rare alleles, offering new phenotypes to the screening of selection.

Keywords: *Mus musculus domesticus*; molar shape; geometric morphometrics; microsatellites; mitochondrial DNA

Symposium: BIOLOGY & EVOLUTION

The partial synchronisation of population cycles through travelling waves

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The dynamics of cyclic populations across space arise from both limited dispersal of activators and inhibitors (i.e. unspecified causal agents of multi-annual population cycles) and the relative strength of synchronising factors able to pull populations into similar cycle phases. While numerous studies have investigated cycles and synchrony in isolation, few consider the potential for the joint influences of synchronisation and activation-inhibition together, largely owing to datasets lacking suitable spatial and temporal coverage. We report here on patterns of partial synchrony in cyclic common vole *Microtus arvalis* populations in NW Spain. Using data collected in the Castilla-y-Leon region, we considered a representative suite of hypotheses, informed by both the theoretical and empirical literature, that were tested using large-scale (>35,000 km^2), multi-year (2011-2017) field observations of vole population growth rates. We find most support for a self-organising, singular spatio-temporal pattern in growth rates (a phenomenological description), itself the cumulative result of two expanding radial travelling waves (with contrasting speeds), which are consistent with activator-inhibitor dynamics.

Keywords: population dynamics; synchrony; spatio-temporal; activator-inhibitor; outbreaks

Symposium: ECOLOGY

Effects of cropping practices on habitat use by pest house mice (*Mus musculus*): implications for management

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In Australia, a shift to conservation agriculture in the last 20 years has led to substantial changes in the post-harvest crop environment. Minimum tillage practices have led to less soil disturbance, allowing rodent burrows to remain intact, while retention of vegetation cover (stubble) after harvest has created a more favourable environment for pest rodents. Consequently, house mouse populations are now resident in Australian crop paddocks year-round, requiring more intensive management than previously. During widespread mouse plagues in Australia in 2020/21, farmers attempted to reduce mouse numbers by creating less favourable conditions for mice by slashing, mulching and burning stubble prior to sowing new crops, which can be severely damaged by resident mouse populations that dig up and eat crop seeds. In this study, we assessed the effect of harvesting and stubble management (cutting and rolling stubble) on mouse populations in crop paddocks. Mouse numbers decreased following harvest, but there was no difference in population size between paddocks with and without stubble management. Other management interventions that aim to reduce food availability in post-harvest cropping paddocks, including from spilled grain and weed seeds, may be more effective for house mouse management.

Keywords: tillage; conservation agriculture; stubble management; habitat manipulation; food availability

Symposium: CONFLICTS & MANAGEMENT

Context-dependent species associations: environmental and seasonal effects on local co-occurrence patterns of two Mediterranean voles

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Species associations are not uniform across space and time. However, this context-dependency remains very difficult to measure, as field experiments are often performed in a limited number of locations and over a short time window. The Cabrera vole (*Microtus cabrerae*) and the southern water vole (*Arvicola sapidus*) are two Mediterranean species that share broadly similar habitat types dominated by wet herbaceous vegetation. The two species may be frequently found together in some regions, particularly where habitat availability is high and the landscape is structurally complex (*e.g.* variable patch sizes and habitat mosaics across the matrix), allowing them to coexist at the landscape scale (*e.g.* through among-patch segregation). Yet, it is possible that seasonal changes resulting in further increases in habitat and food availability in such landscapes (*e.g.* due to increased precipitation) may provide improved conditions for both species, potentially leading to a positive association between them at the local scale. Here we tested this prediction based on replicated presence-sign surveys of the species, conducted in a farmland landscape from southwest Portugal where habitat resources for both species were relatively widespread and both occur at relatively high abundance. Based on two-species occupancy-detection modelling, we found that during the dry season the co-occurrence of the species at the local scale was largely independent, with patch occupancy patterns of each one being mostly linked to its own particular limiting factors related to its niche features and life-history traits. However, during the wet and rainy season, there was a positive association between Cabrera and water voles at the patch-level, suggesting an increased ability of the species to coexist locally, most likely involving fine-scale resource segregation mechanisms. Overall, our study highlights the complex range of possible association patterns that may be established between species, depending on the environmental and seasonal context.

Keywords: *Microtus cabrerae; Arvicola sapidus*; occupancy-detection modelling; co-occurrence dynamics; coexistence mechanism

Symposium: ECOLOGY

Overcoming barriers of poor zinc phosphide bait efficacy for reducing vole damage to grass seed fields in Oregon, USA

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Grass seed is an important crop in the Willamette Valley of Oregon, USA, where >160,000 ha are used to produce >$500M annually. The gray-tailed vole (*Microtis canicaudus*) causes year-round damage in these fields and the only rodenticide allowed for vole management is zinc phosphide (ZnP). Migratory goose (*Branta* spp.) presence further restricts above-ground ZnP applications to only May-September. Farmers claim these ZnP baits are not consistently effective against voles. We formed several hypotheses to test: 1) ZnP baits have low palatability, 2) bait delivery method are insufficient, 3) bait delivery timing is poor due to natural food availability, and 4) ZnP concentrations reduce once baits interact with moist and low pH soils. Our field study tested hypothesis #1, and we measured vole activity before and after farmers applied ZnP baits in summer. Additionally, cameras monitored ZnP baits to determine animal visitors and bait attractiveness. We found that ZnP generally did not reduce vole populations following summer applications. Cameras showed voles frequently passed ZnP baits without interest, which supports our hypothesis that ZnP have low palatability in summer. To test hypothesis #4, we simulated field conditions using a laboratory environmental chamber and applied ZnP baits to acidic soils with differing moisture levels. We then harvested baits and analyzed for ZnP at Days 0, 1, 3, 8, and 15. We determined that ZnP baits are quite stable, even with all baits (4 formulations) showing slight ZnP losses at day 1. The two pellet formulations were slightly more stable than the oat formulations. None of the ZnP losses were so great that they would seem ineffective against voles, leading us to reject hypothesis #4. Currently we are working with formulations chemists, as well as Neogen and Bell Labs, on methods/adjuvents (e.g., masking agents, absorbants) to enhance ZnP bait palatability for improved vole management.

Keywords: *Microtis canicaudus*; acute toxicant baits

Symposium: CONFLICTS & APPLIED SCIENCE

Effectiveness and future utility of goodnature A24 self-resetting rat traps for multiple rodent species

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Rodent pest species threaten resources in agriculture, urban, and natural environments. Goodnature® A24 rat+stoat self-resetting traps (A24s) are used extensively for invasive rat control in several countries and environments, especially in island ecosystems. Unlike traditional single-set kill traps, A24s fire and reset up to 24 times per CO_2 cartridge, and represent a nontoxic device for rodent pest control. Given the rapid rise in use of A24s as a management tool, our goal was to understand why A24s work in some cases and not others. To address this goal, we reviewed A24 literature including a recent special issue of A24 effectiveness and hazard studies, and then we propose future research needs and recommended uses for A24s including a list of potentially susceptible rodent species requiring further investigation. A24 are mostly used against *Rattus rattus* for control on islands in Hawaii and New Zealand. Additionally, A24 effectiveness was compared to toxic bait use against rats in California agricultural landscapes, and snap-traps against house mice (*Mus musculus*) in Colorado pens. Behavioural studies have demonstrated that both rats and mice repeatedly visit and pass by A24s much more frequently than they trigger A24s. Some large-scale trapping grids in Hawaiian forests reduced rat populations, but a few endangered birds were unintentionally killed by A24s, which stimulated research on bird excluder attachments for A24s. Future research may investigate A24 uses on rodent species other than *Rattus*, as the types of species potentially vulnerable to A24s range in size from mice (e.g., *Apodemus, Mus, Peromyscus, Reithrodontomys*; ≥14 g) to squirrels (e.g., *Otospermophilus*, *Sciurus*; 353-527 g). A24s can be used successfully to control rodent populations of some species in particular environments. Studies that compare A24s with alternative and synergistic rodent management methods will help determine the most effective and efficient rodent control methods that minimize non-target risks.

Keywords: *Apodemus*; automatic trap; *Mus*; *Rattus*

Symposium: METHODS & APPLIED SCIENCE

Are associations between zoonotic pathogens driven by host community diversity, gut microbiome and environmental indicators in forests and urban parks throughout Europe?

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Major advances in the understanding of infectious diseases have been achieved these last decades. However, the persistence and re-emergence of pathogens continue to raise public and veterinary health concerns, of which the recent COVID-19 pandemic may be one of the most dramatic examples. Understanding the impact of habitat alterations and concomitant biodiversity loss on pathogen transmission and emergence from wildlife remains challenging. Here, we aim to elucidate the interlinkages between biodiversity and rodent-borne diseases at local and European scales. We present the recently collected host-pathogen data from 27 temperate forest sites and 10 urban green spaces - environments where rodents are abundant and human/domestic – wildlife interactions are likely to occur - throughout 5 European countries. Over 4000 specimens were captured during 2020 – 2022 compromising 18 different host species. Different organ tissues of each specimen were screened by either 16S rRNA amplicon sequencing or specific PCR. The presence of antibodies to different families of viruses was screened using immunofluorescent assays. A multitude of pathogens from several genera including *Bartonella*, *Borrelia*, *Mycoplasma*, *Anaplasma*, *Neoehrlichia, Leptospira, Orthohantavirus and Orthopoxvirus* were detected at non negligeable prevalence. These multi-pathogen multi-host data were analysed using a community ecology approach, based on hierarchical modelling of species community (HMSC), elucidating the different biotic and abiotic factors driving pathogen occurrence and associations throughout Europe. These results will contribute to an improved understanding on the biodiversity-disease relationship and can guide ecosystem management practices and biological conservation strategies in the future.

Keywords: rodent-borne diseases; urbanisation gradient; human-wildlife interface; gut microbiome; dilution and amplification effects

Symposium: RODENT-BORNE DISEASES

Linking climatic variables to wild rodent population dynamics as predictors for zoonotic disease transmission

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Climate can affect tree seed production, which represents the major food resource for several rodent species including *Apodemus flavicollis*, a very common forest rodent species and an important reservoir for different zoonotic pathogens (as Hantavirus, TBEV and *Borrelia burgdorferi* s.l) representing an increasing threat for human public health. We thus investigated how climatic data alone might be useful to predict rodent population dynamics, which in turn might affect rodent-borne disease risk and therefore be used as early warning indicators of great utility for the improvement of prevention and control strategies. A population of *Apodemus flavicollis* was monitored for 17 years (2000-2017) in a forest dominated by beech (*Fagus sylvatica*) in the Province of Trento (northern Italy) using Capture-Mark-Recapture technique. All animals were individually tagged with a subcutaneous transponder and at each session a set of standard parameters related to the site (date, trap and grid) and to the animals (tag ID, species, sex, body mass, status) were recorded. Animal abundance was obtained using the Jolly-Seber method and then averaged over study sites and year of sampling. Temperature and precipitation data were obtained from a ground station close to the study area. Linear models were implemented to assess how yearly average mice abundance was associated with previous years weather conditions. We found that warmer summers two years before sampling were positively related to higher *A. flavicollis* population density. On the other hand, precipitation occurring during the autumn one year before sampling negatively influenced mice density. To the best of our knowledge, this is one of the first attempts at investigating how alpine rodent abundance might be linked to weather conditions. Our results highlight important correlations, which eventually might be used for estimating risk of transmission of rodent-borne zoonotic pathogens.

Keywords: capture-mark recapture; climate; *Apodemus flavicollis*; beech; risk assessment

Symposium: ECOLOGY

Are there more species of the naked mole-rat (*Heterocephalus glaber*)? Species delimitation using phylogenomics

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African mole-rats of genus *Heterocephalus* are considered as monotypic with the only representative, the naked mole-rat (*H. glaber*). This species has attracted attention of scientists from various fields due to numerous peculiarities in its biology, such as longevity, highly cooperative breeding system, hairlessness, cancer resistance, or tolerance to pain and hypoxia. Although there is intensive ongoing research focused on this species, knowledge of the genetic structure is still limited. Several molecular phylogenetic studies have brought genetic support for existence of two naked mole-rat species. Unfortunately, up-to-date studies employ only restricted number of loci (up to two mitochondrial and six nuclear loci) and geographic sampling covers only the western and northern part of the naked mole-rats` distribution – north-eastern Ethiopia, southern Ethiopia, Kenya. Moreover, the most southern part of their sampling, the only specimens from Kenya, is represented only with *cytb* gene. For our analyses, we collect fresh tissue samples of 37 individuals from 17 localities, including new samples from Djibouti, Somaliland, and Kenya. All samples were of sufficient DNA quality for genomic sequencing method, ddRAD sequencing, giving us extensive detailed dataset virtually randomly representing the whole genome of all individuals. In addition, we use Sanger sequencing of *cytb* gene and five nuclear loci for allowing us the combination of already sequenced specimens.

Keywords: phylogeny; ddRAD; population structure; diversification; Eastern Africa

Symposium: TAXONOMY, GENETICS & CONSERVATION

Can animal personalities save human lives? Evidence for repeatable differences in activity and anxiety in african giant pouched rats (*Cricetomys ansorgei*)

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Scent-detection animals are used worldwide. The training success, and their following career, depend not only on their unique sense of smell but also on their behaviour. But current behavioural research is biased towards dogs, which are not the only scent-detection animals. APOPO, a global non-profit organisation based in Tanzania, trains giant African pouched rats (Cricetomys ansorgei) to save human lives by using their exceptional olfactory abilities. The rats are used to detect explosives in post-conflict zones and help combat tuberculosis (TB), the world's deadliest infectious disease, by sniffing out the bacteria in human sputum samples. Their detection abilities are influenced by both external (e.g., scent training) and internal (e.g., instinct) forces, such as their personality. Indeed, animal personality, or consistent behavioural differences among individuals, likely contributes to their success as scent-detection animals since it has been shown to be associated with cognition. It is, therefore, important to consider the rat's personality and related cognitive styles when determining their scent-detection task assignment, which may improve training efficiency. The first step is, however, quantifying personality traits within that species and determining how stable they are over time. In this study, we used a modified open-field test to repeatedly quantify the anxiety, exploratory, and locomotory behaviours of 25 rats over one year. Activity and anxiety were repeatable across time, suggesting consistent differences among rats, which can be considered the first demonstration of two independent personality traits in this species. Anxiety was repeatable in the long term, which is promising for further research, especially since anxiety has been linked with cognitive styles in different species.

Keywords: personality; behavioural repeatability; cognition; activity; exploration

Symposium: METHODS & APPLIED SCIENCE

Community composition of non-volant mammals along a complete elevational gradient in New Guinea: fieldwork, musea, genetics, and ecology

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Community ecology along elevational gradients presents one of the basic pillars of ecology. The issue becomes very topical in connection with climatic change influencing shifts of habitats and possible extinction due to upward migration. It is interesting especially in tropical mountains with high speciation rate in vertebrates. Among them, non-volant mammals belong amongst the worst migrators due to the combination of endothermy (and thus increased need of food intake) and lack of flight. So far, their community ecology along elevational gradients has been studied at every tropical continent except for Australo-Oceania. Therefore, we conducted a long-term study of a complete elevational gradient (25 – 3700 m asl) along Mt. Wilhelm, the highest mountain of Papua New Guinea. This largest and tallest tropical island located east of Wallace line hosts a unique assemblage of highly endemic rodents (tribes Hydromyini and Rattini), Marsupials, and Monotremes. Due to suspected cryptic diversity, we genetically barcoded all of the sampled individuals (cytochrome b or cytochrome c oxidase 1, genus-specific own designed primers) – for the first time in suchlike study. This helped us to reveal a higher diversity previously overlooked by mere morphological determinations. Moreover, we discovered new species and confirmed them also morphologically. Thus, we were able to identify more precisely the community assemblage, diversity distribution, and species turnover along the gradient in this understudied region.

Keywords: Hydromyini; Rattini; altitudinal distribution; Australo-Oceanian region; crypticity

Symposium: ECOLOGY

Invading species and their parasites: spillover of an alien nematode affects personality and reduces survival in a native species

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Spillover of alien parasites to native host species can severely impact naïve populations, conferring a competitive advantage to invading hosts that introduced them. Although such host-switching events commonly occur in biological invasions, studies demonstrating the impact of alien macroparasites on native animal hosts are few. In Europe, native red squirrels (*Sciurus vulgaris)* are replaced by introduced North American grey squirrels (*S. carolinensis*) mainly through resource competition, and, in Britain and Ireland, by competition mediated by a viral disease. In Italy such disease is absent, but spillover of an introduced North American nematode (*Strongyloides robustus*) from grey to red squirrels occurs. We used populations of native red squirrels that were colonised by the alien grey squirrel as experimental sites and compared data of red squirrel parasite infection, fitness and personality with those taken in control sites where only the native species occurred. We found negative correlations between native species' activity and infection with *S. robustus*. Moreover, individuals that acquired *S. robustus* during the study reduced their activity after infection, while this was not the case for animals that remained uninfected. We found no negative effect of the alien parasite on body mass or reproductive success of red squirrels, but intensity of infection by *S. robustus* reduced survival in both sexes. Survival of squirrels co-infected by their native nematode, *Trypanoxyuris sciuri*, was less affected by *S. robustus*, suggesting a protective effect of the native helminth against the new infection. We show that parasite-mediated competition is costly, reducing activity in individuals of the native species and that *S. robustus* spillover adds to the detrimental effects of resource competition, further reducing the fitness of the native species in the presence of the invasive competitor.

Keywords: *Strongyloides robustus; Sciurus vulgaris*; *Sciurus carolinensis*; macroparasites; parasite-mediated competition

Symposium: RODENT-BORNE DISEASES

POSTERS

17th RODENS ET SPATIUM
Valladolid, Spain 2023

Helminths of New Guinean rodents

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On New Guinea two spatially overlapping but temporally separate radiations have occurred after over-sea colonization of the island by two closely related rodent tribes, the Hydromyini (‘Old Endemics’, arrived ~ 8 mya ago) and the Rattini (‘New Endemics’, arrived ~ 2 mya ago). More recently, invasive *Rattus* species (*R. exulans and R. rattus*) have colonized the island via human dispersal. The helminth communities of these rodent species have been only partially explored and some aspects are still unknown. In this study, rodents were sampled along two altitudinal transects (2019 and 2020) covering two geologically distinct mountain ranges: The first is Mount Wilhelm, a complete elevational gradient of relatively undisturbed rainforest (from 200 m to the tree line at 3,700 m.). The second transect is in the Finisterre Range. Our sampling includes at least 15 genera of Hydromyini and at least 9 different species of *Rattus*, and the invasive species *R. exulans* and *R. rattus*. We first investigated the helminths of the caecum and colon. We provide a preliminary taxonomic and genetic characterization of these helminths and explore the distribution of helminth communities along the two altitudinal transects.

Keywords: endemic species, invasive species; parasite; rodent; altitudinal gradient

Burrow architecture of the lusitanian pine vole, *Microtus lusitanicus* in semi-natural habitats

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The Lusitanian pine vole, *Microtus lusitanicus* (Cricetidae), is a fossorial rodent endemic to the Iberian Peninsula and the south of France. Although it is not a strictly subterranean species, coming to the surface to forage and to disperse, the Lusitanian pine vole is known to build extensive underground burrow systems in which the animals live with several family members. Previous work in orchards indicated that the burrows built by this species were complex and could reach several dozen meters long. However, not much is known about the burrow structure of this species when living in more natural habitats. Here, we examined in detail the architecture of *M. lusitanicus*' burrows in a semi-natural habitat, in Sintra, Portugal. Using a differential GPS system, we mapped the burrow systems in detail (average tunnel length and depth, number of intersections, cyclic structures, openings, nests, etc), and evaluated burrow complexity in terms of its linearity, circularity, convolution and fractal dimension. Burrows varied in terms of their length (up to ~100m), area (up to ~190m^2) and depth (up to ~50cm), the system's size being positively correlated with its complexity, and with the number of structural elements present. Additionally, we found several structural elements, some never previously described for this species, namely: siphons and dam-like structures, as well as drainage and escape tunnels.

Keywords: fossorial; rodent; underground architecture; burrow complexity; burrow structural elements

Collaborative science beyond borders: the example of EUROSMALLMAMMALS initiative

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Environmental, climatic and anthropogenic modifications constantly affect worldwide ecosystems altering population and community dynamics and consequently host–parasite pairings with emergence of infectious diseases. To detect these responses and isolate the proximate causes long-term studies and retrospective spatio-temporal longitudinal studies are required. In this sense, knowledge sharing and data reuse among different ecological contexts allow to address unforeseen questions on global changes across a wide range mammalian groups, with relevance for those playing crucial especially ecological and epidemiological roles, such as small mammals. In 2019 within the umbrella project 'EUROMAMMALS' (https://euromammals.org), we have initiated a new branch specifically dedicated to small mammals, named EUROSMALLMAMMALS. The aim of this initiative is to promote collaborative open science and networking among European scientists involved in small mammal ecology, by connecting different species-specific bottom-up projects. Considering the metadata provided by the first 20 partners that joined the network as reference, we translate small mammal data collection protocols into a relational database specifically built under open-software platforms to group the data shared by the partners being thus available for new study themes. Data included all aspects covered during a small mammal study: study area characteristics, types of experimental design, local environmental and climatic data, descriptors of capture event, data derived from laboratory screening and epidemiological analyses. Before being included in the database, the shared raw data passed through quality check and harmonization process to promote reliability, robustness and data standardization. To date (December 2022) 17 partners belonging to 9 European countries joined the network. The data, spanning from 1990 to 2022, included 42158 individuals belonged to 41 small mammal species (e.g., voles, mice, glirids, lemmings and shrews) with 86606 capture events occurred in 150 study areas. We created a specific EUROSMALLMAMMALS website (https://eurosmallmammals.org/), and a mailing list (eurosmallmammals@googlegroups.com) to improve communication and networking among the partners. EUROSMALLMAMMALS collaborative initiative is constantly expanding, involving partners that cover different fields of interest within small mammal ecology. In this sense, by scaling up the knowledge from the individual to the ecosystem and by sharing data and expertise on small mammals, this initiative could give the opportunity to fill some important knowledge gaps and provide novel perspectives to evaluate the effect of global changes on species distribution, ecosystems functioning and epidemics risk.

Keywords: collaboration; database; data-sharing; Europe; small mammals

Rabbit hemorrhagic disease virus – Occurrence of both variants in rodents in the Czech Republic

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Rabbit hemorrhagic disease virus (RHDV) a lagovirus from the family Caliciviridae causes an acute and generally fatal disease in the European rabbit (*Oryctolagus cuniculus*). The origin of the virus is unknown; however, major outbreak was described in China in 1984, where the first variant was described (RHDV). By the late 1990s, outbreaks were documented in other 40 countries including the Czech Republic (CZ). The new variant - RHDV2, which first appeared in France in 2010, has been detected in the CZ since 2017. The virus is transmitted either directly by all secretions and excretions from infected rabbits, by various fomites including contaminated food, water and litter or by an insect vector - flies, fleas, mosquitoes. Birds and mammals that prey on lagomorphs may be mechanical carriers and excrete viruses in faeces after eating infected rabbits. The virus is very infectious and resistant to the environment, which facilitates its transmission. Sporadic report of both variants in the internal organs of rodents has already been reported, but how much rodents participate in the circulation of the virus in the environment is unknown. In this study, we analyzed rabbit samples suspected of RHDV infection. If the infection was confirmed, we trapped rodents in the surrounding of the affected farm. We tested 8 rabbit samples and 19 rodent samples from 2020 to 2021. In total, we obtained 4 positive samples from rodents (RHDV - *Mus musculus musculus*, RHDV2 - *Apodemus flavicolis* and two *Myodes glareolus*). Sequence analyses revealed both variants of the virus in the Highland region of the CZ. Although our results confirm that rodents can carry RHDV, their competence as a host and the direction of transmission of the virus between rodents and rabbits is still unknown. Further research, especially of the experimental type, may help us to determine whether rodents can be a reservoir for this virus.

Keywords: RHDV; lagovirus; transmission; Muridae; Cricetidae

Lymphocytic choriomeningitis virus in the European house mouse hybrid zone

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Lymphocytic choriomeningitis virus (LCMV) is a mammarenavirus that can be pathogenic to humans. Its primary host reservoir is the house mouse (Mus musculus) which explains the worldwide distribution of the virus. The house mouse is a complex of several subspecies that meet at regions of secondary contact (hybrid zones), such as the >2,500 km long and 20-30 km wide region in Europe that stretches from Scandinavia to the Black Sea and where *M. m. musculus* and *M. m. domesticus* mice have contact. Secondary host contacts are ideal places to study the limits of virus specificity for their hosts. In a recent study, while analysing samples mostly collected between 2008 and 2014 in a large transect of 16 000 km^2 across the hybrid zone of *musculus*/*domesticus* in the Bavarian/Bohemian region, we detected LCMV only in *M. m. musculus* individuals in a restricted region of 12 km^2 in the Czech Republic. LCMV was detected in some localities over a 6-year period suggesting that the virus may be endemic to some restricted localities. However, LCMV has not been detected since 2014, but sampling in the area since then has been quite limited. To determine whether LCMV is still present in this area or in other localities in the Bavarian/Bohemian secondary contact region between *musculus*/*domesticus*, we sampled mice and sympatric small mammals in May and September 2022 and screened the samples for LCMV using ELISA assays. We report the results of this screening here.

Keywords: LCMV; *Mus musculus*; secondary host contacts; mammarenavirus; Central Europe

Serologic study of tularemia infection in rodents of Castilla y León, Spain

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Francisella tularensis, a zoonotic pathogen with a broad range of hosts including humans; is the etiological agent of tularemia. Rodents have an important role in the epidemiology of the disease, which is believed to cause rapid onset, acute, and fatal infections in these animals. We carried out a serological survey to explore the disease circulation among two sympatric rodent species (*Apodemus sylvaticus* and *Microtus arvalis*) during a period of 7 years (2013-2019) in which tularemia outbreaks have occurred in the region. We compared results of DNA detection of the pathogen, anatomopathological findings and *Francisella*-antibody screening from the same individuals. Data about corporal weight, liver and spleen weight were collected during necropsies in order to determine the presence of hepatomegaly and/or splenomegaly. A commercial microagglutination kit was used to detect *F. tularensis* antibodies on the sera, and a mixture of liver and spleen tissue was tested for *Francisella spp.* using Real-Time PCR. Positive seroprevalence was only found in 4% (9/237) of sera samples, with titters equal or under 1/4. Within the animals tested, 18.6% (44/237) were positive for *F. tularensis* but none of them had any reaction in the microagglutination test. There was no relevant anatomopathological findings in the seropositive animals. However, hepatomegaly and splenomegaly were found in 3.4% (8/237) and 1.3% (3/237) of the animals, respectively, with no individuals with both anomalies. These findings suggest that there was not enough antibody development against tularemia before the animals die, probably due to their short live spam or the lethality of the disease. Further studies should focus on developing experimental infection models to be able to dive deeper into the disease development on these species and their antibody response.

Keywords: anatomopathology*;* antibodies; *Francisella tularensis*; microagglutination*;* One Health

Alexandromys oeconomus mehelyi in Slovakia – Metapopulation?

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Pannonian root vole (*Alexandromys oeconomus mehelyi*) is geographically isolated postglacial relict, present in Hungary, Slovakia and Austria. Habitats preferred by the root vole, wetlands in river valleys and humid terrain depressions, are drained, converted to croplands and separated by natural and artificial barriers. Therefore, the subspecies consist of scattered, more or less isolated local populations. Threatening factors are mainly: water scarcity, competition, agrotechnical interventions, small habitat size and the absence of their connection. During the projects aimed on practical protection of root vole in Slovakia (Conservation of root vole LIFE08 NAT/SK/000239 and Restoration of habitats for root vole **Microtus oeconomus mehelyi* LIFE17 NAT/SK/000621) in years 2010-2016 and 2019-2022 the extensive monitoring of root vole was held on about one hundred localities. We identified the features of the metapopulation structure in the occurrence of root vole in the habitat fragments. During a regular monitoring, 15 localities were intensively monitored between years 2013-2016. Although the exchange of genetic information between the fragments has already been confirmed, they are relatively isolated. In a circle, around monitored localities, with a radius of a two-day dispersal distance (approx. 1440 m) there are maximally tree suitable or already occupied localities (with maxima in the Danube inundation area). During our regular monitoring, we noted the decline of some subpopulations below a detectable level (extinction) and their subsequent restoration (recolonization). Here, the root vole shows local asynchronous interannual fluctuations, as well as different dynamics within the year. The most often repeated patterns during monitored years are: population maximum occurred in autumn (5 localities), irregular occurrence on locality (3 localities) and population maximum in spring during monitored years (2 localities). Fragments inhabited by subpopulations are of markedly different quality and size (approx 0.7-350 ha), and based on our knowledge we also assume the existence of local source-sink dynamics, and in the extreme cases of an unequlibrial metapopulation.

Keywords: root vole; Slovakia; habitat fragmentation; source-sink population

High δ^{13}c values in red squirrels *Sciurus vulgaris* explained by a reliance on conifer seeds

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Eurasian red squirrels *Sciurus vulgaris* have unusually high δ^{13}C value compared to other forest rodents. A similar pattern was found in some American squirrels. It is usually assumed that high δ^{13}C values in squirrels stem from the consumption of 13C-enriched conifer seeds. To test this hypothesis; we analyzed the hair of wild and zoo-kept red squirrels; seeds of pine and spruce; and feathers of specialized consumers of conifer seeds; crossbills *Loxia spp*.; and opportunistic consumers of conifer seeds; woodpeckers *Dendrocopos major*. Data on the isotopic composition of hair or feathers of other species of forest rodents and birds were obtained from published studies. The range of mean δ^{13}C values of hair of wild forest rodents (19 species) exceeded 10 ‰. All squirrel species had high 13C content; *S. vulgaris* having maximum δ^{13}C values. In contrast; *S. vulgaris* kept in captivity had an isotopic composition similar to other captive rodents. The feathers of crossbills were enriched in 13C compared to other forest birds (15 species); while seeds of coniferous trees often had higher δ^{13}C values compared to seeds of other woody plants. We conclude that high δ^{13}C values of hair (and bone collagen) of S. vulgaris are associated primarily with feeding on conifer seeds; although some patterns in the δ^{15}N values have not been fully elucidated. Distinctiveness of the isotope composition of mammals and birds feeding on the seeds of coniferous trees suggest that this resource can be traced through the entire forest food web.

Keywords: food web; stable isotopes; isotopic outliers; conifer seeds; seasonal variation

Helminth fauna of mouse-like rodents in the city of Moscow

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Urban environmental conditions significantly influence the ecology of animals, including their level of parasitic load. The response of the helminth community of small mammals to ecological imbalances and their adaptation to life in the urban environment remain an urgent problem in ecology. In this study, we aimed to compare the species diversity and distribution of helminths of rodents in urban forest parks with varying degrees of anthropogenic pressure. In urbanized areas of five locations of the city of Moscow, the parameters of infestation of model rodent species were assessed in comparison with a natural, slightly disturbed area (the Chernogolovka scientific and experimental base). The gastrointestinal tract was removed from individuals of the four most common rodent species (n = 158), *Apodemus agrarius, Sylvaemus uralensis, Microtus arvalis*, and *Clethrionomys glareolus*, which were caught using snap traps, followed by the determination of their number and their species identification and assessment of infestation by three parameters. The species composition of helminths and the presence of three parasite classes in the helminth fauna of the studied species predictably corresponded to the characteristics of the disturbed areas. In addition, a succession of the dominant helminth species (*H. polygyrus* for *H. spumosa*) has been recorded, which indicates a significant effect of the helminth fauna of synanthropic species on the composition of parasite communities in wild rodent species living in the city. Our study contributes to the accumulation of information about the species composition of endoparasite communities in mouse-like rodents in the city of Moscow, which is important for compiling an up-to-date epidemiological picture of the urban environments.

Keywords: urbanization; parasite community; *Apodemus agrarius; endoparasites;* helminth biodiversity

Mandible variation in the dwarf fat-tailed jerboa, *Pygeretmus pumilio* (Rodentia: Dipodidae)

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A dwarf fat-tailed jerboa (*Pygeretmus pumilio* (Kerr, 1792)) is a small bipedal ricochet rodent from semideserts and clay deserts of southeastern Europe and Central Asia. It is abundant and polytypic, with five recognized subspecies. The geographic range covers ca. 5350 km in longitude and ca. 1750 km in latitude. Phenotypic plasticity of the mandible of *P. pumilio* was explored with geometric morphometric methods in relation to subspecific taxonomy and desert environment constraints. We studied 283 mandibles from 29 geographical localities grouped into 22 populations from most of the species distribution area. The unguided K-means clustering on mandible shape partitioned populations into two clusters, corresponding to the western and eastern groups of populations. These clusters nearly perfectly matched the two subspecies groups (*pumilio* and *potanini* groups) recognized in an independent study based on the morphology of the glans penis. Mandible size varied with geographic position and demonstrated a strong, nonlinear longitudinal pattern. Moreover, size was associated with several climatic variables but not with soil properties or with proxies for primary productivity. Mandible shape varied clinally along the longitudinal transect and the pattern was affected more by temperature than by precipitation. Our results suggest that the mandible, although under environmental pressure, has retained a sufficient amount of taxonomic information to retrieve grouping closely resembling those derived from a sexually selective trait. We recommend morphometrics of the mandible as a routine step in addressing variations in mammals at species and subspecies levels. We conclude that the success of the dwarf fat-tailed jerboa in occupying an extensive geographic range relies on its ability to meet environmental heterogeneity through cohesive and diverse responses, including physiology, behaviour, lifehistory traits, and morphological plasticity.

Keywords: desert ecology; ecomorphology; geometric morphometrics; longitudinal cline; subspecies

Phylogenetic structuring in skull variation of *Apodemus* species (Rodentia: Muridae)

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We studied phenetic and phylogenetic relationships among *Apodemus* species of the Western Paleartic region. The sample comprised eight filed mice species from three subgenera *Sylvaemus* (*A. alpicola*, *A. flavicollis*, *A. sylvaticus*, *A. uralensis*, *A. witherbyi*), *Karstomys* (*A. epimelas*, *A. mystacinus*) and *Apodemus* (*A. agrarius*). Two species were each represented by two geographically distinct populations, *A. flavicollis* from Slovenia and Türkiye in Asia, and *A. uralensis* from the Czech Republic and Türkiye. The study of skull variation with geometric morphometric methods included the ventral cranium, mandible and upper molars. The analyzed skull structures were the largest in *A. mystacinus* and *A. epimelas* and the smallest in *A. uralensis*. The most distinctive in the mandible shape were *A. mystacinus*, *A. epimelas, A. alpicola* and *A. agrarius*. *Apodemus mystacinus*, *A. epimelas* and *A. alpicola* showed most unique cranium shape *while A. agrarius* was the most distinct in the molar shape. Mapping the geometric morphometric data to a phylogenetic tree of *Apodemus* species based on mtDNA cytochrome *b* sequences showed a phylogenetic signal in size variation in all the studied skull structures. The presence of a phylogenetic signal in shape variation was recorded for the mandible and molars. For the cranium, the permutation test showed the absence of a phylogenetic structure in shape variation. These results confirm the idea that different skull structures have diverse developmental pathways and different functional roles and respond differently to phylogenetic constraints and selective pressures. Nevertheless, contrary to the expectations, the cranial shape variation of the studied *Apodemus* species did not contain phylogenetic structuring.

Keywords: *Sylvaemus; Karstomys*; cranium; geometric morphometrics; mandible; molars

Abundance and diversity of rodents under different degrees of agricultural intensification in South-Eastern Europe

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The agricultural landscape of south-eastern Europe is undergoing a series of changes as result of the adoption of the European Union's Common Agricultural Policy. In this context, we are witnessing on the one hand an intensification of agriculture and on the other an increase in abandoned agricultural areas, aspects that may influence rodent species composition and abundance. Here, we document variations in rodent communities associated with crop fields and adjacent non-agricultural lands in landscapes of varying degrees of agricultural intensification. Rodent trapping using capture-mark-recapture method (CMR), was conducted in four zones with different level of farming intensity. The differences in community composition and abundance of rodent species under different degrees of agricultural intensification, among habitat types and over time were tested using Analysis of Variance (ANOVA) and Tukey Honestly Significant Difference (HSD) post-hoc tests. The dominant species were the striped field mouse (*Apodemus agrarius*), wood mouse (*Apodemus sylvaticus*) and field mouse (*Microtus arvalis*). The highest species diversity, richness and abundance were observed in habitats that provide long-term vegetation cover, such as dykes, canals, fallows or hedgerows. Community composition and abundance depended on the degree of agricultural intensification, habitat type and season. In general, stable habitats supported the most abundant and diverse small mammal communities and as such they have high biodiversity value.

Keywords: agricultural management biodiversity, land-use change, *Apodemus agrarius, Microtus arvalis, Apodemus sylvaticus*

Effects of individual genetic variation and ecological factors on individual growth rates in a wood land rodent

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In this communication, we used an intensively studied population of wood mouse (*Apodemus sylvaticus*) at Silwood Park (Imperial College London, UK) to test the effects of individual level factors and environmental effects on individual growth rate. We include data from 242 male and female individually pit-tagged mice covering a total of more than 6 years of intensive monitoring effort. We recorded mouse weight during bi-weekly trapping sessions. Individual genetic variation was measured using homozygosity by locus, MLH and mean d^2. Regarding extrinsic factors we also tested the effects of intraspecific and interspecific competition, as well as an index of predation risk (as measured by habitat use of protective structures in the landscape) on growth rate. We did so controlling for the effects of individual body condition and ectoparasite load. Finally, we also tested for the effects of abiotic factors such as mean temperature, rainfall and the growing season during which the mice were growing on individual growth rates. We discuss the relative contribution of extrinsic versus intrinsic factors determining a key life history trait with implications across the lifespan.

Keywords: inbreeding; homozygosity by locus; mean temperature; season; *Apodemus sylvaticus*

Association between anthropization and rodent reservoirs of zoonotic pathogens in Northwestern Mexico

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The world is facing a stage of ecological and social changes that may favour the risk of zoonotic outbreaks. Anthropization has been proposed to be one of the main socio-ecological phenomena that promotes the emergence of zoonoses by modifying the host community structure and favouring the increase of pathogen reservoirs and the contact rate between these reservoirs and humans. Among all mammalian reservoirs of zoonotic pathogens, rodents (*Rodentia*) have been suggested to be the most resilient to anthropization. In this study, we evaluated whether anthropization increase or decrease the richness and abundance of reservoir and non-reservoir rodents at a regional scale in Northwestern Mexico. To do this, we first conducted a rodent monitoring and identified species previously reported as reservoirs of directly transmitted zoonotic pathogens; then, we developed an Anthropization Index to rate the anthropization degree of each study site in the region; and finally, we analyzed the statistical association between richness and abundance of rodent reservoirs and non-reservoirs with the anthropization degree. We captured a total of 683 rodents corresponding to 27 species of 14 genera, of which nine species have been identified as reservoirs of zoonotic pathogens (359 individuals, 53%). We found a significant positive association between anthropization and zoonotic reservoirs abundance ($p<0.01$). When we individually analyzed *M. musculus* and *P. maniculatus*, two reservoirs previously reported and the most significant species in this survey, the association was positive and negative ($p<0.01$ and $p=0.04$, respectively). The abundance and richness of non-reservoir species had a negative relationship with anthropization ($p<0.01$), while reservoir richness was positive but non-significant ($p=0.25$). These findings are in accordance with other studies indicating that reservoir species of zoonotic pathogens tend to increase their abundance in disturbed environments, which may increase the risk of pathogen exposure to humans.

Keywords: *Mus musculus*; *Peromyscus maniculatus*; richness; abundance; Principal Component Analysis

Comparing sign surveys and owl pellet analysis for detecting Cabrera voles at large spatial scales

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The monitoring of rare, threatened or endemic species that are targeted by international agreements is needed for conservation management and policy purposes. The context of monitoring depends largely on the scale at which population trends are to be considered, influencing the choice of sampling methods. When the focus is on regional or national levels, most important challenges relate to the high logistic and field efforts necessary to achieve a reliable result, particularly when using direct sampling methods such as life-trapping. In the case of rodents, sign surveys and owl pellet analyses are among the non-invasive methods most often used for population monitoring over large scales. However, it is still largely unknown how efficient each of these techniques might be when sampling and monitoring particular target species. Here, we addressed this issue, focusing on the Cabrera vole (*Microtus cabrerae*), a threatened small mammal, listed in the Habitats Directive (Annexes II and IV), hence requiring regular evaluation of its population status and trends. We sampled 56 grids (10×10 km^2) in central and southern Portugal using (whenever possible) both sampling techniques, and then estimated and compared the detection probability of the species from sign surveys and owl pellet analysis, using detection-occupancy models. Results provided evidence for a greater effectiveness of sign surveys compared to owl pellet analysis for detecting the species, suggesting that large-scale population monitoring of Cabrera voles may fairly rely on sign surveys alone, with owl pellet analysis providing a less effective and more costly alternative. Therefore, while owl pellet analysis is generally considered a valuable option for detecting and monitoring multiple small mammal species in a region, our study emphasises the need to use other complementary methods for certain species, in order to increase their detectability and improve the assessment of their population status and trends.

Keywords: biodiversity conservation; cost-effective sampling; grid-based surveys; detection-occupancy model; population monitoring

Rodents in the updated Portuguese mammal red book

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Red Books are essential tools for efficient management of species and habitats at a regional or global level, providing key information on the rate of biodiversity loss over time. In the previous revision of the Red Book of Vertebrates from Portugal (2005), 24% of the 75 species of marine and terrestrial mammals analyzed were listed as threatened. Rodents were the group including more species classified as *Least Concern* (LC) (82%), with only 9% of the *taxa* considered threatened and 9% categorized as *Data Deficient* (DD). The project 'Review of the Red Book of Mammals in mainland Portugal and contribution to the evaluation of their conservation status' (2021) aimed to fill previous information gaps and to reassess species category of threat, in order to improve conservation measures. Regarding rodents, over the period between the last and present evaluation (from 2005 to 2021), there was an overall increased risk of extinction, with about 33.3% of the species evaluated being classified as threatened or near threatened. The water vole *Arvicola sapidus*, the Cabrera vole *Microtus cabrerae* and the Portuguese field vole *Microtus rozianus* were classified as *Vulnerable* (VU) and the garden dormouse *Eliomys quercinus* was considered *Near Threatened* (NT). Two species were classified as DD, meaning that more information is required for an accurate assessment, the European snow vole *Chionomys nivalis*, a recent new species for Portugal, and the common vole *Microtus arvalis*, previously not evaluated. The percentage of LC species dropped to 50%. Overall, comparing both assessments, rodents were among the mammal groups for which increased knowledge allowed to fill more information gaps, leading to a significant decrease in the number of species classified as DD. At the same time, the percentage of threatened species has increased, pointing out the need of regular population monitoring and the implementation of selected conservation measures.

Keywords: extinction risk; IUCN categories; regional evaluation; rodent conservation; threatened species

Unmanned Aerial Systems (UAS) imagery for the automatic detection of burrows of the common vole

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The common vole (*Microtus arvalis* Pallas 1778) is a cricetid rodent that finds its primary habitats in meadows, field edges and alfalfa plots. However, during periods of population outbreaks, they spread out, invading and colonizing other suboptimal habitats, such as cultivated areas of cereals, legumes, rapeseed, sunflower, etc. For this reason, this species is considered one of the most damaging pests in agricultural systems in the Mediterranean regions. Usually, common vole monitoring is carried out through laborious field work, based on trapping and/or observation of signs of the pest's presence (droppings, activity in burrows, vegetation clipping, etc.). However, remote technologies, particularly those based on images captured with Unmanned Aerial Systems (UAS), commonly known as drones, provide a spatial resolution high enough to extract reliable results on common vole activity in a specific area. The present work provides an alternative based on UAS and different airborne sensors (RGB and multispectral) to detect common vole burrows in an agricultural field. A field campaign was carried out in October 2021 on an agricultural plot highly affected by these rodents, located in the municipality of Villalón de Campos (Valladolid, Spain). Different data acquisition protocols were evaluated, depending on the equipment used, flight altitude and image processing algorithm. Overall, the results showed a good performance of the different studied methodologies, with an accuracy rate of more than 60% in all cases. It was the Support Vector Machine (SVM) the one that exhibited better results in the object-oriented classification process, regardless the flight height. The results of this research can provide a new tool for its application in monitoring the abundance of vole populations and its co-evolution with the affectation or damage to crops.

Keywords: rodent pest; object-oriented classification; *Microtus arvalis*; drones; airborne data

Detection of zoonotic *Babesia microti* strain in rodents from different habitats of Lithuania

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Small rodents are natural reservoir hosts of various pathogens, including *Babesia microti* (Aconoidasida: Piroplasmida), an emerging tick-borne parasite. Worldwide, zoonotic and non-zoonotic *B. microti* strains have been identified in rodents. However, the distribution of *B. microti* in Europe is insufficiently characterized. This study aimed to investigate the prevalence of *Babesia* parasites in different species of small rodents collected in Lithuania and to characterize the detected *Babesia* strains using partial sequencing of the 18S rRNA gene. A total of 1180 rodents were trapped in 19 locations of different habitats in the western and eastern parts of Lithuania by using live or snap traps. DNA was extracted from rodent spleens. *Babesia* DNA was detected in 2.8% of rodents. Infected rodents were trapped in nine sampling locations. The species-based differences in the prevalence of *Babesia* parasites were significant, with the highest prevalence found in *Microtus oeconomus* (14.5%) and *Microtus agrestis* (7.1%) followed by *Clethrionomys glareolus* (2.3%), *Apodemus flavicollis* (2.2%) and *Micromys minutus* (1.3%). A higher prevalence of *Babesia* parasites was detected in rodents trapped in the meadow (5.67%) than in the ecotone (1.69%) and forest (0.31%). The sequence analysis of the partial 18S rRNA gene reveals that *Babesia* isolates were 99–100% identical to the human pathogenic *Babesia microti* Jena/Germany strain. Our findings show that small rodents, especially *Microtus* voles, are involved in the circulation of the zoonotic *B. microti* Jena/Germany strain in Lithuania. This study also is the first report documenting *Babesia* infection in *M. minutus*. Funding: Part of this research is funded by the European Social Fund under the Nr. 09.3.3-LMT-K-712-09-0270 “Development of Competences of Scientists, other Researchers and Students through Practical Research Activities” measure.

Keywords: mice, voles, Babesia parasites, 18S rRNA gene

Phylogeography of *Heterakis spumosa* (Nematoda, Heterakidae) in Southeast Asia

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The helminth *Heterakis spumosa* (Nematoda, Heterakidae) is a parasite of rodents, mainly reported across the world in the invasive black rat *Rattus rattus*, the brown rat *Rattus norvegicus*, and the house mouse *Mus musculus*. The origin of this parasite is in Asia and, according to literature, this helminth species is widespread in Southeast Asia (SEA) parasitizing in several rodent species of the Subfamily Murinae. In the present study, we analyzed these nematode specimens obtained from several localities in Thailand and Lao PDR. The worms were isolated from a variety of murine rodent genera, i.e., *Bandicota*, *Berylmys*, *Cannomys*, *Mus* and *Rattus*. In addition, the representative nematode specimens from the localities out of the original range of *H. spumosa* were obtained from the invasive rodent species, *R. norvegicus* and *Mus domesticus*. PCR primers were designed using sequences available in GenBank to obtain species-specific primers for the mitochondrial cytochrome oxidase subunit1 gene (mtCOI) and the genus-specific primers for ribosomal internal transcribed spacer1 gene (ITS1). Our results showed the genetic structure and phylogeographical pattern of this parasite species across all the surveyed localities.

Keywords: invasive species; helminth; rodent; Murinae; mtCOI; ITS1

Rodent helminth community in ecological succession systems during post-mining restoration

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Successional events have been key to understanding how the composition of wild communities varies, tending to occur after key landscape change events. Within this framework, open-pit mining is one of the human activities that generates the greatest change in the landscape, so it is necessary to evaluate the composition of wild communities in the affected area. We analyzed the composition of the helminth community in an open-pit mining area in the Czech Republic through the 5 years of study within 4 different environments (meadow, wetland, coniferous forest, and deciduous forest), in both post mining as well as in adjacent control plots. The sampling allowed the capture of different rodent species, these were used to analyze the presence of the different helminth species, prevalences and abundances of helminths, differences on life cycles of worms in the studied successional stages. The evaluation of the helminth community and the comparison between both types of areas may allow to assess whether the succession of newly created ecosystems is moving towards the state of the adjacent biotopes, which were not directly affected by mining; and thus, whether the restoration process of post-mining plots is successful.

Keywords: biodiversity; Czech Republic; open-pit mining; parasite; succession

Hymenolepidids in Southeast Asian murine rodents

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Hymenolepiasis is a worldwide parasitosis of humans caused by the rat tapeworm (*Hymenolepis diminuta*) and the dwarf tapeworm (*Rodentolepis nana*). Murine rodents, particularly the invasive and synanthropic species (e.g., *Rattus rattus*-complex, *Rattus norvegicus*, *Rattus exulans*) are recognized as the main hosts. The presence of both zoonotic cestode species has been reported in Southeast Asia in agricultural landscapes and urbanized areas with species determination largely based on morphology. To date, there is very limited molecular data on Hymenolepididae from this region. In the case of *H. diminuta*, the absence of scolex hooks, a taxonomic diagnostic character, makes its specific determination difficult. In addition, diagnosis of *R. nana* remains challenging despite the presence of hooks on the scolex. A long-term study in SEA of helminth infection in rodents from this region allowed us to obtain a representative collection of hymenolepidids for molecular characterization. These cestode specimens, originating from a variety of Murinae rodent species and captured from several localities in Cambodia, Lao PDR, Philippines, Thailand and Vietnam, were studied based on morphological and molecular data (mitochondrial cytochrome oxidase subunit 1 and 28S rRNA markers). Our study refines the taxonomy of these hymenolepidid cestodes.

Keywords: invasive species; helminth; rodent; Murinae; mtCOI; 28S

Seasonal changes in small mammal abundance and in their ectoparasites in agricultural and riparian habitats from northeastern Spain

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Small mammals are key components in most ecosystems and, consequently, ecosystem characteristics shape small mammal communities. Agricultural and riparian habitats are profoundly modified by agricultural practices, crop phenology, and river dynamic, affecting small mammals. Here we show the initial results of monitoring a small mammal community in a Mediterranean region from northeastern Spain comparing cultivated and riparian habitats along Ebro River (Zaragoza). In 2022, 519 animals were live captured 4-times a year (winter, spring, summer, and autumn) in two habitats (agricultural and riparian) with 4800 traps night. Data of species, sex, weight, age and ectoparasite occurrence (fleas, ticks, and mites) were recorded from each individual. The small mammal community was composed of three species: *Apodemus sylvaticus* (26.3%), *Mus spretus* (52.9%) and *Crocidura russula* (18.2%), showing marked differences in their abundances between seasons and habitats. *M. spretus* was the main species in cultivated habitats, showing a peak of abundance in autumn (abundance index, AI=20.04), while in riparian habitats, *A. sylvaticus* was the dominant species, with the highest records in spring (AI=6.12). GLMs with family binomial were used to test if overall ectoparasites prevalence in the host community was dependent on host species, season, and habitat. Dead animals were excluded. *M. spretus* occurrence increased ectoparasite prevalence in the small mammal community. Separated models were also tested for each group of ectoparasites. Overall flea prevalence increased in riparian habitats, while it decreased with *M. spretus* occurrence, in summer and winter. Overall tick prevalence increased in summer and with *M. spretus* occurrence, while it decreased in autumn and with *C. russula* occurrence. Finally, overall mite prevalence increased with *M. spretus* occurrence and in winter, decreasing in summer and in riparian habitats. Future monitoring will allow us to know long-term small mammal response to changes in habitat characteristics, parasite infestation, disease transmission and climate variables.

Keywords: dynamic habitats; Mediterranean region; monitoring; population dynamic; species abundance

Geographical Information Systems-based insights of a large, long-term database of common vole abundance in Castilla y León (Spain)

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The common vole (*Microtus arvalis* Pallas 1778) shows cyclical population outbreaks ranging approximately from 2 to 5 years, although temporal and spatial patterns of its behaviour remain unclear. This species is present in Castilla y León (the largest Spanish region), having detected in recent decades recurrent episodes associated with risk situations in agricultural areas and damage to crops. In this work, an extensive database of 10 years of a common vole abundance index (VAI) monitored in alfalfa fields was analysed (13,262 observations along 2,921 plots within Castilla y León, comprising an area of more than 90,000 km^2 wide). To examine the potential spatial and temporal patterns of the VAI expression, we propose a Geographical Information System (GIS)-based analysis using the so-called HotSpot tool, which is able to identify significant spatial clusters of high values of the variable. The results reveal that common vole abundance is not spatially random distributed but a spatially clustered process, with a significance level of 99%. The northern of Valladolid, southern of Palencia and north eastern of Zamora provinces stand out as their clear accumulation of VAI hotspots. The temporal pattern highlighted years 2012, 2014, 2016 and 2019 as the most affected, with higher incidence of hotspots in the summer and fall seasons. The investigation of the relationship between those affected regions and their specific climatic, ecologic, agronomic and topographic characteristics is underway.

Keywords: rodent pest; *Microtus arvalis*; hotspots; GIS

The effect of elevation on the community and population structure of small mammals in mountain forests

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The most diverse mammalian group, terrestrial small mammals have been the subject of numerous ecological studies. Given their adaptability and the high rate of speciation, small mammals can be found worldwide in variety of habitats. Elevation is one of the most impactful gradients shaping their community structure and species abundance. Most studies on the effect of elevation on small mammal communities have been carried out in tropical areas. In Europe, this topic has been approached less often. Consequently, the scarcity of research has prompted us to address this topic, aiming to test the (1) effect of elevation on small mammal species composition and abundance, (2) yearly changes in community structure and the (3) combined effect of year and elevation, (4) influence of elevation on the population structure (sex ratio and age structure) in dominant rodents. We conducted a two-year survey in the Cindrel Mountains, Romania. The study area (500 - 1850 m elevation) covered four habitat types: oak, mixed oak-beech and spruce forests, and timberline. Live-trapping of small mammals was conducted in autumn, in 8 stations, 2 in each type of habitat, in 8 x 8 trapping grids, with traps checked for 3 consecutive days. We had 286 capture events of 234 individuals belonging to 6 species. The most abundant species were the yellow-necked mouse (*Apodemus flavicollis*) and the bank vole (*Clethrionomys glareolus*) in 2021 and the yellow-necked mouse in 2022. The other species were captured just once. In 2021, the total abundance of the small mammal community increased with elevation, with *A. flavicollis* having decreased ratios within the community along the gradient. *C. glareolus* showed an opposite pattern. In 2022, the overall abundance was much lower. Our results reveal how the elevational gradient and the interaction between space and time shape small mammal community structure.

Keywords: elevational gradient; species composition and abundance; Carpathian Mountains; forest habitats; rodents

Detection of *Borrelia* pathogens in small mammals and their ticks in Lithuania

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Borrelia spp. are Gram-negative spirochaetes transmitted by ticks that cause Lyme borreliosis and tick-borne relapsing fever. Small mammals are important reservoir hosts for *Borrelia* pathogens. The aim of our study was to investigate the presence of *Borrelia* spp. in small mammals and their ticks. A total of 149 small mammals belonged to seven species (*Apodemus flavicollis*, *Microtus arvalis*, *Microtus oeconomus*, *Clethrionomys glareolus, Micromys minutus*, *Sorex araneus* and *Sorex minutus*) were captured in the Curonian Spit of Lithuania. Ticks were carefully removed from the rodents, identified morphologically and using molecular methods. In total, 800 ticks (673 *Ixodes ricinus* and 127 *Dermacentor reticulatus*) were collected. Urine bladders samples of small mammals and ticks were analysed for the presence of *Borrelia* DNA using real-time PCR, conventional and nested PCR targeting 16S rRNA, outer surface protein A (ospA) genes and 16S-23S intergenic spacer region. *Borrelia* species and strains were determined using sequence analysis of the ospA gene and 16S-23S intergenic spacer region. *Borrelia* DNA was detected in 4.7 % of examined urine bladders, 11.8% *D. reticulatus* and 7.7% *I. ricinus* samples. Sequence analysis revealed the presence of *Borrelia afzelii* and *Borrelia miyamotoi* in *M. arvalis* and *M. oeconomus* rodents and both tick species. This study is the first report documenting the presence of *B. afzelii* and *B. miyamotoi* DNA in *D. reticulatus* ticks from small rodents in Lithuania.

Keywords: rodents; *Ixodes ricinus; Dermacentor reticulatus; Borrelia afzelii; Borrelia miyamotoi*

Population outbreak of fossorial water voles in NW uplands of Spain: consequences and management

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The presence of fossorial water voles, *Arvicola scherman*, in pastures and orchards can lead to significant agricultural losses due to its feeding and activity. In 2019, a population outbreak was recorded in Lugo (Galicia, NW Spain), affecting 8 municipalities and more than 3,000 plots. Damage of between 40% - 90% of the harvest has been registered in almost 1,700 declared hectares, and economic losses exceed half a million euros. A decrease in ploughed land (3,996 ha) and forests (11,375 ha), and an increase of plots devoted to mowing instead of grazing (4,921 ha) in the last decade seem to be key factors. In autumn 2020, the SERIDA and the Xunta de Galicia started a demographic study and an integrated management program of these populations. Demographic densities were registered in autumn 2021 and 2022 across the whole affected area. In this way, a variation in vole abundance was observed in most plots associated with a spatial spreading during this time. Despite the patchy landscape and relatively low percentage of suitable habitats (30.12%), colonisations processes have led to a recent 80% increase in the distribution range of fossorial water voles in Lugo. Integrated control of this species included promotion of natural enemies, snap traps, barriers, habitat disturbance (studded roller prototype) and zinc phosphide application (double truck dispenser prototype) with landowner key participation. A total of 151 landowners participated with traps gathering 20,352 individuals so far. However, due to the large number of people who should necessarily be involved and the lack of coordination between them, the measures taken were generally ineffective during this population peak. Ultimately, fossorial water vole multiannual cycle in abundance should be characterized for this geographic area to synchronize coordinated control measures with the initial low-density phase of population growth.

Keywords: crop damage; distribution range; integrated pest management; multiannual cycle; vole pest

Variations in the reproductive cycle of fossorial water voles according to different environmental conditions in the Iberian Peninsula

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Rodents living at temperate areas typically use day length as the main factor to adapt reproductive cycle to seasonal changes. However, breeding regulation is unclear in those species influenced by different local environmental conditions across the same latitude. This is the case of fossorial water voles, *Arvicola scherman*, an agricultural rodent pest that occur discontinuously in the northern fringe of the Iberian Peninsula, from the sea level up to 2,000 m.a.s.l. In this research we compiled data on testis length (TL) and seminal vesicle length (SVL) in mature males, and the percentage of pregnant females from three populations separated more than 150 km each other and located at different altitudes: 0 – 600 m.a.s.l. (Asturias); 700 – 900 m.a.s.l. (Pyrenees); 900 – 1300 m.a.s.l. (Ancares mountains). Monthly rainfall, temperatures and daylength were registered for each location throughout the corresponding study period. A continuous breeding was observed at low altitude (Asturian population) with no seasonal differences in the percentage of pregnant females. Conversely, significant ($p < 0.05$) and nearly significant ($p = 0.06$) seasonal differences were observed in the Pyrenean and the Ancares populations, respectively. The Pyrenean population stopped breeding in winter, whereas the Ancares one also decreased its breeding activity in summer, presumably associated with a period of drought. Day length and temperature, which showed high autocorrelation, had a positive influence on mean TL, mean SVL and the percentage of pregnant females in the Pyrenean population. This percentage was also positively correlated with rainfall in the Asturian population. However, neither the percentage of pregnant females nor the mean TL correlated with environmental conditions in the Ancares population. Results indicate that in the Iberian Peninsula fossorial water voles may display variations in the reproductive cycle according to local environmental condictions regardless the effect of day length.

Keywords: Altitude; breeding characteristics; climate; day length; vole pest

The fossorial water vole as a potential reservoir for *Borrelia burgdorferi* sensu lato

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Borrelia burgdorferi, causal agent of Lyme disease, is a Gram-negative bacterium that can be transmitted to humans by tick bites. Rodents are considered potential reservoirs for some *Borrelia* genospecies and hosts of different blood-sucking ectoparasites. Sampling on rodents could be a suitable method for this pathogen surveillance, especially in those species which can reach high population densities. In that sense, the potential role in the transmission cycle of *Borrelia* is little known in fossorial water voles (*Arvicola scherman*) an overabundant vole species in agroecosystems of western Europe. The aim of this study was to determine *B. burgdorferi* sensu lato prevalence in this species during two different population outbreaks in neighbouring regions from NW Spain. A total of 144 fossorial water voles gathered during 2021-2022 (57 from Asturias and 87 from Galicia) were necropsied and their ectoparasites were collected. DNA from pinna samples was extracted with commercial kits and PCR-screened for the presence of *B. burgdorferi* s.l. (*flaB* gene). Since the pathogenicity level may vary among different *Borrelia* genospecies, positive samples were sequenced for their identification and phylogenetic analysis. *Borrelia burgdorferi* s.l. was detected in 4.86% (7/144) of the samples. Sequences analysis showed different *Borrelia* genospecies for each region: *Borrelia lusitaniae* in Galician specimens (5/7, 71.42%) and *Borrelia afzelii* in Asturian ones (2/7, 28.57%). No ticks but Laelapids (31/144, 21.52%) and fleas (21/144, 14.60%) were found on these fossorial water voles. These results complement those formerly obtained in other municipalities in Asturias, showing that *B. afzelii* is present in different fossorial water vole populations across this region. To our knowledge, the infection by *B. lusitaniae* genospecies in fossorial water voles is first reported here. Further studies are needed to unravel the role of non-tick vectors in *Borrelia* transmission and the current health threat in both geographic areas.

Keywords: *Arvicola scherman*; ectoparasites; PCR; vector-borne pathogen; zoonosis

high prevalence of endoparasites during a fossorial water vole outbreak in NW Spain

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The fossorial water vole, *Arvicola scherman*, is considered a key intermediate host of *Echinococcus multilocularis*, *Taenia taeniformis* and *Toxoplasma gondii* in western Europe. These parasites can infect many endothermic vertebrates, including humans, especially whether their host reach high population densities. In 2019, a population outbreak was recorded in uplands of 8 municipalities of Lugo (Galicia, NW Spain), where the interaction between wild animals, livestock and humans is high. We analysed 296 fossorial water voles gathered during 2021 and 2022. Careful examination was performed at the opening of thoracic and peritoneal cavities, and organs, in particular the liver, were attentively examined. Metacestodes were collected and identified by morphological characteristics and by sequencing the *rrn*S gene in case of doubt. Brain, masseter muscle and heart tissues of seventeen winter specimens were histologically processed and stained with haematoxylin and eosin and then coccidian cysts were identified using a microscope. Six histological sections at two levels (twelve in total) were examined in each brain. Macroscopic liver lesions were observed in 38 of 296 dissected specimens, with an overall percentage of *T. taeniformis* of 15.2% (range between municipalities: 34.8 - 7.4%). Its incidence was maximum in winter and minimum in summer, and neither the body length, related with age, nor the sex was determinant. No cysts morphologically compatible with *Toxoplasma* were found in masseter muscle, liver, or heart. Conversely, high prevalence of these cysts (46.7%) was observed in brain tissues, with a very high infection (presence of cysts in all histological sections) in 20% of specimens. These preliminary results have revealed fossorial water voles are probably important in the transmission of these parasites that use predator-prey interactions in NW Spain. As cats are potential definitive hosts, domestic cats may easily increase the risk of human infection with these parasites in this area.

Keywords: *Arvicola scherman*; health risk; parasites; vole pest; zoonosis

Living on the edge: morphology and personality of red squirrels in marginal habitat

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Local environmental conditions that characterize a specific habitat can influence both behavior and morphology of species, which can result in habitat-dependent phenotypic differences among animals living in heterogeneous environments. Here, we studied three populations of Eurasian red squirrels (*Sciurus vulgaris*) in alpine study areas: one living in a marginal high-elevation habitat at the edge of the species' altitudinal distribution, and two occurring in higher-quality habitats (based on average seed-crop size and annual fluctuations in seed production). We investigated whether squirrels living in the marginal area differed in 2 morphological parameters (body size and body mass) and/or in the expression of 4 personality traits (activity, exploration, activity-exploration, and social tendency) estimated with an open field test and a mirror image stimulation test. Furthermore, we calculated whether the within-individual variance of the personality traits (behavioral plasticity) was higher in the marginal habitat. We found that male squirrels were smaller and lighter in the edge habitat, a relationship that was less marked among females, suggesting differential selective pressures among sexes in the marginal habitat than in the other two populations. Furthermore, personality differed in squirrels living in the edge habitat, which showed higher activity, exploration and sociability scores, than individuals in higher-quality habitats. In accordance with previous studies, the non-random distribution of individuals' personality traits between heterogeneous areas suggests that squirrels chose the habitat that best fits their personality. In this study this seems associated with the advantage that these traits confer in acquiring resources. Moreover, in contrast to our predictions, we found smaller behavioral plasticity in the marginal habitat, but only for the trait exploration. This study provides information about the role of personality in habitat selection and how variation in habitat quality can shape morphological adaptations and influence differences in behavioral plasticity among populations.

Keywords: *Sciurus vulgaris*; phenotype; behavioral plasticity; heterogeneous environments; alpine populations

Spatial behaviour of farm dwelling Norway rats treated with an anticoagulant rodenticide

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Norway rats (*Rattus norvegicus*) cause damage to stored food and infrastructure and transmit zoonotic pathogens. Therefore, rats are managed, often with anticoagulant rodenticides (ARs). ARs are easy to use and effective but bio-accumulative and persistent and can be transferred along food chains. Little is known about spatial behaviour of wild Norway rats and how the consumption of ARs affects spatial behaviour. In a replicated field study on livestock farms the AR brodifacoum (BR) was delivered to rats by oral gavage or free fed bait presented in bait stations. Rats were radio-collared to monitor spatial behaviour. BR residues in rat liver tissue were analysed using liquid chromatography coupled with tandem mass spectrometry. Norway rats that consumed BR preferred the same habitat as untreated control rats but there was a decrease in distances moved and in home range size of treated rats that set in rapidly. None of the 71 BR-treated rats left the area where they were radio-collared. None of them was removed by predators but predatory birds killed three of 16 untreated control rats. 92% of rats that succumbed to BR died in well-hidden locations, where removal by scavenging birds and most terrestrial scavengers is unlikely. Rats that ingested bait from bait stations had 65% higher residue concentrations in liver tissues than rats that died from dosing with a two-fold LD_{50} BR solution but individual residues were highly variable. The results indicate a minor role of poisoned rats in the transfer of BR into the food chain via predators and scavengers but secondary exposure of these non-target species is evident. The risk of transferring ARs to food chains could be minimized by using additives inducing a stop-feeding effect, the optimization of pulse baiting strategies, bait stations that exclude non-target species and the advancement of best practice measures including non-chemical alternatives.

Keywords: brodifacoum; home range; non-target exposure; *Rattus norvegicus*; rodent management

Sex differences in hematological and hepatic parameters in *Gerbillus tarabuli*

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The aim of this study is to determine the sexual dimorphism of biological parameters (hematological and hepatic) in *Gerbillus tarabuli*. We used 25 adult gerbils freshly captured in the Algerian Sahara desert during the breeding period and divided into 13 males and 12 females. The gerbils are kept in the laboratory facility under a photoperiod of 12hL :12hD, and a temperature varying between 22 to 24°C and subjected to a specific diet. After the sacrifice carried out by decapitation, the whole blood is collected into EDTA tubes for the hematological and transaminases analytes and into heparin tubes for alkaline phosphatase assay. Livers and other organs are fixed in formalin for further study. The numerical blood formula (NFS) was carried out by a "mindray-bc-30-auto-hematology-analyzer-500x500" automatic device and transaminases and alkaline phosphatases by colorimetric assay. The results revealed the presence of a sexual dimorphism in favor of the female for the weight of the liver and in favor of the male in most hematological parameters with exception to lymphocytes more numerous in the female, It is interesting to note, that the mean corpuscular hemoglobin concentrations and the monocytes do not exhibit dimorphism. For hepatic markers (transaminases and alkaline phosphatase), the dimorphism is in favor of the female. As a result, it appears that the weight parameters (body weight and liver weight) and the haematological and hepatic parameters are sensitive to male and female sex hormones in *Gerbillus tarabuli*

Keywords: *Gerbillus tarabuli*; sexual dimorphism; NFS; transaminases; alkaline phosphatase

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