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Abstracts of the 18th *Rodens et Spatium* – International Conference on Rodent Biology

Rodents (order Rodentia) are the most diverse mammalian group, crucial for ecosystem health through dispersing seeds, aerating soil, and serving as primary prey for predators. They function as ecological engineers and keystone species, although some species act as significant pests and disease vectors (e.g., plague, leptospirosis) to humans.

The *Rodens et Spatium* conferences started in France in 1987, under the title 'Le rongeur et l'espace'. In 1993, at its 4th edition held in Poland, the conference became international. Ever since, the conference has been organised, 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), the Czech Republic (15th 2016), Germany (16th 2018), and Spain (17th 2023). The next – the 18th – edition of the conference will for the first time be held in Kaunas, Lithuania, from 18 to 22 May 2026. Its main purpose is to bring together researchers, scientists, veterinarians, ecologists, and other experts to exchange knowledge and the latest research in the fields of rodent biology, ecology, medicine, and care, as well as to promote interdisciplinary collaboration and seek solutions to current challenges involving rodents.

At the 18th *Rodens et Spatium*, over 80 participants from the Baltic countries, Belgium, Brazil, Canada, the Czech Republic, Ethiopia, France, Germany, Israel, Italy, Luxembourg, Poland, Republic of South Africa, Scandinavia, Serbia, Singapore, Slovakia, Spain, Switzerland, Tanzania, Turkey, the United Kingdom, United States of America took the opportunity to exchange ideas, views, and knowledge about rodents biology, their impact on human and ecosystem, and the development of effective strategies for monitoring, prevention, and control. The most important research results shared at the 18th *Rodens et Spatium* are presented here in 77 abstracts, including three plenary talks, 49 oral presentations, and 25 poster presentations.

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Algimantas Paulauskas
Editor-in-Chief

Plenary presentations

DETECTING CHANGE BEFORE IT MATTERS: LESSONS FROM LONG-TERM SMALL MAMMAL COMMUNITIES

Linas Balčiauskas
State Scientific Research Institute Nature Research Centre, Vilnius, Lithuania
Email: linas.balciauskas@gamtc.lt

Ecological change is often framed in terms of endpoints such as species extinctions, invasions, population crashes, or ecosystem collapse. Yet across much of the temperate world, ecosystems remain stable despite decades of climatic, land-use, and anthropogenic pressures [1]. This raises a question: what forms of ecological change occur before they become visible, and how can they be detected in time to matter?

In this presentation, I synthesise decades of standardised data on small mammals from a mid-latitude European country to show that the most important ecological transitions are hidden, gradual, and internal; they unfold at biological levels that are rarely monitored [2]. Rather than focusing on population abundance or species richness alone, this presentation integrates individual condition, morphology, diet, dominance structure, genetics, and pathogens. Together, these layers reveal a consistent pattern: ecosystems can reorganise profoundly without collapsing, so abundance-based monitoring underestimates the tempo and depth of change.

In Lithuania, small mammals occur in a climatically moderate, human-dominated landscape, which is neither pristine nor extreme. Precisely for this reason, they capture subtle change early. Over 50 years of trapping across different habitats shows that stability and invasion can occur simultaneously. Some species persist with little change for decades [3], while others quietly expand and become dominant without obvious demographic explosions [4].

Expansion does not necessarily imply success. Range expansion fronts may be genetically fragile, while communities undergoing long-term change simplify: species richness declines, dominance increases, and functional redundancy erodes, even as total abundance often remains stable. This creates a powerful illusion of resilience [2].

The strongest early-warning signals emerge at the level of traits. The body condition responds to environmental stress earlier and more clearly than population size. Fitness declines often precede demographic change [5]. Morphological shifts, including body size reduction, occur without population loss and increasingly override classical eco-geographic rules. Dietary plasticity differentiates winners from losers: generalist species capable of decoupling diet from habitat thrive in disturbed systems, while specialists, particularly insectivores, decline early through bottom-up trophic filtering.

Human-modified systems play a central and counterintuitive role. Agricultural landscapes, orchards, colonies of nutrient-transporting birds, and commensal habitats are not degraded but productive and selective ecosystems. Nutrient pulses and disturbance rapidly restructure food webs, while maintaining high biomass. Commensal environments can act as refugia, buffering climate variability, yet simultaneously concentrate ecological and epidemiological risk.

Parasites and pathogens provide a final integrative perspective. Disease dynamics are structured primarily by dominance and trophic connectivity, not species richness. Across the system, zoonotic risk tracks dominant hosts and landscape connectivity, particularly hydrology.

Together, these findings support a set of general principles: ecological change begins in individuals before populations respond; fitness erodes before abundance; dominance hides vulnerability; disturbance simplifies small mammal communities before degrading them; traits and parasites respond faster than demography; range edges and human landscapes reveal change first. The broader implication is that long-term ecology is not about predicting collapse but about identifying the signals that matter early enough to understand change and respond before it becomes irreversible.

Keywords: long-term ecological change, small mammal communities, early-warning signals, trait-based ecology, illusion of resilience

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LONG-TERM DYNAMICS OF MULTISPECIES ARVICOLINE COMMUNITY IN NORTHERN LAPLAND

Heikki Henttonen

Natural Resources Institute Finland, Helsinki, Finland

Email: HeikkiHenttonen@luke.fi

Dynamics of voles and lemmings in Finland have been monitored for decades. I will first briefly cover some patterns at the whole-country level. Then I will concentrate more on the long-term research in Lapland. Fluctuations there have been monitored at Kilpisjärvi since the late 1940s and at Pallasjärvi since 1970 [1]. A drastic change in the population dynamics took place in the mid and late 1980s. The earlier 'beautiful' cycles turned to primarily seasonal dynamics [2]. However, after a 'noncyclic' period of 25 years, recently the cycle has returned! These patterns also included drastic changes in the species composition of arvicoline communities (five vole and two lemming species). In the cyclic times, the deepest crash phase was synchronous in all sympatric species. The disappearance and return of the cycle took place quite simultaneously in a large geographic area in northern Fennoscandia. Cyclic times are characterised by large geographic synchrony, while during noncyclic times geographic synchrony is weaker. Synchronous events are indicative of climatic factors; climate change affecting the snow structure and subnivean space [3]. However, different species react in different ways: some change from cyclic to seasonal dynamics, some decline to low densities for a long period. I emphasise the community approach: following the whole arvicoline community helps to understand the roles of various species for cyclic events.

Keywords: voles, lemmings, population dynamics, northern Fennoscandia, Lapland

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FROM RODENT POPULATION DYNAMICS TO ZOONOTIC RISK: A MULTI-SCALE ECO-EPIDEMIOLOGICAL APPROACH IN EUROPE

Valentina Tagliapietra*, Daniele Arnoldi, Francesca Dagostin, Giulia Ferrari, Giovanni Marini, Fausta Rosso, Annapaola Rizzoli

Fondazione Edmund Mach, Research and Innovation Center, San Michele a/A (TN), Italy

** Corresponding author. Email: valentina.tagliapietra@fmach.it*

Global biodiversity loss, habitat fragmentation, and climate change are significantly reshaping the landscape of public health in Europe through the disruption of the natural transmission cycles of rodent-borne zoonotic pathogens, including tick-borne encephalitis virus (TBEV), hantaviruses, and arenaviruses. A multi-scale One Health approach integrates individual host traits with predictions of human risk, from local to broad European spatial patterns. A key role in these complex dynamics is played by rodent populations, largely governed by bottom-up factors such as climate and food availability. Resilient generalist species such as the bank vole (*Clethrionomys glareolus*) and the yellow-necked mouse (*Apodemus flavicollis*) play pivotal roles in driving these dynamics across latitudes. While northern rodent populations follow multiannual cycles, southern European populations exhibit dramatic, mast-driven outbreaks linked to tree seed production and resource availability [1]. These population fluctuations are also statistically predictable using specific climatic drivers. For instance, warmer summers occurring two years prior correlate with population peaks, whereas autumnal precipitations in the preceding year serve as a limiting factor [2].

At the local level, the transmission of tick- and rodent-borne pathogens is often regulated through specific interactions among key hosts. In the case of TBE, the virus spreads effectively through non-viraemic co-feeding [3]central and eastern Europe, Russia and the Far East, with considerable altitudinal and latitudinal shifts described during recent decades. The reported routes of transmission for TBE virus include the saliva-activated non-viraemic transmission between co-feeding ticks taking place on rodent hosts. During the period 2001–2014, a population of the yellow-necked mouse (Apodemus flavicollis, a mechanism where infected and uninfected ticks exchange the pathogen while simultaneously feeding on the same rodent host. The presence of larger animals, such as deer, introduces a further layer of complexity. Ungulates act as tick amplifiers by providing necessary blood meals for reproduction, yet they simultaneously serve as pathogen dilution hosts, as they are incompetent to transmit the virus back to the ticks. This effect is highly scale-dependent, meaning that the local density of deer can either exacerbate or mitigate the risk of infection [4]. Directly transmitted viruses, such as arenaviruses (e.g., lymphocytic choriomeningitis virus) and hantaviruses, spread horizontally through density-dependent mechanisms. The transmission is primarily driven by aggressive encounters between older males, making these pathogens highly susceptible to stochastic fadeouts if host density thresholds are not maintained. This vulnerability highlights the fragility of viral persistence during low phases of rodent population [5].

At regional and continental scales, pathogen risk can be forecasted by integrating various ecological and environmental indicators. Factors such as habitat richness indices, host community composition (specifically deer and rodents), and specific climatic variables serve as robust predictors for TBE occurrence [6–7]. Furthermore, a biological indicator for tree masting, the airborne pollen abundance, acts as a particularly innovative proxy for TBE risk. Monitoring of pollen levels enables the prediction of human TBE risk with a significant two-year lag time [8].

An effective One Health strategy must harness together these multiscale ecological complex threads, from individual scale events to continental climatic trends. Transitioning from reactive monitoring to proactive early warning systems allows for effective anticipation of zoonotic spill over events before they impact human populations.

Keywords: rodent dynamics, One Health, ecological predictors, zoonotic pathogens

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Oral Presentations

SPATIOTEMPORAL DRIVERS OF SMALL MAMMAL COMMUNITY ASSEMBLY IN AN AFROALPINE ‘SKY-ISLAND’ ECOSYSTEM

Birara Abraham[1, 2, 3*], Abdul A. S. Katakweba[4], Alfan A. Rija[1]
[1] Department of Wildlife Management, Sokoine University of Agriculture, Morogoro, Tanzania
[2] Department of Biology, Mekelle University, Mekelle, Ethiopia
[3] African Centre of Excellence for Innovative Rodent Pest Management and Biosensor Technology, Sokoine University of Agriculture, Morogoro, Tanzania
[4] Institute of Pest Management, Sokoine University of Agriculture, Morogoro, Tanzania
** Corresponding author. Email: abraham.birara@mu.edu.et / adesalegn2@gmail.com*

Afroalpine ecosystems function as isolated ‘sky-islands’, harbouring unique vertebrate assemblages highly vulnerable to environmental change. While foundational work has described the spatial and temporal dynamics of rodent communities in other systems [1] and recent studies have advanced the taxonomic and biogeographic understanding of Ethiopia’s small mammals [2–3], the hierarchical interplay of these drivers in structuring Afroalpine assemblages remains poorly quantified. We dissected these drivers in the Guassa Menz Community Conservation Area, an Afroalpine plateau in the Ethiopian highlands characterised by a fine-scale mosaic of five distinct habitats and a strong tri-modal seasonal climate. Using a fully factorial, stratified design across habitats and seasons (dry, early dry, wet), we conducted standardised live-trapping (33,750 trap-nights) to document the rodent population. We analysed patterns of abundance, alpha diversity (Shannon-Wiener index) and beta-diversity (Bray-Curtis dissimilarity) using multivariate and redundancy analyses, building upon frameworks used to understand elevational diversity patterns [4–5]. Our results reveal a hierarchical assembly process. First, the habitat structure acted as the primary spatial filter, with complex *Helichrysum* shrubland supporting significantly higher alpha diversity than simplified habitats like plantation forest. Second, seasonality was the dominant temporal modulator, driving synchronised landscape-wide fluctuations in rodent abundance (peak capture success in wet season) but leaving core species composition within habitats unchanged, mirroring patterns observed in other arid-adapted small mammal communities [1]. Third, a sharp hydrological gradient defined a critical environmental barrier: the permanently saturated swamp grassland hosted a compositionally distinct rodent assemblage driven by specialist species (*Otomys typus*, *Arvicanthis abyssinicus*) and was the paramount source of beta-diversity across the landscape. The community was numerically dominated by a generalist core (*Lophuromys flavopunctatus*, *Stenocephalemys* spp.) across upland habitats, a finding consistent with the regional species pool described by Bryja et al. (2019) [2]. We conclude that rodent community assembly in this Afroalpine ecosystem is governed by a persistent template of habitat heterogeneity, upon which climatic seasonality superimposes abundance dynamics, with edaphic thresholds creating definitive turnover. These findings provide a mechanistic framework for understanding vertebrate community assembly in insular ecosystems and identify critical environmental filters that maintain gamma diversity in sky-islands worldwide.

Keywords: community assembly, Ethiopian highlands, habitat filtering, Rodentia, sky-island ecosystems

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PREVALENCE AND MOLECULAR CHARACTERISATION OF *MYCOPLASMA* SPP. INFECTION AMONG POLISH BANK VOLES. INSIGHTS INTO *MYCOPLASMA* GENETIC DIVERSITY

Mohammed Alsarraf[1*], Dorota Dwużnik-Szarek[1], Mustafa Alsarraf[2], Dagmara Wężyk[1], Wiktoria Romanek[1], Maciej Grzybek[3], Joanna Górska[3], Martyna Krupińska[3], Aleksander Goll[3], Jolanta Behnke-Borowczyk[4], Jerzy Behnke[5], Anna Bajer[1]

[1] *Department of Eco-Epidemiology of Parasitic Diseases, Faculty of Biology, University of Warsaw, Warsaw, Poland*

[2] *Department of Microbiology, Molecular Genetics and Genomics, Centre for Advanced Materials and Technologies, CEZAMAT, Warsaw, Poland*

[3] *Department of Tropical Parasitology, Medical University of Gdańsk, Gdynia, Poland*

[4] *Department of Forest Entomology and Pathology, Faculty of Forestry and Wood Technology, Poznań University of Life Sciences, Poznań, Poland*

[5] *School of Life Sciences, University of Nottingham, Nottingham, UK*

** Corresponding author. Email: m.al-sarraf3@uw.edu.pl*

Haemotropic mycoplasmas, known as haemoplasmas, are widespread bacteria that adhere to the surface of mammalian erythrocytes and can induce varying levels of haemolytic anemia, particularly in hosts with compromised immunity [1–2]. This study investigated the prevalence and genetic diversity of *Mycoplasma* spp. in bank voles *Clethrionomys glareolus* in Poland.

Between 1999 and 2022, a total of 1,514 rodents were captured across three forested sites in the Mazurian Lake district. *Mycoplasma* spp. infections were identified through microscopic examination of stained blood smears (200 fields of view) and by PCR amplification and sequencing of a 600 bp fragment of the 16S rRNA gene. Additional *Mycoplasma* spp. sequences were obtained from *Apodemus flavicollis* (n = 8), *A. sylvaticus* (n = 1), and *A. agrarius* (n = 5).

The overall prevalence of *Mycoplasma* spp. was 66.4%. Phylogenetic analyses revealed multiple *Mycoplasma* spp. lineages, including strains closely related to those previously detected in small rodents such as *Akodon montensis* from Brazil, as well as potentially novel genotypes unique to Polish rodent populations. These results highlight the ecological diversity of *Mycoplasma* spp. in wild rodents in Poland and raise important questions regarding their impact on wildlife health and their possible zoonotic significance. This study documents the high prevalence and substantial genetic diversity of *Mycoplasma* spp. in *C. glareolus* across several decades and locations in the Mazurian Lake district. The detection of both known and potentially new *Mycoplasma* spp. lineages underscores the complex ecology of these bacteria in wild rodent reservoirs. Continued monitoring and molecular characterisation of *Mycoplasma* spp. in wildlife are essential, particularly considering their potential relevance for animal health and zoonotic transmission.

Keywords: *Mycoplasma* spp., *Clethrionomys glareolus*, prevalence, genetic diversity, Poland

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ANALYSIS OF CRANIAL AND MANDIBULAR MORPHOLOGICAL DIVERSITY IN *NANNOSPALAX* SP. (2N = 60) NF VARIANTS USING 3D GEOMETRIC MORPHOMETRICS

Ömer Faruk Arslan[1]*, Ferhat Matur[1], Marko Djurakic[2], Mustafa Sözen[3]

[1] Dokuz Eylul University, Faculty of science, Department of Biology, İzmir, Türkiye
[2] University of Novi Sad, Faculty of Sciences, Department of Biology and Ecology, Novi Sad, Serbia
[3] Zonguldak Bülent Ecevit University, Faculty of Science, Department of Biology, Zonguldak, Türkiye
** Corresponding author. Email: farukarslan.v@gmail.com*

The blind mole rat (*Nannospalax*) represents a unique evolutionary model characterised by high chromosomal polymorphism (specifically diverse cytotypes) but notable morphological convergence in skeletal elements. The 2n = 60 chromosomal form, which is widely distributed across Türkiye, exhibits remarkable variation in the fundamental number of chromosomal arms (NF). Previous studies utilising traditional morphometric measurements have remained limited in differentiating this cytotype. This study aims to analyse the cranial and mandibular variation within 2n = 60 cytotype using high-resolution 3D geometric morphometric methods. In order to infer correspondence between phenotypic (size and shape) and chromosomal variation, we employed Procrustes ANOVA, canonical variate analysis (CVA), and multivariate regression (allometry tests). Procrustes ANOVA results showed that NF variants significantly differed in both cranial and mandibular shape, while centroid size showed no significant difference across NF groups for either structure. As these findings suggest the phenotypic variation in *Nannospalax* 2n = 60 is dominantly structured across shape space rather than size, it may explain the insufficiency of traditional morphometrics in previous studies [1–3]. Regarding sexual dimorphism, a significant difference was observed only in the mandibular shape, while no sexual shape dimorphism was detected in the cranium. The absence of dimorphism

in the cranium compared to its presence in the mandible suggests that these two structures evolved under different selection pressures. The mandibular variation is largely shaped by biomechanical demands for 'chisel-tooth' digging function [2–4]. Serving as the functional unit for transmitting forces and overcoming soil resistance, the mandible shows higher adaptive diversification than the cranium, which appears to be more conservative. These findings suggest that NF variants represent distinct cryptic species, underscoring the necessity of 3D morphological data for *Nannospalax* taxonomic revisions.

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Keywords: *Nannospalax*, 3D geometric morphometrics, 2n = 60, NF, cryptic speciation

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REASSESSING THE DIVERSITY AND DISTRIBUTION OF AFRICAN ROPE SQUIRRELS IN THE CONGO BASIN

Pascal Baelo[1‡], Léa Fourchault[2, 3‡], Ann Ceulemans[4], Nicolas Laurent[2, 5], Claude Mande[6, 7], Anne Laudisoit[6], Nicaise Amundala[6], Ganiyat Temidayo Saliu[2], Herwig Leirs[6], Guy-Crispin Gembu[1, 7], Martine Peeters[8], Audrey Lacroix[8], Simon-Pierre Ndimbo Kumugo[9], Eddy Kinganda Lusamaki[9], Meris Matondo Kuamfumu[9], Steve Ahuka[9], Sophie Gryseels[2, 6], Jan Hulselmans[6], Erik Verheyen[2, 6‡], Joachim Mariën[4, 6*‡]

[1] Biodiversity surveillance centre, University of Kisangani, Kisangani City, Democratic Republic of Congo
[2] Vertebrate Group, Directorate Taxonomy and Phylogeny, Royal Belgian Institute of Natural Sciences, Brussels, Belgium
[3] Systems Ecology and Resource Management, Free University of Brussels, Brussels, Belgium
[4] Department of Biomedical Sciences – Virus Ecology, Institute of Tropical Medicine, Antwerp, Belgium
[5] Department of Environmental Sciences, Open Universiteit, Heerlen, The Netherlands
[6] Evolutionary Ecology Group, Department of Biology, University of Antwerp, Antwerp, Belgium
[7] Faculty of Science, University of Kisangani, Kisangani, Kisangani City, Democratic Republic of the Congo
[8] Institute of Research for Development, Montpellier, France
[9] National Institute for Biomedical Research, Kinshasa, France
** Corresponding author. Email: jmarien@itg.be*
‡Equal contribution of coauthors

Rope squirrels (*Funisciurus*) have been suggested as important hosts of mpox virus, which causes recurrent outbreaks in Central Africa [1]. Yet the taxonomy, phylogeny, distribution, and ecology of sub-Saharan tree squirrels remain poorly resolved, limiting our ability to identify reservoir species and define their ranges [2]. Here, we clarify the diversity and biogeography of *Funisciurus* Trouessart, 1880 across the Congo Basin and evaluate their relevance for mpox ecology. We assembled the most comprehensive genetic and morphometric dataset to date ($N = 488$), spanning a large portion of the geographic and taxonomic range of the group. Integrating craniometrics with mitochondrial and nuclear markers, we recovered six major lineages: *Funisciurus anerythrus* (comprising four sublineages); two genetically and morphologically distinct, sympatric taxa that resemble *Funisciurus* cf. *bayonii*; a lineage attributable to *Funisciurus pyrrhopus akka* de Winton, 1895; and one previously undescribed taxon. Based on craniometric data only, we also delineated a species that looks like *Funisciurus cf. congicus*. Mapping lineage distributions revealed the Congo and Kasaï Rivers as major biogeographic barriers, consistent with river-driven diversification in Central African forests. Finally, we generated three whole genomes of mpox virus from *Funisciurus* specimens, providing direct evidence that rope squirrels are mpox virus hosts and reinforcing their role as likely reservoirs.

Keywords: mpox virus, Democratic Republic of Congo, squirrels, reservoir

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USING GENOME-WIDE SNPs TO UNDERSTAND GENETIC DIVERSITY AND THE POPULATION GENETICS OF AFRICAN GIANT POUCHED RATS (*CRICETOMYS* SPP.)

Allan A. Baino[1, 2*], Cynthia D. Fast[5], Rhodes H. Makundi[4], Daniel P. Bray[1], Rodrigo Vega[3], Steven R. Belmain[1]

[1] Natural Resources Institute, University of Greenwich, Chatham Maritime, Kent, UK

[2] Institute of Pest Management, Sokoine University of Agriculture, Morogoro, Tanzania

[3] School of Psychology and Life Sciences, Canterbury Christ Church University, Kent, UK

[4] African Centre of Excellence for Innovative Rodent Pest Management and Biosensor Technology Development, Institute of Pest Management, Sokoine University of Agriculture, Morogoro, Tanzania

[5] Anti-Personnel Landmines Detection Product Development (APOPO) Training Research Centre, Sokoine University of Agriculture, Morogoro, Tanzania

** Corresponding author. Email: allanbaino69@gmail.com*

African giant pouched rats (*Cricetomys* spp.) are one of the world's largest rodents of importance to human welfare as disease reservoirs, source of bushmeat and biosensors in programmes to detect land mines [1], tuberculosis [2] and illegally traded wildlife [3]. Continuation of their role as biosensors is contingent on the availability of genetically healthy and diverse stock populations from the wild, which could be under threat from unregulated bushmeat consumption. This study sets out to elucidate the genetic diversity of captive and wild populations of pouched rats using genome-wide single nucleotide polymorphisms (SNPs). A DNA sequencing library (ddRAD) comprising 108 pouched rat samples was sequenced on a NovaSeq X series system to generate 624,950,206 reads. Common bioinformatic tools were used to call 626,004 SNP genotypes that were filtered down to a high confidence dataset of 2,762 SNP genotypes. Genotypes were analysed with various population genetics and statistical packages in R to inform genetic diversity. As anticipated, we found wild populations of pouched rats to be more differentiated and genetically diverse (F_{ST} and H_e) compared to the captive population. Despite elevated levels of inbreeding (F_{IS}) across populations, computed levels of genetic relatedness for individuals across populations (unadjusted AJK statistic) were low. No signals of selection were detected but, surprisingly, SNP genotypes unique to individuals were found in the two groups of captive pouched rats. Coupled with partially sequenced cytochrome b ~ 756 bp, analyses suggested the presence of a third lineage of *Cricetomys* in Tanzania (*C. sp*2), one additional instance from two lineages initially described to be present in southern Africa by the IUCN and the work by Olayemi et al., 2012 [4]. Our study presents the first ever SNP genotype profiles for an understudied small mammal of sub-Saharan Africa and its implications for conservation management and captive breeding for continued use in biosensor training.

Keywords: small mammals, rodents, ddRAD sequencing, SNP genotyping, molecular ecology

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ALTERNATIVE LIFE-HISTORY TACTICS IN BODY MASS DYNAMICS INFLUENCE WINTER SURVIVAL IN THE ROOT VOLE

Kamil A. Bartoń[1]*, Zbigniew Borowski[2]

[1] *Institute of Nature Conservation, Polish Academy of Sciences, Kraków, Poland*

[2] *Department of Forest Ecology, Forest Research Institute, Sękocin Stary, Poland*

* *Corresponding author. Email: kbarton@iop.krakow.pl*

Body mass in small rodents is highly dynamic, varying in response to environmental seasonality and intrinsic factors such as sex and age cohort [1]. Within a single population, individuals may adopt alternative tactics characterised by distinct trajectories of body mass change [2]. We examined whether these tactics influence overwinter survival in populations of the root

vole (*Microtus oeconomus*) in temperate grasslands. Using capture-mark-recapture data with multiple sampling throughout the year, we quantified individual body mass trajectories and identified distinct patterns of seasonal mass change using latent class models. We then related these trajectories to survival probabilities during the critical winter period. We found that individuals reducing their body mass prior to winter exhibited higher overwinter survival than those maintaining higher body mass. This suggests that pre-winter mass reduction may represent an adaptive tactic, potentially lowering energetic demands or predation risk under winter conditions [3]. Our results demonstrate that within-population variation in life-history tactics can shape demographic outcomes during seasonal bottlenecks. Accounting for individual heterogeneity in body mass dynamics may therefore be essential for understanding the dynamics of small rodent populations in seasonal environments.

Keywords: voles, life-history, body mass, winter survival, population structure

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RODENTS IN THE GREEN ZONE OF RIGA

Anton Basovs*, Tanya Zorenko

Department of Zoology and Animal Ecology, University of Latvia, Riga, Latvia

** Corresponding author. Email: bullsquid59@gmail.com*

Of 21 Latvian rodent species, 13 were found in Riga [1]. Of these, synanthropic brown rats, the house mouse, and the muskrat are allochtonous. Other species are autochthonous and native to local biotopes. Riga is a large city with an extensive green area. We assume that forest parks, meadows, and other green spaces, combined with rivers, form a single green-blue complex of natural ecosystems. Based on the data collected between 2000 and 2014, most species maintain ecological stability in their habitat preferences. The bank vole lives exclusively in forest parks (37%), while the yellow-necked mouse is recorded less frequently (12.5%). Since forest communities alternate with meadow biotopes in forest parks, they are home to the striped field mouse (20%) and the common vole (17%). The composition of species in each biotope is constant. The striped field mouse inhabits all biotopes of the city and is the dominant species in the green zone (42.2%), followed by the common vole (29%). The striped field mouse dominates the shelterbelt along railways (74.5%), while other rodents account for 2–3.9%. Also, this species is dominant along the banks of bodies of water (75.6%). Synanthropic species are primarily found in built-up areas. Along railways, house mice account for 5.9% of the captured animals, while brown rats account for 2%. The banks of water bodies, especially rivers, as well as the rights-of-way along railways are becoming an important ‘green corridor’ for the dispersal of rodents. The settlement of the Daugava islands by field mice and common voles occurred before their artificial formation about 300 years

ago. We monitored rodent species in the green zone based on ecological criteria: species diversity, abundance, and formation of interspecific associations. The next step is molecular and morphological analysis to assess genetic diversity and to determine if the urban environmental stress affects rodents' mandible shape.

Keywords: urban ecology, urban green zone, small rodents

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RESPONSES OF MONTANE RODENTS' ABUNDANCE AND COMMUNITY COMPOSITION TO PRESENT AND PAST WEATHER

Ana Maria Benedek[1]*, Marius-Victor Bîrsan[2]

[1] *Faculty of Sciences, Lucian Blaga University of Sibiu, Sibiu, Romania*

[2] *Institute of Geography, Romanian Academy, Bucharest, Romania*

* *Corresponding author. Email: ana.benedek@ulbsibiu.ro*

Rodents show a strong response to weather, which is one of the main factors shaping their dynamics [1]. We evaluated the effects of past and present weather on rodent abundance and community composition, using trapping data collected between 2000 and 2008 in the Southern Carpathian Mountains (Romania). For each sampling site, we used the interpolated seasonal rainfall and mean temperature in the trapping year and each of the three years before. We assumed that meteorological conditions in the year of survey would have both a direct and an indirect effect on rodent abundance, whereas the past weather would have an indirect effect, mediated through tree masting, with seed production influenced by conditions of up to two years before [2]. Thus, we hypothesised that (1) species and community abundance respond to both present and past meteorological conditions, (2) responses to past weather are strongest in the seed specialist *Apodemus flavicollis* (yellow-necked mouse) and weaker in the more herbivorous *Clethrionomys glareolus* (bank vole), (3) if meteorological conditions were not favourable for masting, rodent populations are expected to be low, therefore their density will be little affected by the past and more by synchronous weather; in contrast, if weather favours masting, population densities depend on past conditions and these responses would be stronger in the seed specialist *A. flavicollis*, (4) because conifer seeds have low nutritive value [3], we expected the responses to past weather be stronger in beech- compared to spruce-dominated forests. Our results confirmed the first three hypotheses. However, contrary to expectations, the response of *A. flavicollis* abundance was significant only in spruce forests. Overall, *A. flavicollis* had a positive response to temperature and negative to precipitations, warm and dry summers being often cited as preceeding mast years [4]. These responses would favour the abundance of yellow-necked mouse in the context of climate change.

Keywords: climate change impacts, spatio-temporal patterns, direct and indirect effect, *Apodemus flavicollis*, *Clethrionomys glareolus*

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TRAPPED IN THE CITY: GENETIC ISOLATION OF SMALL RODENTS IN THE URBAN FORESTS OF BELGRADE

Jelena Blagojević*, Aleksa Rončević, Ivana Budinski, Marija Rajičić, Mladen Vujošević, Milan Miljević, Branka Bajić

Department of Genetic Research, Institute for Biological Research 'Siniša Stanković' National Institute of the Republic of Serbia, University of Belgrade, Belgrade, Serbia

** Corresponding author. Email: jelena.blagojevic@ibiss.bg.ac.rs*

Urbanisation is a defining feature of contemporary global social transformation, drastically altering natural landscapes and reshaping the interactions between humans and wildlife [1]. In the context of rapid urban development and environmental change, understanding the genetic consequences of urban fragmentation on native fauna is essential for promoting urban biodiversity and sustainable green planning. This study investigates the genetic structure of the yellow-necked mouse, *Apodemus flavicollis*, the most common small mammal in European woodlands, within the ruminant forest fragments of the city. Using microsatellite markers, we analysed the genetic diversity and connectivity of populations in isolated urban forests and compared them with populations from larger, geographically distinct natural habitats in the surrounding region.

Our findings reveal that urban populations of *A. flavicollis* are highly genetically differentiated from one another and their peri-urban and rural counterparts. The observed genetic structuring indicates limited gene flow between forest fragments, suggesting that roads, buildings, and other urban infrastructures act as significant barriers to movement. These results indicate the existence of 'urban genetic islands' within Belgrade, where small mammal populations are effectively trapped, increasing their risk of inbreeding, reduced adaptive potential, and long-term decline.

The consequences of this fragmentation extend beyond biodiversity loss. Urban green spaces support ecosystem services essential to human health, including air purification, temperature regulation, and psychological well-being. Ensuring the genetic connectivity of urban wildlife populations is thus critical not only for conservation but also for building healthier and more resilient cities.

Future city planning should prioritise the development and implementation of green corridors and ecological networks to reconnect fragmented habitats across urban landscapes. These initiatives would support wildlife movement and gene flow, thereby preserving native biodiversity, enhancing ecosystem resilience, and advancing the broader vision of sustainable urban living in the face of global social and environmental change.

Keywords: genetic diversity, native species, forest fragments

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HOW DO BIRDS OF PREY AFFECT THE VOLE POPULATION? A PREDATION EXCLUSION EXPERIMENT IN A TEMPERATE MEADOW

Zbigniew Borowski[1*], **Kamil A. Bartoń**[2]
[1] Department of Forest Ecology, Forest Research Institute, Sękocin Stary, Poland
[2] Institute of Nature Conservation, Polish Academy of Sciences, Kraków, Poland
** Corresponding author. Email: z.borowski@ibles.waw.pl*

Birds of prey are thought to have a strong impact on small rodent populations and their dynamics throughout the year, particularly in winter, which is a key period for individual survival [1–3]. Unlike the impact of mammalian predators, the impact of birds of prey is underexplored [4]. To fill this gap, we conducted a field experiment in a temperate grassland, in which we excluded bird predation in populations of the root vole (*Microtus oeconomus*) throughout the year. We covered open plots in three locations with netting and used capture-mark-recapture method to estimate the effect of this treatment on vole survival and population size, accounting for body mass and sex of individuals. We found that avian predation exclusion increased vole survival in winter and spring (November–May). Survival of voles with bird predation was up to 22% lower than in plots with no bird access and was not sex-selective, but heavier voles showed reduced overwinter survival. This research adds to our knowledge of the causes of winter vole population collapses by showing that bird predation has the greatest impact on vole survival and abundance during the winter-spring period, even under persistent snow cover. Our results highlight how seasonal predation may be altered by climate-driven changes in snow conditions and vegetation phenology.

Keywords: voles, population dynamics, winter survival, avian predation, population structure

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INTEGRATING METAVIROMIC DATA INTO THE INFECTIOUS DISEASE DYNAMICS MODELLING PIPELINE OF RODENT POPULATION DYNAMICS

Ioana Bouros*, Jayna Raghawani
The Royal Veterinary College, London, UK
** Corresponding author. Email: ibouros@rvc.ac.uk*

Most emerging viral zoonotic diseases originate from wild animal reservoirs. However, unlike for most human pathogens, we often have little to no knowledge of the viruses circulating within wildlife populations or their transmission dynamics, even for well-known zoonotic viruses. This gap greatly limits our ability to predict outbreaks and design effective interventions. As sequencing becomes cheaper and more efficient, metagenomics makes it easier to more readily characterise virus diversity and abundance within individual samples. Here, we explore how we can use these rich data to inform general population dynamics and robustly determine long-term epidemic trajectories in wild rodent populations living in variable environments.

Semi-quantitative measures that are intrinsically linked to time since infections and/or pathogen load, such as seroprevalence and quantitative PCR (qPCR) data, have been successfully used to infer epidemic dynamics. Viral read counts from metaviromic data also reflect sample viral loads, suggesting that these approaches could be extended to study multiple viruses simultaneously, even in poorly understood host–virus systems, transforming our ability to investigate transmission dynamics in wildlife populations. We started developing an inference framework to estimate epidemic dynamics directly from metaviromic read counts [1], and our preliminary results using simulated epidemic data indicate that this approach produces reliable results even under complex infection dynamics, including seasonal or a precipitation-dependent birth rate, as observed in many wild rodent ecosystems.

Future research will focus on assessing the robustness of this method when contact structure is incorporated into the transmission model dynamics, and on determining limits of the sampling process, such as the incidence of infection and sample size, required to obtain reliable results. These investigations will help validate the method under realistic capture-mark-recapture conditions, where wild rodent populations may be sampled weeks apart and capture numbers can vary over time.

Keywords: epidemic models, metaviromics, rodent ecology, Bayesian inference

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USING HAMSTER-DERIVED CELL LINES TO ASSESS THE CYTOTOXICITY OF ANTICOAGULANT RODENTICIDES IN CRICETIDS

Clara Bravo-Jiménez*, Noelia Marín-Prat, José M. Navas, Azucena Bermejo-Nogales

National Institute for Agricultural and Food Research and Technology (INIA),
Department of Environment and Agronomy, Madrid, Spain

** Corresponding author. Email: clara.bravo@inia.csic.es*

Rodents of the family Cricetidae, including voles and hamsters, can become the most persistent and problematic pests worldwide, causing substantial economic losses in agriculture and serious public health risks as reservoirs of zoonotic diseases because of their high reproductive rate and adaptability to humanised environments [1–2]. Anticoagulant rodenticides (ARs) remain the primary chemical tool for rodent control due to their high efficacy through inhibition of vitamin K epoxide reductase complex 1 (VKORC1). However, the widespread emergence of resistance, frequently associated with mutations in the *vkorc1* gene, challenges the sustainability of current pest management programmes [3–5]used as one of the most effective ways to control rodent populations worldwide, inhibit the vitamin K 2,3-epoxide reductase (VKORC1. Most of the work on toxicological responses has concentrated on murid species; however, data for cricetids are very scarce. *In vitro* assays represent New Approach Methodologies that reduce reliance on live animal testing, while providing insights into cellular responses to toxic compounds.

We hypothesise that cricetid-derived cellular models exhibit specific cytotoxic responses to anticoagulant rodenticides. The objective of this study is to evaluate and compare the cytotoxic effects of seven first- and second-generation ARs in two hamster-derived cell lines: Chinese hamster (*Cricetulus griseus*) ovary cells (CHO-K1) and Syrian hamster (*Mesocricetus auratus*) kidney cells (BHK-21).

Cytotoxicity was evaluated by measuring alterations in mitochondrial activity, membrane integrity, and lysosomal activity following exposure to a concentration range of 0.78–100 μg/ml for 24, 48, and 72 h. Results indicate compound and cell line-specific differences in cytotoxicity, suggesting distinct cellular sensitivities and potential variability in the mechanisms underlying cytotoxicity. Overall, this work aims to generate toxicological data for cricetid models, contributing to a better understanding of anticoagulant rodenticide effects and supporting more ethical and effective strategies for rodent pest management within a One Health framework.

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Keywords: anticoagulant rodenticides, cytotoxicity, cricetid cell lines, New Approach Methodologies, One Health

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A ONE HEALTH APPROACH TO MANAGING RODENT PESTS IMPACTING HUMAN HEALTH AND WELLBEING IN SOUTH AFRICAN TOWNSHIPS: OHRATSA

Peter John Taylor[1*], Lourens Swanepoel[2], Samie Amidou[2], Felicity Burt[1, 8], Shingirai Chamisa[1], Fanie Coetzee[2], Lethlogonolo Diseko[1], Armand Engelbrecht[7], Zandile Fakude[1], Sibusile Hadebe[1], Tanya Fouche[5], Arun Gokul[4], Aliza Le Roux[1], Lefty Mahlodi Mpya[1], Lehlohonolo Mofokeng[1], Ara Monadjem[7], Thabang Mokoena[1], Shadreck Muchaku[3], Jolly Musoke[1], Lesly Nembudani[2], Nthatisi Nyembe[1], Patricks Otomo[1], Shilpa Parbhu[1], Nonhlahla Radebe[1], Mpho Ramoejane[1], Hayley Thompson[3], Afsatou Traore[2], Thobeka Ziqubu[1], Manqoba Zungu[2], Steven Belmain[6]

[1] *University of the Free State, QwaQwa Campus, South Africa*
[2] *SARChI Chair on Biodiversity Value & Change, University of Venda, Thohoyandou, South Africa*
[3] *University of Fort Hare, South Africa*
[4] *University of Mpumalanga, South Africa*
[5] *University of South Africa, Pretoria, South Africa*
[6] *Natural Resources Institute, University of Greenwich, UK*
[7] *University of Pretoria, South Africa*
[8] *National Health Laboratory Service, Free State, South Africa*
** Corresponding author. Email: taylorpj@ufs.ac.za*

This project examines the multifaceted challenges caused by rodents in South African townships, focusing on their impacts on human health, food and nutrition safety, and mental wellbeing. Using One Health, an ecology-based approach, it aims to identify safer, more sustainable rodent management technologies in partnership with communities and public authorities. Rodents contaminate food with urine and faeces, increase disease risks, promote aflatoxin growth, and reduce nutritional value through selective feeding [1]. Heavy reliance on toxic rodenticides further threatens human and environmental health, while endemic rodent-borne diseases remain frequently misdiagnosed despite millions of global cases each year. The project addresses three core questions: (i) how rodent activity affects food quality, safety, and nutrition in urban households, (ii) how infestations influence mental health, particularly through stigma, social pressure, and reduced personal agency among vulnerable community members [4], and (iii) whether innovative, ecologically based tools – such as rodent fertility control [2, 3] – can provide safer, more socially acceptable alternatives to conventional poisons while reducing disease transmission. Ultimately, the project seeks to generate evidence to support sustainable rodent management strategies that lessen zoonotic spillover and protect livelihoods in low- and middle-income communities.

Keywords: contraceptives, Rodentia, Muridae

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ANTROPOGENIC IMPACT ON RODENT ZOONOSIS IN MANIEMA, THE DEMOCRATIC REPUBLIC OF THE CONGO

Tine Cooreman[1, 2‡*], Patrick Mpoyo[3‡], Pascal Baelo[4], Steve Ngoy[4], Madeleine Alimasi[4], Daddy Kanonge[3], Augustin Twabela[3], Josef Brya[6], Herwig Leirs[1], Justin Masumu[3], Guy-Crispin Gembu[4], Erik Verheyen[1, 5], Sophie Gryseels[1, 5], Joachim Mariën[1, 2]

[1] Evolutionary Ecology Group, University of Antwerp, Belgium

[2] Virus Ecology Group, Institute of Tropical Medicine Antwerp, Belgium

[3] Central Veterinary Lab, Kinshasa, Democratic Republic of the Congo

[4] Biodiversity Surveillance Center, University of Kisangani, Democratic Republic of the Congo

[5] Vertebrate group, Directorate Taxonomy and Phylogeny, Royal Belgian Institute of Natural Sciences, Belgium

[6] Institute of Vertebrate Biology, Czech Academy of Sciences, Brno, Czechia

** Corresponding author. Email: Tine.Cooreman@uantwerpen.be*

‡Equal contribution of coauthors

In recent years, the incidence of emerging infectious diseases (EIDs) has increased markedly, placing growing pressure on global health systems and economic stability. Anthropogenic land-use change is a major driver of this rise, reshaping host communities and human-wildlife interfaces [1–2]. In rodents, such changes often reduce biodiversity and favour disturbance-tolerant generalist species in human-dominated landscapes [3]. Yet it remains unclear whether biodiversity loss and functional homogenisation consistently decrease, maintain, or increase the risk of zoonotic disease. This study assessed how anthropogenic land-use change influences pathogen transmission in rodent communities in Maniema Province, Democratic Republic of the Congo. A total of 381 rodents were sampled across two villages and different forest plots and screened for six pathogen families: *Poxviridae*, *Bartonellaceae*, *Anaplasmataceae*, *Leptospiraceae*, *Hepatozoidae*, and *Orthoherpesviridae*. Village communities were strongly dominated by *Rattus rattus*, whereas forest plots harboured 28 species and showed a substantially higher diversity (Shannon index of 2.61 vs. 0.10 in villages). *Bartonellaceae* had the highest infection rate (22%), followed by *Hepatozoidae* (5.8%), *Orthoherpesviridae* (3.9%), and *Anaplasmataceae* (0.8%). Despite frequent Mpox outbreaks in the region, no rodents tested positive for *Poxviridae*. *Bartonellaceae*

was significantly more prevalent in villages, probably due to the high infection rate in *R. rattus*, which accounted for 74% of positives. Phylogenetic analyses of the *Bartonellaceae* ITS and gltA genes identified a distinct forest-associated cluster comprising two different molecular operational taxonomic units (MOTUs). Bartonellaceae in *R. rattus* formed species-specific clusters including worldwide Rattus populations and exhibited higher MOTU diversity than forest sequences, suggesting multiple introductions during the *Rattus* global expansion. The other pathogens of this study were more frequently detected in forest species, indicating a limited role of *R. rattus* in their transmission and a potentially lower spillover risk to humans. Overall, our findings highlight pathogen-specific responses to anthropogenisation and a complex relationship between biodiversity change and zoonotic disease risk.

Keywords: zoonosis, rodents, DRC, anthropogenisation

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YEAR-ROUND MONITORING OF SMALL MAMMAL POPULATIONS: CAMERA-TRAPS, AI, AND BAYESIAN MODELS

Bolduc David[1]*, Fauteux Dominique[1, 2], Legagneux Pierre[1]
[1] *Biology Department and Northern Studies Center, Laval University, Quebec, Canada*
[2] *Centre for Arctic Knowledge and Exploration, Canadian Museum of Nature, Ottawa, Ontario, Canada*
* *Corresponding author. Email: david21bolduc@hotmail.com*

Small mammal research is largely dedicated to population dynamics. However, empirical estimation of population densities remains a logistical challenge. Live trapping provides precise estimates but can only be conducted over limited spatial and temporal scales given the required manual labour and the meteorological constraints. As a result, density time series are often constrained to the summer and miss the winter period – when major population changes may occur – and the gaps between surveys can be too large to distinguish between competing hypotheses on what drives population dynamics. Hence, while these time series have provided incredible insight into the population dynamics of vertebrates in general, we are now approaching their explanatory limits. Addressing this issue, we developed a complete methodology to continuously monitor small mammal populations and estimate their density across seasons. Inspired by other enclosed camera-trap designs [1–2], we built a system encouraging the passage of animals at fixed distances from the camera-trap. This allows us to measure traits (e.g., body size, tail length, colour) on most images with a custom AI instance segmentation model. Then, we integrate the trait and spatial information of each observation in spatial partial-identity Bayesian model [3], where we probabilistically link observations, create capture histories, and estimate density. In this presentation, we discuss the prospects of using this methodology to monitor small mammal populations, focusing on (1) the diversity of sampled mammals, (2) the performance of species-recognition model and trait measurement tools, and (3) the model development and the limits of the generated density estimates.

Keywords: camera-traps, image analysis, density estimation, population dynamics

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'TO BE OR NOT TO BE' (KILLED BY PREDATION): PREDATORS CAN MASK OTHER MORTALITY AT MASS OUTBREAKS OF WOOD LEMMINGS

Frauke Ecke[1, 2*], Björn Wallgren[2, 3], Henrik Johansen[2, 4], Hussein Khalil[2], Magnus Magnusson[2, 5], Bo Niklasson[6], Hein Sprong[7], Birger Hörnfeldt[2]

[1] *Organismal and Evolutionary Biology Research Programme, Faculty of Biological and Environmental Sciences, University of Helsinki, Finland*

[2] *Department of Wildlife, Fish, and Environmental Studies, Swedish University of Agricultural Sciences (SLU), Umeå, Sweden*

[3] *County Administrative Board of Västmanland, Västerås, Sweden*

[4] *Southern Swedish Forest Research Centre, Swedish University of Agricultural Sciences (SLU), Alnarp, Sweden*

[5] *Swedish Forest Agency, Umeå, Sweden*

[6] *Jordbro Medical Center, Jordbro, Sweden*

[7] *Centre for Infectious Disease Control, National Institute for Public Health and the Environment (RIVM), Bilthoven, The Netherlands*

* *Corresponding author. Email: frauke.ecke@helsinki.fi*

The population dynamics of rodents at northern latitudes have been suggested to be mainly driven by predators that induce mortality especially during the peak phase of the rodent cycle [1]. Here, we took the rare opportunity to test the predation hypothesis by investigating 131 wood lemmings (*Myopus schisticolor*) that were found dead in Sweden during outbreaks of wood lemmings in 2014 and 2017 followed by mass mortality. Among the 110 (84%) females and 21 (16%) males, we investigated whether they were killed by predators by examining the presence of haemorrhages. Predators killed 57 (44%) of the wood lemmings, while 45 (34%) were attacked by predators after their death (scavenged) and for 29 (22%) no signs of predator-induced damage was found. Generalised linear modelling showed that the cause of death by predators was not related to the sex and weight of wood lemmings. Spatial analyses revealed that prior to death, most wood lemmings had dispersed from their preferred spruce forest habitats into non-preferred habitat. Our study demonstrates that predation alone did not

cause mass mortality among wood lemmings, but that predation is an important cause of death. Our study leaves the mystery of mass mortality among wood lemmings unsolved. However, it highlights the need to better understand non-predation related drivers of rodent population dynamics since predation might mask any underlying physiological conditions that could increase susceptibility to predation.

Keywords: mutation, population cycle, population outbreak, predation hypothesis, sex ratio

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IS URBANISATION A DRIVER OF DIFFERENCES IN BACTERIAL COMMUNITIES AMONG NATIVE AND INVASIVE RODENTS IN NORTHERN SENEGAL?

Julia Emerit[1*], Johannes Tavoillot[1], Maxime Galan[1,] Lily Cesari[1], Ambroise Dalecky[2], Cheikh Moustapha Dia[1], Gaye Laye Diop[3], François Diouf[4], Youssoupha Niang[1], Ibrahima Sow[2, 4], Laurent Granjon[1], Carine Brouat[1], Christophe Diagne[1*]

[1] *CBGP, IRD, INRAE, CIRAD, Montpellier SupAgro, Montpellier University, Montferrier/Lez, France*

[2] *IRD, Aix Marseille University, LPED, Marseille, France*

[3] *Senegalese Institute for Agricultural Research, National Laboratory for Livestock and Veterinary Research, Dakar – Hann, Senegal*

[4] *UFR S2ATA, Gaston Berger University, Saint-Louis, Senegal*

** Corresponding author. Email: julia.emerit@ens-lyon.fr, Christophe.diagne@ird.fr*

Urbanisation is a major cause of environmental disturbances that have strong consequences on the nature and evolution of interactions between and/or within host communities and their pathobiomes (viruses, bacteria, helminths and protozoans, including pathogenic taxa) [1]. This pathobiome may include zoonotic agents, with rodents acting as major reservoirs of such pathogens and key components of the urban fauna worldwide [2]. In West Africa, where urban transition is among the fastest throughout the world, rodent-borne zoonotic risks associated with these changes still remain to be investigated [2]. More particularly, biological invasions of exotic rodent species are increasingly documented in this region, yet these processes remain insufficiently integrated into urban health ecology [3]. Here, we investigate the links between ongoing urbanisation and bacterial community dynamics within native and invasive rodent host populations in North Senegal. Specifically, we aim to test two alternative hypotheses, whereby urbanisation may either reduce (*urban refuge*) or increase (*urban burden*) zoonotic carriage by (rodent) reservoirs [4]. To this end, we analysed samples from natural rodent populations collected between 2013 and 2025 across 31 urban or rural sites in North Senegal. Our dataset includes 1,430 individuals from two species: the invasive *Mus musculus domesticus* and the native *Mastomys erythroleucus*. We performed 16S metagenomics on spleen samples to characterise their bacterial communities based on operational taxonomic units (OTU). Our preliminary analyses identified nine bacterial genera, most of them shared by both host species. Interestingly, genus-level diversity was higher than previously reported [5]. Based on a broad-scale classification of sampling sites, our analyses highlighted host-specific differences between urban and rural localities, suggesting patterns consistent with either *urban refuge* or *urban burden* hypotheses depending on the bacterial genus considered. Further analyses will include a finer landscape characterisation and the description of helminth communities to explore potential co-infection patterns.

Keywords: bacteria, community ecology, house mouse, small mammals, zoonoses

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INVESTIGATION INTO SELECTION PRESSURE ON COHESIN AND CONDENSIN GENES IN *NANNOSPALAX XANTHODON*

Başak Esgin[1]*, Ferhat Matur[2], Seda Baykal[3]

[1] *Dokuz Eylul University, Faculty of science, Department of Biology, İzmir, Türkiye*

[2] *Dokuz Eylul University, Faculty of science, Department of Biology, İzmir, Türkiye*

[3] *Seda Baykal, Izmir Institute of Technology IZTECH, Faculty of science, Department of Molecular Biology and Genetics, İzmir, Türkiye*

* *Corresponding author. Email: bskesgn@gmail.com*

Accurate chromosome segregation is essential for genomic stability, and cohesin and condensin complexes – members of the structural maintenance of chromosomes (SMC) family – are key regulators of this process [1–2]. These evolutionarily conserved complexes control sister chromatid cohesion, chromosome condensation, DNA repair, and gene regulation during cell division [2]. Although dysfunction in SMC components is linked to chromosomal instability and cancer, their evolutionary dynamics remain poorly understood in non-model organisms [1]. This project investigates selection pressures acting on cohesin and condensin genes in *Nannospalax xanthodon*, a subterranean rodent characterised by extensive chromosomal diversity and distinctive adaptations such as hypoxia tolerance and cancer resistance [3–4]. Much of its karyotypic variation arises from Robertsonian translocations, which may contribute to genomic restructuring and speciation [3]. We integrate comparative genomics and gene expression analyses across four Turkish populations representing major cytotypes (2n = 60, 52, and 38). These localities share similar ecological and geological conditions, enabling chromosomal divergence to be evaluated as the primary variable. Exhibiting stable karyo-

types, *Microtus* species from the same regions serve as evolutionary controls. Whole genome sequencing of 19 cohesin and condensin genes and Western blot analyses will assess molecular and protein-level variation. Selection signatures will be examined using dN/dS ratios and McDonald–Kreitman tests, following established phylogenetic model selection frameworks [5]. This study provides novel insights into the evolutionary dynamics of essential chromosome architecture proteins in relation to cytotypic divergence.

Acknowledgements: supported by the TÜBİTAK 1001 programme (Project No. 124Z079).

Keywords: selection pressure, chromosomal evolution, cohesin, condensing

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ASYMMETRIC PREDATION ON FEMALE VS MALE BROWN LEMMINGS

Dominique Fauteux[1, 2*], Camille Gaudreau-Rousseau[2], Glenn Yannic[3], David Bolduc[2], Pierre Legagneux[2]

[1] *Arctic Centre, Canadian Museum of Nature, Gatineau (QC) Canada*

[2] *Centre for Northern Studies, Laval University, Quebec (QC) Canada*

[3] *University Savoie-Mont-Blanc, Chambéry, France*

* *Corresponding author. Email: dfauteux@nature.ca*

In the Canadian High Arctic, the bottom-up and top-down control of lemming populations have been tested several times to understand which causal mechanism is predominantly leading to their 3–4-year cycles. On Bylot Island, direct density-dependence appears to be particularly strong in summer and fall because of the impact of migrant avian predators and resident foxes. In addition, delayed density-dependence of predation by ermines has been recently uncovered by Bolduc et al. [1], which appears necessary to extend the low phase to shape the longer 4–5-year cycles. In 2022 [2], we published a result that was quite puzzling for us: the only demographic parameter that varied over the lemming cycles was a strong male-biased sex-ratio during low-abundance years. Considering this, we initiated new work to identify a mechanism leading to such rarity of females. Our most recent results, based on molecular sexing of prey remains like mandibles and pieces of skin, suggest that female brown lemmings are much less hunted than males by both ermines and snowy owls, which cannot explain the male-biased sex-ratios observed previously. This concurs with a previous study showing higher summer survival in adult

females than males [2]. These results show a potential mechanism evolved by lemmings to survive extirpation during each population cycle. Unfortunately, we are still puzzled by the strong male-biased sex-ratios observed at low abundance. That being said, the most recent results may indicate strong behavioral responses at low density, involving intense and risky mate searching, leading to higher trappability of males.

Keywords: trophic interactions, demography, predator-prey interactions, population dynamics, Cricetidae

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ECOLOGICAL CONSEQUENCES OF EXTREME CLIMATIC EVENTS: FROM SMALL MAMMALS COMMUNITY COMPOSITION TO POPULATION DYNAMICS AND TICKS ENCOUNTER IN THE ITALIAN ALPS

Giulia Ferrari[1, 2*], Valentina Tagliapietra[1, 2], Daniele Arnoldi [1], Andrea Busolin[3], Ilaria Di Giovanni[4], Piergiovanni Partel[5], Heidi C. Hauffe[1], Annapaola Rizzoli[1, 2]

[1] Fondazione Edmund Mach, Research and Innovation Centre, San Michele all'Adige (TN)
[2] National Biodiversity Future Center (NBFC), Palermo, Italy
[3] University of Parma, Department of Chemical, Life and Environmental Sustainability Sciences, Parma, Italy
[4] University of Eastern Piedmont, Department of Sustainable Development and Ecological Transition, Vercelli, Italy
[5] Paneveggio Pale di San Martino Natural Park, Villa Welsperg, Primiero San Martino di Castrozza, Italy
** Corresponding author. Email: giulia.ferrari@fmach.it*

Climate change is intensifying extreme meteorological events and altering ecosystem disturbances globally, with mountain regions being particularly vulnerable. In Europe, an average of two extratropical storms strike annually, leaving wind as the primary driver of forest destruction [1]. In 2018, the Vaia windstorm, an extreme meteorological event, hit the Italian Alps toppling an estimated 40 million trees across 41,000 hectares in north-eastern regions [2]. As part of the PNRR and BEPREP project, we investigated how catastrophic disturbances influence small mammal community composition, dynamics, and tick burden [3].

The study was conducted in the Paneveggio-Pale di San Martino Natural Park (Trento, Italy). We selected two habitat types – Vaia windthrow and undisturbed forest (non-Vaia) – at two contrasting altitudinal levels: low (1,100 m a.s.l.) and high (1,650 m a.s.l.). From 2022 to 2025, we performed seasonal capture-mark-recapture (CMR) of small mammals and screened for tick infestation. Spatially explicit capture-recapture (SECR) models were used to estimate rodent density and space use, while generalised linear mixed models (GLMMs) were applied to analyse the effects of habitat disturbance, host condition, and altitude on tick burden.

We captured 468 individuals including *Apodemus flavicollis*, *A. sylvaticus*, *Clethrionomys glareolus*, *Microtus* spp., and *Sorex* spp. Small mammal species richness was higher in Vaia windthrows than in undisturbed forests, characterised by the presence of *Microtus* spp. and an increased relative abundance of shrews and density of *C. glareolus*, while contracting the spatial range of the latter. Interestingly, *Apodemus* spp. density was primarily driven by altitude. Of the 295 *Ixodidae* ticks counted, 73% were found in windthrow areas. Tick burden was highest at low altitude sites and among heavier males in both *C. glareolus* and *Apodemus* spp. Notably, a significant increase in tick burden was observed in *C. glareolus* in Vaia-affected areas.

Natural reforestation in windthrow areas creates complex, heterogeneous habitats that modulate small mammal community composition, density, and space use [4]. These successional environments promote host-parasite encounters, potentially enhancing zoonotic circulation in this mid-term recovery phase, until forest is fully restored [5].

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Keywords: extreme meteorological events, Italian Alps, small mammals, tick burden, natural restoration

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TRACING LCMV LINEAGES THROUGH HYBRID ZONES: IMPLICATIONS FOR HUMAN INFECTION

Alena Fornuskova[1*], Ivana Jezkova[1], Maria Kachamakova[2], Veronika Bartakova[1], Polina Nikova[2], Ludovit Dureje[1], Stela-Teodora Trendafilova[2], Natalia Martinkova[1], Yordan Koshev[2], Joelle Gouy de Bellocq[1]

[1] Institute of Vertebrate Biology, Czech Academy of Sciences, Brno, Czech Republic

[2] Institute of Biodiversity and Ecosystem Research, Bulgarian Academy of Sciences, Sofia, Bulgaria

** Corresponding author. Email: a.fornuskova@seznam.cz*

Lymphocytic choriomeningitis virus (LCMV) is a globally distributed zoonotic arenavirus maintained primarily by the house mouse (*Mus musculus*). In humans, infection can result in severe disease, particularly in immunocompromised individuals and following congenital transmission.

In Europe, LCMV circulation is strongly shaped by the genetic structure of its main reservoir host. Two house mouse subspecies, *Mus musculus musculus* and *M. m. domesticus*, meet in a well-defined hybrid zone across Central Europe. Our studies show that the major phylogenetic lineages of LCMV closely correspond to this subspecies division. Consequently, the viral lineage with zoonotic potential can be predicted based on the dominant mouse subspecies present at a given locality [1].

Long-term monitoring in the Czech Republic further demonstrates that LCMV persists in geographically restricted hotspots, remaining stable within local mouse populations for at least 24 years. This highlights the ability of LCMV to maintain long-term endemic cycles without extensive spread [2].

In Bulgaria, where two subspecies of the house mouse (*M. m. musculus* and *M. m. domesticus*) occur in sympatry with the wild mouse *Mus macedonicus*, we found that LCMV circulation is not restricted to house mice. The wild species *M. macedonicus* also harbours the virus and shows a higher prevalence (11%) than house mice (4.2%). Phylogenetic analyses indicate that LCMV infections in Bulgarian house mice most likely result from spillover from *M. macedonicus*. Genomic data further reveal that all Bulgarian samples form a distinct lineage closely related to viruses typical of *M. m. musculus*, including a human-derived strain isolated in Bulgaria in 1956.

Overall, our findings demonstrate that understanding the genetic structure and phylogeography of rodent hosts is crucial for predicting viral circulation patterns and assessing human infection risk, with important implications for public health in central and south-eastern Europe.

Keywords: LCMV, house mouse, hybrid zone, spillover, arenavirus

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THE ROLE OF *MICROTUS* DIVERSITY IN THE EMERGENCE OF NEW HANTAVIRUSES

Gerald Heckel
University of Bern, Institute of Ecology and Evolution, Bern, Switzerland
Email: gerald.heckel@unibe.ch

The evolutionary history of rodents and their pathogens often appears tightly associated but the decisive factors remain mostly unknown. The rapid diversification of the vole genus *Microtus* has led to many species across the palearctic but phylogeographic evidence suggests that associated hantaviruses are unlikely to have emerged simply by co-divergence [1]. Vicariance plays a key role for the diversification of *Microtus*, while the functional diversity of hantaviruses depends apparently much more on adaptive processes than on geographic isolation [2–3]. Our work on intraspecific hybrid zones between evolutionary lineages in the common vole *Microtus arvalis* revealed full isolation between parapatric phylogenomic clades in Tula Orthohantavirus (TULV). Genetic polymorphisms in the host relevant for adaptive divergence of TULV probably emerged during an earlier vicariant phase of *M. arvalis* [4]. Genome-wide association studies identified

candidate polymorphisms in the host explaining up to 38% of variance in infection with either virus clade [5]. There was no evidence of reassortment in this hybrid zone, but reassortment is probably rarely detected in nature because of its detrimental fitness effects. However, extended regional surveys of *M. arvalis* populations enabled us to find genomic evidence of multiple reassortment events between other TULV clades which were phylogenetically dated to more than 30 years ago. Reassortants have since replaced the ancestral TULV clades regionally which suggest they may represent a novel transgressive phenotype in admixed common vole populations. Taken together, our results show that evolutionary divergence in *Microtus* hosts can promote TULV speciation through reciprocal adaptation, but host hybridization may also provide the genetic substrate for the emergence of novel hantaviruses.

Keywords: *Microtus arvalis*, Tula hantavirus, speciation, hybrid zone, reassortment

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THE IMPORTANCE OF DEMOGRAPHY IN RODENT DISEASE ECOLOGY

Heikki Henttonen
Natural Resources Institute Finland, Helsinki, Finland
Email: HeikkiHenttonen@luke.fi

Small rodents are increasingly used as model animals in ecological disease research. However, many students in the field have inadequate knowledge of the significance of demographic heterogeneity of reservoir rodent populations and how that affects infection parameters. This heterogeneity can vary seasonally, and in density- and phase dependent ways [1]. Here I summarise some of the common problems and give a solution, the use of the concept of *functional groups*, to gain more detailed information and to avoid common mistakes, e.g., by drawing conclusion from pooled heterogeneous population samples. I emphasise the importance of seasonality and demography (the roles of various population functional subgroups) for parasite/pathogen studies and sampling design to cover the essential components of populations.

Keywords: disease ecology, rodents, demography, population structure

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FERTILITY CONTROL FOR OVERABUNDANT VERTEBRATES

Jens Jacob[1*], **Giovanna Massei**[2]

[1] *Julius Kuehn-Institut (JKI), Federal Research Centre for Cultivated Plants, Institute for Epidemiology and Pathogen Diagnostics, Rodent Research, Muenster, Germany*

[2] *Botstiber Institute for Wildlife Fertility Control, University of York, UK*

* *Corresponding author. Email: jens.jacob@julius-kuehn.de*

Management of overabundant vertebrates such as invasive goose species, rodents, and ungulates is challenging when conducted in urban and agricultural environments at a landscape scale. Traditional methods are usually based on killing (hunting, trapping, rodenticides) that can create vacant territories for reinvasion and disrupt social behaviour. For large mammals, culling is often ineffective in reducing population size. In many parts of the world, public opinion favours non-lethal approaches, which are regarded as more humane and sustainable than traditional methods [1].

Fertility control – alone or in concert with other management techniques – could help because it might be more species-specific, humane, and accepted by the public. An ideal contraceptive would be effective for several breeding cycles, is delivered to a proportion of the population required to be effective, has no or minimal side-effects nor environmental impact, and has a positive benefit-cost-ratio.

Fertility control could be useful in several contexts including the protection of human and animal health, conservation, and plant protection. However, so far, efficacy has rarely been demonstrated at the landscape scale, interest by big international companies and regulators is lacking, and very few products have been registered [2]. More and more restrictions for the use of rodenticides and banning of certain rodenticidal compounds in several countries may prompt more intensive work on fertility control, at least for rodents.

Whilst injectable contraceptive vaccines and multi-year implants work well in large species, fertility control for rodents is likely to rely on oral contraceptives delivered in baits. This presentation reviews the progress in the development of oral contraceptives such as chemosterilants, synthetic steroids, and plant extracts. The presentation will also address remaining challenges, such as legal issues in some regions regarding endocrine disruptors, and suggest future work to make contraceptives (many by default endocrine disruptors) acceptable to regulators.

Keywords: human wildlife conflict, contraceptives, infertility, reproduction, wildlife management

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REGIONAL ASSEMBLAGES OF RODENTS (AND OTHER SMALL MAMMALS) AND THEIR FLEA PARASITES FORM BIOGEOGRAPHICAL BUT NOT ECOLOGICAL CLUSTERS

Boris Krasnov*, Georgy Shenbrot

[1] *Jacob Blaustein Institutes for Desert Research, Swiss Institute for Drylan Environmental and Energy Research, Ben-Gurion University of the Negev, Midreshet Ben-Gurion, Israel*

** Corresponding author. Email: krasnov@bgu.ac.il*

Step-down factor analyses (SDFAs) [1] and cluster analyses were used to identify biogeographic (across the entire globe) and ecological (within a realm across the main terrestrial biomes) clusters of regional assemblages of fleas and their small mammalian hosts (mostly rodents) from six biogeographic realms. At the global scale, the clusters of regional assemblage loadings on SDFA axes reflected well the assemblage distribution, according to the biogeographic realms to which they belong except for fleas and hosts from Madagascar (belonging to the Afrotropics but clustered with the Indo-Malay and the Australasian assemblages, respectively) and hosts from Morocco and Egypt (both belonging to the Palearctic, but clustered with the Afrotropical assemblages) The cluster topology, corresponding to the biogeographic realms, was similar between flea and host assemblages, but the topology of subtrees within realm-specific clusters substantially differed between fleas and hosts. At the scale of biogeographic realms, the distribution of regional flea and host assemblages did not correspond to the predominant biome types. Assemblages with similar loadings on SDFA axes were often situated in different biomes and vice versa. The across-biome, within-realm distributions of flea versus host assemblages suggested weak congruence between these distributions. These results indicate that dispersal is a predominant mechanism of flea and host community assembly across large regions.

Keywords: biogeography, global scale, species composition

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RODENTS OF ETHIOPIA: WHAT HAS CHANGED SINCE 2019 IN THE MOST BIODIVERSE AFRICAN COUNTRY?

Lucie Kubáčková[1, 2]*, Getachew Mulualem[1, 2, 3], Josef Bryja[1, 2]

[1] *Institute of Vertebrate Biology, Czech Academy of Sciences, Studenec, Czech Republic*

[2] *Department of Botany and Zoology, Faculty of Science, Masaryk University, Brno, Czech Republic*

[3] *Ethiopian Biodiversity Institute, Mekelle, Tigray, Ethiopia*

** Corresponding author. Email: kubluci@seznam.cz*

Ethiopia is one of the most significant centres of biodiversity in Africa, mainly due to its remarkable spectrum of geographical and ecological conditions. Pronounced environmental and

elevational gradients in the Ethiopian Highlands, along with their geographical isolation and position at the border of multiple biogeographical regions, have contributed to exceptionally high levels of diversity and endemism in Ethiopian fauna, with rodents forming the most species-rich group of mammals. In 2019, Bryja et al. published the monograph *Annotated checklist, taxonomy and distribution of rodents in Ethiopia* [1], which summarises the results of long-term research and international collaboration. However, since this publication, a number of taxonomic revisions and field expeditions have significantly improved our knowledge of species composition and distribution of Ethiopian rodents. The updated information is being published in the online database Rodents of Ethiopia (https://asm.ivb.cz/), which provides a valuable data resource for further research and nature conservation. This contribution reviews recent taxonomic and faunistic changes, evaluates the biogeographical structure of Ethiopian rodent fauna, and proposes further directions and priority areas for biodiversity research.

Keywords: biodiversity, biogeography, Ethiopian Highlands, endemism, Rodentia

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RED SQUIRRELS (*SCIURUS VULGARIS*) AS POTENTIAL RESERVOIRS OF *BORRELIA* SPP.

Indrė Lipatova*, Ugnė Medikaitė, Justina Snegiriovaitė, Irma Ražanskė, Povilas Sakalauskas, Jana Radzijevskaja, Algimantas Paulauskas

Vytautas Magnus University, Kaunas, Lithuania

** Corresponding author. Email: indre.lipatova@vdu.lt*

Lyme disease, caused by spirochete bacteria of the *Borrelia burgdorferi* sensu lato complex, is the most common vector-borne disease in North America and Europe [1]. Its prevalence has increased in recent decades due to climate change, environmental changes, and the expansion of tick populations and their hosts [2]. Numerous cases have been reported across several European countries, including Germany, Austria, Slovenia, and Lithuania [1]. Understanding the role of wildlife in the maintenance and transmission of these pathogens is essential for assessing public health risks. The Eurasian red squirrel (*Sciurus vulgaris*), which inhabits natural, suburban, and urban environments, frequently encounters ticks while moving on the ground and may act as potential reservoir hosts for *Borrelia* spp. [3]. This study aimed to determine the presence of *Borrelia* spp. in red squirrels and their associated ticks collected in urban parks of Kaunas city, Lithuania, using molecular detection methods. Red squirrels and their ticks were tested for the presence of *Borrelia* DNA. Detection was performed using real-time PCR with *Borrelia*-specific primers. Positive samples were further analysed by conventional PCR targeting the intergenic spacer (IGS) region and *ospA* and *fla* genes, followed by sequencing for species identification. *Borrelia* DNA was detected in 39.6% of red squirrels. Among ticks, all identified as *Ixodes ricinus*, 26.0% were positive for *Borrelia*. Detection frequency rates varied among the genetic markers analysed. Sequencing analysis revealed three human pathogenic species: *B. afzelii*, *B. garinii*, and *B. burgdorferi* sensu stricto. These findings suggest that red squirrels may contribute to the circulation of Lyme disease pathogens in urban ecosystems and highlight the importance of continuous monitoring of wildlife hosts and tick populations in endemic regions.

Keywords: *Borrelia* spp., *Siurus vulgaris*, ticks, Lithuania

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DRIVERS OF PATHOGEN TRANSMISSION RISK BY TICKS IN MOUNTAIN ECOSYSTEMS

Aurelio F. Malo[1, 2*]**, Esther Llorente**[1]**, Giovanni Forcina**[1]**, Ignacio Bueno**[3]**, Paloma Prieto**[3]

[1] *University of Alcalá, Global Change Ecology and Evolution Research Group Madrid, Spain*

[2] *Imperial College London, Silwood Park, Ascot, UK*

[3] *Natural Park Sierra de Cazorla, Segura y las Villas Jaen, Spain*

* *Corresponding author. Email: aurelio.malo@uah.es*

We report on the results of a two-year project [1] aimed at disentangling the effects of biotic and abiotic factors on tick density and tick species composition in Mediterranean mountain ecosystems. Abiotic factors included weather conditions, altitude, ground-level temperature and humidity, microhabitat cover and composition, and slope direction. Biotic factors included the species composition and density of potential tick hosts such as ungulates and carnivores. The experimental design allowed statistical control of the effects of herbivores plus rodents versus rodents alone (using herbivore-exclusion zones) on tick presence, density, and tick species composition. Likewise, we separated the effects of herbivore aggregation (salt lick plots) from those under optimal high-humidity conditions (water hole plots) on tick density and composition.

Tick surveys were conducted with drag sampling; each drag stretch covered a minimum of 30 m^2 per sampling plot, and a minimum of four were conducted per plot. Each tick was collected and later identified in the lab at the species level. The tick's microbiome was sampled in the lab to identify potential pathogens. The host species composition (mainly ungulates and some carnivores) was quantified using 70 camera traps installed in two mountain regions in central and southern Spain (Sierra de Guadarrama and Sierra de Cazorla). Over 3500 censuses were conducted in over 75 census plots, and over 1200 ticks were collected, identified, and tested for pathogens. The results show how biotic and abiotic drivers affect tick density and their potential to spread diseases in mountain ecosystems, exemplifying an interesting One Health methodological approach to better understand the complexity underlying tick distribution and the risk of pathogen transmission to humans and livestock.

Keywords: One Health, tick density, host ungulates, host rodents, pathogens

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PROGRAMMABLE CRISPR-CAS9 HOST DEPLETION IMPROVES MICROBIAL DETECTION IN METAGENOMIC RODENT SURVEILLANCE

Joachim Mariën[1, 2*], Emilie Van Vyve[1], Mare Geraerts[1, 2], Baraka E Mwamundela[3], Tine Cooreman[2], Apia Massawe[3], Sophie Gryseels[2, 4], Lucinda Kirkpatrick[2, 5], Herwig Leirs[2], Kevin Arien[1, 6], Philippe Selhorst[1]

[1] Department of Biomedical Science, Institute of Tropical Medicine Antwerp, Antwerp, Belgium
[2] Evolutionary Ecology group, Department Biology, University of Antwerp, Wilrijk, Belgium
[3] Institute of Pest Management, Sokoine University of Agriculture, Morogoro, Tanzania
[4] OD Taxonomy and Phylogeny, Royal Belgian Institute of Natural Sciences, Brussels, Belgium
[5] Prifysgol Bangor University, Bangor, United Kingdom
[6] Department of Biomedical science, University of Antwerp, Antwerp, Belgium
** Corresponding author. Email: jmarien@itg.be*

Unbiased pathogen surveillance in reservoir hosts is often constrained by the overwhelming abundance of host nucleic acids in metagenomic sequencing libraries. Here, we combine a flexible CRISPR-Cas9 host-depletion approach with metagenomic sequencing to improve detection of low-abundance microbes in small mammals, and we report the pathogen diversity recovered from wild-caught rodents in Morogoro, Tanzania [1].

First, we designed a rodent DASH (Depletion of Abundant Sequences by Hybridization) [2] panel targeting cytoplasmic and mitochondrial rRNAs (18S, 5.8S, 28S, 12S, 16S) and an abundant mitochondrial transcript (ND2) in *Mus musculus* and *Mastomys natalensis.* In serum samples, host depletion markedly reduced rRNA backgrounds and increased the proportion of viral reads, outperforming a commercial depletion reagent and enabling ND2 depletion not achieved by the kit. We then applied this workflow to 436 wild small mammals (pooled into 93 serum libraries) sampled in 2021 and 2023, dominated by *M. natalensis*. After stringent filtering against controls, we detected mammal-associated sequences from nine viral families, 15 bacterial genera, and 17 eukaryotic parasite genera.

Viral reads were identified in 39 pools and yielded complete genomes from multiple taxa. Notably, we recovered six full mammarenavirus genomes clustering within the Morogoro/Mopeia arenavirus clade, all from pools containing only *M. natalensis*. We also retrieved two orthohepadnavirus genomes related to musk hepatitis shrew virus from pools containing *Crocidura* spp., highlighting shrews as potentially underappreciated viral reservoirs. A complete rotavirus A genome was recovered from *M. natalensis*, alongside cycloviruses, a mammastrovirus related to rat mammastrovirus, and multiple picobirnavirus segment 2 sequences. Among bacteria, *Mycoplasma* was most frequently detected, followed by *Anaplasma* and *Ehrlichia*, with additional detections including *Borrelia*, *Bartonella*, and *Salmonella*. Together, these results demonstrate that programmable host depletion can make metagenomic wildlife surveillance more sensitive and cost-effective, while revealing substantial viral and microbial diversity in a key African rodent reservoir system.

Keywords: viral enrichment, metagenomic sequencing, CRISPR-cas9, Mastomys natalensis

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USING MOLECULAR DOCKING TO VKORC1 TO PREDICT RODENT SUSCEPTIBILITY TO ANTICOAGULANT RODENTICIDES

Noelia Marín-Prat*, David Hernández-Moreno, José María Navas, Azucena Bermejo-Nogales

Department of Environment and Agronomy, National Institute for Agricultural and Food Research and Technology (INIA, CSIC), Madrid, Spain

** Corresponding author. Email: nmarin@inia.csic.es*

Rodents pose a significant agricultural and public health threat. Anticoagulant rodenticides (ARs), widely used for rodent control in urban and rural settings, disrupt vitamin K-dependent blood clotting and cause lethal haemorrhage by inhibiting vitamin K epoxide reductase complex 1 (VKORC1). Their extensive use has resulted in resistance-linked mutations in target brown and black rats [1–2] and exposure of non-target species [3], raising conservation concerns. Computational molecular docking offers a promising approach for assessing chemical risks across species [4] by characterising ARs-VKORC1 interactions based on predicted binding affinity (BA). We considered the hypothesis that amino acid and structural differences among Rodentia VKORC1 do not significantly affect AR binding or species susceptibility. Therefore, non-target rodents might be as susceptible to ARs as target rodents. Using available *vkorc1* sequences and structural data, we applied a computational framework combining protein structure prediction and molecular docking to evaluate the susceptibility of 57 rodent species to nine ARs (brodifacoum, bromadiolone, chlorophacinone, coumatetralyl, diphacinone, difenacoum, flocoumafen, warfarin). Susceptibility was assessed based on the difference in BA (ΔBA) between vitamin K and ARs, using brown rat VKORC1 interactions as a reference. Resulting ΔBA values ranged from –1.30 to 4.53 kcal/mol, being generally higher for second-generation ARs, indicating a greater susceptibility. Five species were identified as susceptible to at least one AR: *Acomys russatus*, *Apodemus sylvaticus*, *Arvicanthis niloticus*, and *Bandicota bengalensis* (Muridae) and *Arvicola amphibius* (Cricetidae). All were susceptible to flocoumafen. Additionally, *A. sylvaticus* and *A. amphibius* showed susceptibility to chlorophacinone, diphacinone, coumatetralyl, and bromadiolone. Only *A. sylvaticus*

was susceptible to brodifacoum. Therefore, considering the species present at application sites is essential. This approach provides a mechanistic basis for predicting cross-species susceptibility and supports next-generation risk assessment by prioritising species for further testing while reducing animal use.

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Keywords: rodent control, non-target exposure, next generation risk assessment, *in silico*, binding affinity

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SYLVATIC MAINTENANCE OF HUMAN *TRICHURIS TRICHIURA* IN ENDEMIC HYDROMYINI RODENTS, PAPUA NEW GUINEA

Nona Moradpoor[1, 2], Daniel Solomon Okena[3, 4, 5], František Vejmělka[3, 4, 5], Vojtěch Novotný[3, 4], Anna Bryjová[1], Dagmar Čížková[1], Alexis Ribas[6, 7], Joëlle Goüy de Bellocq[1*]

[1] Institute of Vertebrate Biology, Czech Academy of Sciences, Brno, Czech Republic
[2] Department of Botany and Zoology, Masaryk University, Faculty of Science, Brno, Czech Republic
[3] Faculty of Science, University of South Bohemia, České Budějovice, Czech Republic
[4] Biology Centre of the Czech Academy of Sciences, České Budějovice, Czech Republic
[5] Faculty of Science, Charles University, Prague, Czech Republic
[6] Parasitology Section, Department of Biology, Healthcare and Environment, Faculty of Pharmacy and Food Science, University of Barcelona, Barcelona, Spain
[7] Biodiversity Research Institute (IRBio), University of Barcelona, Barcelona, Spain
** Corresponding author. Email: joellegouy@gmail.com*

Soil-transmitted helminths remain a major global health burden, and control strategies for *Trichuris trichiura* assume humans are the primary reservoir. However, the ecology and host range of whipworms are incompletely understood. We investigated the occurrence and genetic identity of *Trichuris* spp. in non-volant wild mammals in Papua New Guinea (PNG), where epidemiological data are scarce [1] and wildlife–human interactions are frequent [2]. We examined the caecum and colon of 874 mammals (rodents and marsupials) collected in 19 localities

between 2019 and 2023 [3]. Whipworms were recovered and characterised using morphometrics and genome skimming to assemble mitochondrial genomes, complemented by nuclear ITS2 analyses. Morphometric variation was assessed using principal component analysis and cluster-based inference. All marsupials ($n = 43$) were negative for *Trichuris*. Sixteen rodents were infected (overall prevalence 1.8%), with infections distributed across multiple Hydromyini species and localities. Genomic analyses revealed that eight rodent-derived specimens clustered robustly within the *T. trichiura* clade alongside human and non-human primate isolates, while three belonged to rodent-associated lineages. Infections were patent, with gravid females and high worm burdens observed. Morphometric analyses showed significant differentiation between *T. trichiura* and rodent-associated clusters and indicated that the historically described *Trichuris germani* [4] likely represents *T. trichiura*. Our findings provide molecular evidence that wild rodents in PNG can harbour *T. trichiura*, suggesting that humans may not be the only natural reservoir. The presence of patent infections across multiple rodent hosts suggests the potential for a sylvatic transmission cycle. These results highlight the need for One Health approaches integrating wildlife surveillance into soil-transmitted helminth control programmes, as non-human reservoirs could undermine progress toward WHO 2030 elimination targets [5].

Keywords: trichiuriasis, neglected tropical disease, zoonotic reservoirs, endemic rodents, sylvatic cycle

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UNCOVERING CRYPTIC RESERVOIRS AND HIDDEN HOTSPOTS: A SURVEY OF SAVANNA SMALL MAMMALS FOR LASSA VIRUS WITHIN BENIN AND NIGERIA

Ayodeji Olayemi[1, 2*], Adetunji Samuel Adesina[3], Akinlabi Oyeyiola[1], Adeoba Obadare[1], Umaru Bangura[2], Nnennaya Anthony Ajayi[4], Kingsley Ukwaja[4], Liman Mohammed[5], Adamu Ibrahim[5], Toni Rieger[6], Stephan Günther[6], Anges Yadouleton[7] Elisabeth Fichet-Calvet[2]

[1] Natural History Museum, Obafemi Awolowo University, Ile Ife, Osun State, Nigeria
[2] Zoonoses Control Research Group, Bernhard Nocht Institute for Tropical Medicine, Hamburg, Germany
[3] Department of Biochemistry and Molecular Biology, Obafemi Awolowo University, Ile Ife, Osun State, Nigeria
[4] Federal Teaching Hospital Abakaliki, Abakaliki, Ebonyi State, Nigeria
[5] Ministry of Health, Nasarawa State, Nigeria
[6] Virology Department, Bernhard Nocht Institute for Tropical Medicine, Hamburg, Germany
[7] Laboratory of Viral Haemorrhagic Fevers and Arboviruses, Cotonou, Benin
** Corresponding author. Email: aolayemi@oauife.edu.ng*

Killing thousands of people annually, the zoonotic Lassa virus (LASV) is maintained majorly by the multimammate mice *Mastomys natalensis* and *M. erythroleucus*, but other rodent reservoirs also exist [1–2]. Knowledge regarding LASV ecology remains limited in certain areas where Lassa fever continues to be incident and even recently emergent [3]. Here, we assess community composition and LASV infection status of small mammals in key localities across the Guinea savanna belt that spans the countries of Benin and Nigeria. Active LASV infection was determined by conventional (gel based) and quantitative PCR screening, while previous infection was determined by an immunofluorescent assay on IgG antibodies. Surprisingly, *M. natalensis* and *M erythroleucus*, known to be sympatric across the Guinea savanna [4], co-occurred in only one locality and were PCR-negative for the virus, but showed IgG antibodies in localities endemic for Lassa fever within Nigeria. Viremia, alternately, was detected in *Mus* (*Nannomys*) *baoulei* and *Lemniscomys striatus* (a newly-discovered reservoir), carrying relatively ancient LASV lineages, VIII & IX respectively, within Benin. Our results suggest that non-*Mastomys* rodents assume an increased role in LASV ecology within the Guinea savanna belt of Benin and Nigeria, especially in central Benin, which turns out to be a long-overlooked hotbed of early evolution, host-switching, and contemporary emergence.

Keywords: ecological zonation, Lassa virus reservoir, multimammate mice, non-*Mastomys* rodents, novel lineage, savanna

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IS LASSA FEVER BURDEN LINKED TO RODENT ABUNDANCE?

Ayodeji Olayemi[1], **Elisabeth Fichet-Calvet**[2]*

[1] *Natural History Museum, Obafemi Awolowo University, Ile Ife, Osun State, Nigeria*

[2] *Zoonoses Control Unit, Bernhard Nocht Institute for Tropical Medicine, Hamburg, Germany*

* *Corresponding author. Email: fichet-calvet@bnitm.de*

Lassa fever is a viral haemorrhagic disease endemic to West Africa and primarily transmitted to humans from its main reservoir, the Natal multimammate mouse (*Mastomys natalensis*) [1]. Although this rodent is widespread across the region, patterns of human disease vary markedly. Many epidemiological models attribute outbreaks, particularly in Nigeria, to seasonal increases in rodent abundance that elevate contact with humans [2].

We reassessed this assumption using longitudinal field data collected from 12 sites in Guinea, Sierra Leone, and Nigeria, representing more than 64,000 trap-nights in domestic environments [3–5]. *M. natalensis* dominated rodent communities in Guinea, where it comprised 95% of captures, but was far less common in Sierra Leone (55%) and Nigeria (19%), where other commensal species were prevalent. Rodent abundance was 3–6 times higher in Guinea than in the other countries. Despite this, Lassa virus prevalence in *M. natalensis* was similarly high in Guinea and Nigeria (around 40%) and much lower in Sierra Leone (about 10%).

When these ecological findings were compared with human case data from the same regions and periods, a striking mismatch emerged. Guinea, despite high rodent abundance and substantial viral prevalence, reported almost no human cases. Nigeria, in contrast, experienced hundreds of confirmed infections even where rodent abundance was relatively low.

These results indicate that the burden of Lassa fever cannot be explained solely by reservoir occurrence or density. Instead, additional ecological and sociological factors are likely critical, including human mobility, trade networks, contaminated environments, and possibly under-recognised human-to-human transmission. Variations in population immunity may also contribute. We conclude that Lassa fever dynamics arise from a complex system requiring integrated, interdisciplinary investigation within a One Health framework.

Keywords: Lassa fever, *Mastomys natalensis*, abundance, occurrence, Lassa virus

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NICHE AND ECOLOGICAL DIFFERENTIATION PATTERNS OF THE *SPERMOPHILUS* COMPLEX IN ANATOLIA AND IRAN

Şakir Önder Özkurt[1]*, Emin Seyfi[2], Mohammad Moradi Gharakhloo[3]
[1] *Department of Science Education, Faculty of Education, Kırşehir Ahi Evran University, Kırşehir, Türkiye*
[2] *Yeni Bağlıca Mahallesi, Etimesgut, Ankara, Türkiye*
[3] *Department of Biology, Faculty of Science, Zanjan University, Zanjan-Iran*
* *Corresponding author. Email: onderozkurt64@gmail.com*

Previous studies concerning the known distributions, habitat preferences, and taxonomic status of *Spermophilus* species (*S. citellus*, *S. xanthoprymnus*, *S. torosensis* and *S. fulvus*) occurring in different habitat types in Türkiye and Iran were taken as a basis. Anthropogenic pressures, bioclimatic variables and topographic parameters were evaluated together in order to examine patterns of interspecific niche differentiation and ecological divergence [1–5]. The results indicate that the *Spermophilus* complex in Anatolia does not constitute a homogeneous steppe assemblage; rather, it consists of distinct lineages differentiated by specific habitat preferences. Broad and continuous suitable areas across the Central and Eastern Anatolian steppe belt are particularly evident for *S. xanthoprymnus*. The species exhibits high environmental tolerance within semi-arid steppe ecosystems, and this pattern is consistent with previously reported ecological and physiological characteristics [3–4]. In contrast, *S. torosensis* has adapted to elevation-dependent habitats along the Taurus Mountains and to steppe meadows within ancient lake basins and depressions. This spatial structure suggests that topographic barriers have functioned as long-term isolation mechanisms and is consistent with molecular, karyological and morphological evidence supporting the recognition of the species as an independent evolutionary lineage [2]. The suitability areas of *S. citellus*, restricted to Thrace, correspond to meadow-steppe systems and do not show distributional continuity within Anatolia. This pattern supports the role of the Marmara and Bosphorus system as a biogeographical barrier [3–4]. For the Iranian *S. fulvus*, suitability areas largely coincide with the Zagros region; ecological data from Zanjan and surrounding areas indicate the species' association with semi-arid Iranian plateau systems [4–5]. Overall, Anatolia represents not a dispersal corridor for *Spermophilus* species, but a multi-centred evolutionary structure shaped by topographic and climatic heterogeneity.

Keywords: *Spermophilus*, ecological niche differentiation, ecological divergence, biogeographic barriers, Türkiye-Iran

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TICK-BORNE ENCEPHALITIS VIRUS IN WILD RODENTS FROM ENDEMIC AREAS: PREVALENCE AND VIRAL RNA LEVELS

Arnoldas Pautienius[1, 2*], Austėja Žilinskaitė[2], Evelina Šimkutė, Juozas Grigas[1, 2], Marina Sidorenko[3], Jana Radzijevskaja[3], Algimantas Paulauskas[3], Arūnas Stankevičius[1]

[1] Department of Anatomy and Physiology, Lithuanian University of Health Sciences, Kaunas, Lithuania

[2] Institute of Microbiology and Virology, Lithuanian University of Health Sciences, Kaunas, Lithuania

[3] Faculty of Natural Sciences, Vytautas Magnus University, Kaunas, Lithuania

** Corresponding author. Email: arnoldas.pautienius@lsmu.lt*

Wild rodents are considered key reservoir hosts of tick-borne encephalitis virus (TBEV) and are widely used as sentinel animals for identifying natural foci of virus circulation [1–2]. However, detecting TBEV in wildlife reservoirs remains challenging because infections in natural hosts are typically associated with very low viral RNA concentrations.

To assess the suitability of rodents for confirming TBEV foci, small wild rodents (n = 139) were trapped in confirmed endemic locations in Lithuania and tested for viral RNA in brain and internal organ samples. TBEV RNA was found in 74.8% of rodent tissue suspensions (95% CI: 66.7–81.1). After culturing samples in Neuro-2a cells, the detection rate increased to 96.4% (95% CI: 91.8–98.0), confirming the presence of viable virus in most rodents captured at endemic sites.

Quantitative analysis of selected rodent samples with the lowest Ct values showed a moderate increase in viral RNA levels after cell culture isolation (5.71 vs 6.35 log10 copies/mL; $p < 0.05$). However, quantitative analysis using digital PCR across a larger dataset revealed that TBEV RNA copy numbers in natural samples were generally very low and highly variable, with an average of 6.72 copies/μL (range: 0.11–69.41 copies/μL) in uncultured samples. When these samples were subsequently propagated in mammalian cell lines (Vero, Neuro-2a, and MARC-145), no consistent or statistically significant increase in viral RNA copy numbers was observed.

Overall, these findings suggest that cell culture primarily increases the likelihood of detecting the virus, whereas viral RNA concentrations in natural hosts remain low. This highlights the significance of using sensitive molecular methods in studying TBEV ecology and indicates that the choice of samples and sampling strategy can greatly affect viral amplification results.

Keywords: TBEV, TBEV prevalence, tick-borne encephalitis, digital PCR

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RAPID CHROMOSOMAL RADIATION ACROSS SUB-SAHARAN AFRICA: A PHYLOGENOMIC PERSPECTIVE ON THE GENUS *TATERILLUS*

Barbora Pavlíčková[1, 2*], Anna Bryjová[1], Laurent Granjon[3], Gauthier Dobigny[3], Josef Bryja[1, 2]
[1] Institute of Vertebrate Biology CAS, Brno, Czech Republic
[2] Department of Botany and Zoology, Faculty of Sciences, Masaryk University, Brno, Czech Republic
[3] Biology Centre for Population Management, Montferrier-sur-Lez, France
** Corresponding author. Email: pavlickova.barbora910@gmail.com*

Gerbils of the genus *Taterillus* (Gerbillini), distributed in a wide belt of sub-Saharan Africa from Mauritania to Somalia, represent a case of cryptic diversity combined with extensive karyotypic variation. To date, species delimitation within the genus has relied mostly on karyotypic differences [1] because reliable molecular data have been largely unavailable. Universal barcoding primers for rodents often amplify nuclear mitochondrial pseudogenes (NUMTs) rather than the intended mitochondrial cytochrome b gene, or do not work at all, preventing species-level identification. To overcome this limitation, we sequenced complete mitogenomes of several *Taterillus* species using high-throughput sequencing and designed *Taterillus*-specific primers. In the next step, we generated 90 cytochrome b sequences, including many from karyotyped individuals. Based on mitochondrial phylogeny, we selected representatives of each mitochondrial lineage for genomic sequencing of *ca* 4000 ultra-conserved elements (UCE) loci. Using this integrative approach enabled us to delimit species, test the karyotype-based taxonomy, and reconstruct the evolutionary history of the genus.

Keywords: *Taterillus*, karyotypic radiation, phylogenomic, gerbils, Sahelo-Sudanian savanna

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RODENTS AND THEIR ROLE IN THE TRANSMISSION OF ZOONOTIC VECTOR-BORNE PATHOGENS IN LITHUANIA

Jana Radzijevskaja*, Dalytė Mardosaitė-Busaitienė, Indrė Lipatova, Evelina Kaminskienė, Algimantas Paulauskas
Vytautas Magnus University, Kaunas, Lithuania
** Corresponding author. Email: jana.radzijevskaja@vdu.lt*

Besides their ecological roles, small mammals are important for public health as reservoirs of zoonotic pathogens and hosts for vectors such as fleas and immature ticks, contributing to the circulation of vector-borne infections. We investigated the prevalence and genetic diversity of *Borrelia*, *Bartonella*, *Rickettsia*, and *Babesia* in rodents and their ectoparasites to better understand the role of different rodent species in the maintenance and transmission of these pathogens in Lithuania

[1–5]. Pathogen detection and characterisation were performed using PCR amplification of different genomic regions followed by sequence analysis. Our findings show that *Borrelia burgdorferi* s.l. circulates widely among rodents, with *B. afzelii* as the predominant genospecies. *B. garinii* and *B. miyamotoi* were also detected in some voles and mice species. Voles, particularly *Microtus arvali*s and *Clethrionomys glareolus*, were shown to be efficient reservoirs, significantly contributing to transmission of *B. afzelii* to larval ticks. Screening for rickettsial agents identified *Rickettsia helvetica* in rodents, while analysis of associated ectoparasites revealed a broader diversity of rickettsial species, including *R. helvetica*, *R. felis*, and *R. monacensis*. Infection rates differed among ectoparasite groups, with the highest prevalence detected in fleas, followed by ticks and mites. Investigation of protozoan parasites demonstrated the presence of the zoonotic *Babesia microti* strains, with voles of the genus *Microtus* representing key hosts in its natural cycle, particularly in meadow habitats. *Bartonella* spp. were highly prevalent in rodent populations, with sequence analysis revealing *B. grahamii*, *B. taylorii*, *B. rochalimae*, *B. tribocorum*, *B. coopersplainsensis*, and *B. doshiae*. Our studies demonstrate that small rodents and their ectoparasites play an important role in the maintenance and circulation of zoonotic pathogens in Lithuania, highlighting their significance in the epidemiology of vector-borne diseases in the region.

Keywords: small rodents, ectoparasites, vector-borne pathogens

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THE ROLE OF HABITAT COMPLEXITY IN THE TRANSMISSION OF A RODENT-BORNE ZOONOTIC PATHOGEN

Riana V. Ramanantsalama[1]*, Joni Uusitalo[2], Janne Sundell[2], Sironen Tarja[3], Frauke Ecke[1]

[1] Department of Organismal and Evolutionary Biology, University of Helsinki, Finland

[2] Lammi Biological Station, University of Helsinki, Finland

[3] Department of Virology, University of Helsinki, Helsinki, Finland
** Corresponding author. Email: riana.ramanantsalama@helsinki.fi*

Pathogen transmission is influenced not only by the traits of host species but also by environmental and habitat characteristics [1]. However, the ecological mechanisms linking habitat structure to disease dynamics remain poorly understood [2]. Clarifying these mechanisms is essential for predicting how biodiversity and landscape change influence the emergence and spread of zoonotic pathogens. Here, we experimentally tested how habitat complexity affects disease-related processes using the Puumala virus (PUUV; *Orthohantavirus puumalaense*) and its natural reservoir host, the bank vole (*Clethrionomys glareolus*), in Lammi, Finland. We conducted a large-scale enclosure experiment using 16 outdoor enclosures (40 × 30 m), manipulating two ecological factors: vegetation complexity (mowed vs. unmowed habitats) and host density (high density of ten individuals; low density of four individuals). This factorial design enabled us to evaluate the influence of the habitat structure and host density on key parameters of pathogen transmission, including individual contact rates and home-range size. Each enclosure was equipped with nine live traps, camera traps, and small mammal tracking boxes, allowing continuous monitoring of individually marked voles implanted with PIT (Passive Integrated Transponder) tags. Contact patterns and spatial behaviour were analysed using Generalised Linear Mixed Models. Infection outcomes were assessed through PCR screening of saliva and faecal samples for PUUV. By integrating the habitat structure, host behaviour, and infection data, this study identifies ecological conditions influencing zoonotic risk and contributes to a broader understanding of biodiversity–disease relationships, providing insights for ecosystem-based habitat management aimed at mitigating disease emergence.

Keywords: Puumala virus, bank vole, habitat complexity, pathogen transmission, zoonotic disease

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BEYOND THE ENCLOSURE: A DECADE OF MONITORING REVEALS ALTERED TRAITS IN A EUROPEAN GROUND SQUIRREL WITH IMPLICATIONS FOR A RECOVERY PROGRAM

Irena Schneiderová[1]*, Jitka Matoušová[2], Roman Vodička[3], Jan Matějů[4]
[1] Department of Zoology, Faculty of Science, Charles University, Prague, Czech Republic
[2] Nature Conservation Agency of the Czech Republic, Prague, Czech Republic
[3] Prague Zoological Garden, Praha, Czech Republic
[4] Museum Karlovy Vary, Karlovy Vary, Czech Republic
** Corresponding author. Email: irena.schneid@gmail.com*

Effective integrated conservation programmes critically depend on high-quality animals from *ex situ* breeding, yet insufficient scientific rigour in husbandry protocols can lead to unintended consequences that compromise reintroduction success. Drawing on over a decade of monitoring data for the European ground squirrel (*Spermophilus citellus*), we compared a semi-captive, supplementary-fed colony with an adjacent free-ranging population to assess the effects of enclosure management on key population traits. Our findings reveal that the semi-captive system significantly altered traits in ways that could negatively impact long-term viability. Notably, non-lactating females inside the enclosure exhibited a statistically significant mean body mass increase of 28.4% compared to free-ranging counterparts, while males also showed a tendency toward higher body mass. These trends, along with a high proportion of non-lactating females, mirror patterns found in supplementary-fed wild populations [1], suggesting that intensive provisioning may inadvertently impair reproductive success. Conversely, juveniles born inside the enclosure were significantly lighter, likely due to intense competition with dominant adults. Our results demonstrate that practitioners must implement science-based husbandry protocols and feeding strategies that minimise adult-juvenile competition, such as using diets that resemble natural nutritional intake [2]. This study highlights the necessity of close cooperation between zoos and academic institutions [3] and the adoption of systematic long-term monitoring. Such a rigorous, integrated approach is essential to mitigate unintended negative consequences, prevent resource waste [4] and maximise conservation outcomes for this critically endangered species.

Keywords: *ex situ* conservation, husbandry protocols, Rodentia, *Spermophilus citellus*, supplementary feeding

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IMPACT OF HUMAN DISTURBANCE ON SMALL MAMMAL BIODIVERSITY AND PATHOGEN PREVALENCE IN THE DEMOCRATIC REPUBLIC OF THE CONGO

Vincent Sluydts[1*‡], Rianne van Vredendaal[1‡], Lea Joffrin[1], Claude Mande[1, 2], Nicolas Laurent[1], Pascal Baelo[2], Steve Ngoy[2], Jana Tesikova[1], Herwig Leirs[1], Sophie Gryseels[1], Erik Verheyen[3], Guy-Crispin Gembu[2], Joachim Marien[1, 4]

[1] *Evolutionary Ecology Group, Department of Biology, University of Antwerp, Wilrijk, Belgium*
[2] *Centre for Biodiversity Monitoring, University of Kisangani, Kisangani, Democratic Republic of the Congo*
[3] *Vertebrate Group, Directorate Taxonomy and Phylogeny, Royal Belgian Institute of Natural Sciences, Brussels, Belgium*
[4] *Virus Ecology Group, Department of Biomedical Sciences, Institute of Tropical Medicine, Antwerp, Belgium*
* *Corresponding author. Email: vincent.sluydts@uantwerpen.be*
‡Equal contribution of coauthors

Biodiversity in Afrotropical forests is declining rapidly due to deforestation and intensified bushmeat trade. Concurrently, the frequency of emerging infectious disease outbreaks linked

to small mammal reservoirs is increasing. Because shifts in biodiversity alter local community assemblies, they may either reduce (dilution effect) or enhance (amplification effect) the community's competence to transmit pathogens [1]. However, how this biodiversity loss impacts the risk of pathogen spillover to humans remains poorly understood.

In this study, small mammal communities were surveyed across a degradation gradient, ranging from primary forest and secondary forest to agricultural land and villages, at two sites in the Democratic Republic of the Congo (Kponyo and Inkanamongo). A substantial sampling effort of 8,816 trap-nights resulted in the identification of 101 different small mammal species. Pathogen screening via PCR revealed significant prevalence levels for paramyxovirus, (9.7%), hepacivirus (4.0%), and coronavirus (6.8%), as well as the bacterial genus *Bartonella* (6.4%).

Two primary hypotheses were investigated: (1) that small mammal diversity peaks at an intermediate human disturbance, and (2) that these community shifts drive changes in pathogen prevalence and diversity contingent on local host assembly. These findings contribute to a deeper understanding of the biodiversity-disease relationship and provide critical insight for future ecosystem management and biological conservation strategies.

Keywords: rodent-borne diseases, human-wildlife interface, Africa, dilution effect, community assembly

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THE ROLE OF THE SOUTHERN AFRICAN GREAT ESCARPMENT IN THE PHYLOGENY OF VLEI RATS (MURINAE: *OTOMYS*)

Peter Taylor[1]*, Josef Bryja[2], Nkanyiso Sishange[1], Zandile Fakude[1], Nico Avenant[3], Lehlohonolo Mofokeng[1], Guila Ganem[4], Shilpa Parbhu[1], Andries Phukuntsi[5], Mpho Ramoejane[1]

[1] *University of the Free State, Bloemfontein, South Africa*
[2] *Institute of Vertebrate Biology, Czech Academy of Sciences, Brno, Czechia*
[3] *National Museum, Bloemfontein, South Africa*
[4] *CNRS Researcher, Institute of Evolutionary Sciences, Montpellier University, France*
[5] *South African Environmental Observation Network, South Africa*
** Corresponding author. Email: taylorpj@ufs.ac.za*

The African murid genus *Otomys* comprises 39 species and six additional genetically defined lineages of stocky, short-tailed rodents known as vlei rats. The group has a South African origin, followed by multiple dispersals from southern to eastern Africa and vice versa, as well as dispersals and vicariance events between different ranges within east and west Africa [1–3]. Despite relatively intensive research in the last two decades, the phylogenetic relationships and biogeography of the South African *irroratus* clade are not completely resolved. We present new molecular and morphological data from 16 newly collected individuals from the eastern Free State Province of South Africa, which illuminate the phylogeny and biogeography of this group and add one new, very small-sized and pallid-coloured species from the highveld of South Africa, distinct on cytochrome-b and cranial characters from other species. On mitochondrial and nuclear gene sequences and genomic UCE analysis, this new species belongs to the *irroratus* clade, bringing the number of species in this clade to six. As found by earlier authors, we found a distinct genetic discontinuity (cytochrome-b distance of 4.4%) between populations of the widespread *O. auratus* to the west and east of the High Drakensberg, with both clades present in the midlands of KwaZulu-Natal, with chromosomal but not morphological characters distinguishing them, suggesting possible incipient speciation and at least subspecific separation.

Keywords: Rodentia, Muridae, Otomyini, integrative taxonomy

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A ONE HEALTH APPROACH TO MANAGING RODENT PESTS IMPACTING HUMAN HEALTH AND WELLBEING IN SOUTH AFRICAN TOWNSHIPS: OHRATSA

Peter John Taylor[1*], Lourens Swanepoel[2], Samie Amidou[2], Felicity Burt[1], Shingirai Chamisa[1], Fanie Coetzee[2], Lethlogonolo Diseko[1], Armand Engelbrecht[7], Zandile Fakude[1], Sibusile Hadebe[1], Tanya Fouche[5], Arun Gokul[4], Aliza Le Roux[1], Lefty Mahlodi Mpya[1], Lehlohonolo Mofokeng[1], Ara Monadjem[7], Thabang Mokoena[1], Shadreck Muchaku[3], Jolly Musoke[1], Lesly Nembudani[2], Nthatisi Nyembe[1], Patricks Otomo[1], Shilpa Parbhu[1], Nonhlanhla Radebe[1], Mpho Ramoejane[1], Hayley Thompson[3], Safi Traore[2], Thobeka Ziqubu[1], Manqobo Zungu[2], Steven Belmain[6]

[1] University of the Free State, Bloemfontein, South Africa
[2] SARChI Chair on Biodiversity Value & Change, University of Venda, South Africa
[3] University of Fort Hare, Dikeni, South Africa
[4] University of Mpumalanga, South Africa
[5] University of South Africa, Pretoria, South Africa
[6] Natural Resources Institute, University of Greenwich, London, UK
[7] University of Pretoria, Pretoria, South Africa
** Corresponding author. Email: taylorpj@ufs.ac.za*

This project examines the multifaceted challenges caused by rodents in South African townships, focusing on their impacts on human health, food and nutrition security, and mental wellbeing. Using One Health, an ecologically based approach, it aims to identify safer, more sustainable rodent-management technologies in partnership with communities and public authorities. Rodents contaminate food with urine and faeces, increase disease risks, promote

aflatoxin growth, and reduce nutritional value through selective feeding [1]. Heavy reliance on toxic rodenticides further threatens human and environmental health, while endemic rodent-borne diseases remain frequently misdiagnosed despite millions of global cases each year. The project addresses three core questions: (1) how rodent activity affects food quality, safety, and nutrition in urban households; (2) how infestations influence mental health, particularly through stigma, social pressure, and reduced personal agency among vulnerable community members; and (3) whether innovative, ecologically based tools, such as rodent fertility control [2–3], can provide safer, more socially acceptable alternatives to conventional poisons while reducing disease transmission. Ultimately, the project seeks to generate evidence to support sustainable rodent-management strategies that lessen zoonotic spillover and protect livelihoods in low- and middle-income communities.

Keywords: contraceptives, Rodentia, Muridae

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REPRODUCTIVE IMPACTS OF ETHANE DIMETHANESULFONATE (EDS) IN PRE-PUBERTAL AND ADULT FEMALE WISTAR RATS

Karolina da Silva Tonon[1], Jorge Willian Franco de Barros[1], Wilma De Grava Kempinas[1, 2*]

[1] *Institute of Biosciences, São Paulo State University (UNESP), Botucatu, Brazil*

[2] *Institute of Biotechnology (IBTEC), São Paulo State University (UNESP), Botucatu, Brazil*

* *Corresponding author. Email: wilma.kempinas@unesp.br*

Ethane dimethanesulfonate (EDS) is a cytotoxic agent known for its effects on Leydig cells [1]. Our research group has previously demonstrated that EDS administered via diet promotes transient infertility in male rats (data unpublished due to a patent application). The impact of EDS on female rodents is less documented. This study compared the reproductive effects of EDS administered via gavage to adult and pre-pubertal female Wistar rats. Adult females received EDS daily in two doses for 30 days, while pre-pubertal rats were treated for five days starting at postnatal day (PND) 22. The animals in the control groups received the vehicle (DMSO). In adults, EDS gavage resulted in transient weight gain reduction, prolonged oestrus, and significantly lower sexual receptivity, as indicated by lordosis coefficients below 80%. Immunohistochemical analysis revealed a decrease in tertiary follicles marked by anti-Müllerian hormone (AMH) in high-dose gavage groups, suggesting an impact on ovarian reserve. Conversely, pre-pubertal exposure via gavage exhibited marked systemic toxicity, with a survival rate of only 57%. Surviving females showed a significant delay in vaginal opening and the absence of a first

oestrus within two weeks post-opening. Long-term effects in these females included a 50% reduction in the lordosis quotient and compromised reproductive performance, characterised by fewer corpora lutea, reduced implantation sites, and higher post-implantation loss. Additionally, absolute weights of the ovaries and gravid uterus were significantly lower at PND 85. These results demonstrate that while EDS disrupts reproductive regularity and follicular reserve in adults, pre-pubertal exposure leads to severe developmental delays and permanent subfertility. Therefore, EDS negatively impacts the female rat reproductive health, with effects varying significantly based on the age of exposure.

Keywords: ethane dimethanesulfonate, female reproduction, Wistar Rats

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COMBINING DATA ON RESERVOIR HOST DENSITY AND INFECTIONS TO PREDICT A ZOONOTIC EXPOSURE HAZARD

Katherine E. Wearing[1, 2*], Jasmine S. M. Veitch[3, 4], Janine Mistrick[1, 5], Tarja Sironen[6], Meggan E. Craft[5], Clayton E. Cressler[7], Richard J. Hall[8, 9, 10], Sarah A. Budischak[3], Kristian M. Forbes[1]

[1] Department of Biological Sciences, University of Arkansas, Fayetteville, AR, USA
[2] Lammi Biological Station, University of Helsinki, Lammi, Finland
[3] Department of Natural Sciences, Pitzer and Scripps Colleges, Claremont, CA, USA
[4] Faculty of Veterinary Medicine, University of Calgary, Alberta, Canada
[5] Department of Ecology, Evolution, and Behavior, University of Minnesota, St. Paul, MN, USA
[6] Department of Virology, University of Helsinki, Helsinki, Finland
[7] School of Biological Sciences, University of Nebraska, Lincoln, NE, USA
[8] Odum School of Ecology, University of Georgia, Athens, GA, USA
[9] Department of Infectious Diseases, College of Veterinary Medicine, University of Georgia, Athens, GA, USA
[10] Center for the Ecology of Infectious Diseases, University of Georgia, Athens, GA, USA
** Corresponding author. Email: kwearing@uark.edu*

It is necessary to understand reservoir host biology to estimate the hazard of human exposure to zoonotic pathogens [1]. This is particularly true in systems where every human infection is an individual spillover event from reservoir hosts, as is the case for Puumala hantavirus, a zoonotic virus environmentally transmitted to humans from bank vole reservoir hosts [2]. Despite the connection between reservoir hosts and human exposure hazard, it remains challenging to determine what environmental factors and reservoir host characteristics are informative for estimating this hazard. We used the Puumala hantavirus-bank vole system to examine factors impacting the exposure hazard. We manipulated resource availability and coinfecting nematodes in a large-scale field experiment and longitudinally monitored wild bank vole populations for three consecutive years. We then combined data on vole density, number of infected individuals, and viral shedding to estimate an index for the exposure hazard. We found evidence of spatial and temporal variation in the exposure hazard. Importantly, high density and

high numbers of infected hosts increased the exposure hazard, but density was not sufficient by itself to increase this hazard. Resource availability impacted likelihood of reservoir infection at the population scale, while coinfecting parasites impacted likelihood of reservoir viral shedding at the individual level. These results indicate that, for environmentally transmitted pathogens, it is important to understand both the density of reservoir hosts and the number of infected hosts to properly evaluate human exposure hazard.

Keywords: exposure hazard, zoonotic pathogen, reservoir

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PREDATORS OR SECONDARY DISPERSERS? EVALUATING THE ROLE OF SCATTERHOARDING RODENTS IN THE RECRUITMENT OF A BIRD-DISPERSED TREE

Aleksandra Wróbel[1]*, Milena Zduniak[1], Eike Lena Neuschulz[2], Rafał Zwolak[3]

[1] *Mammal Research Institute, Polish Academy of Sciences, Białowieża, Poland*

[2] *Senckenberg Biodiversity and Climate Research Centre, Frankfurt am Main, Germany*

[3] *Department of Systematic Zoology, Adam Mickiewicz University in Poznań, Poznań, Poland*

* *Corresponding author. Email: a.wrobel@ibs.bialowieza.pl*

Abiotic factors have traditionally been considered the primary determinants of range limits of species and their responses to climate change [1]. However, biotic interactions, such as seed predation and dispersal, also play crucial roles in shaping plant distributions and influencing range shifts [2]. In this study, we investigated how scatterhoarding rodents affect the recruitment of Swiss stone pine (*Pinus cembra*) at its upper elevational limits in the Swiss Alps. We focused on interactions between the pine and the rodent community, exploring how these interactions affect the effectiveness of seed dispersal by the spotted nutcracker (*Nucifraga caryocatactes*). We conducted seed crop estimations, rodent live-trapping, seed-tracking experiments, and seedling emergence trials across an elevational gradient over three years. We tested whether rodents act as mutualists by caching seeds in favourable microsites or as antagonists by predating seeds and pilfering caches. Our results showed that rodents acted consistently as seed predators and cache pilferers. In seed-tracking experiments, they consumed 97% of the seeds they removed, caching only 3%. Furthermore, rodents reduced seedling emergence from simulated nutcracker caches by two-thirds. These findings indicate that rodents suppress *P. cembra* recruitment by reducing the effectiveness of nutcracker-mediated dispersal. The negative impact was most pronounced when rodent populations were high and seed availability was low, aligning with the predator satiation hypothesis [3]. Our study suggests that climate warming, which is expected to increase rodent abundance at higher elevations, may intensify these negative effects, impeding the upward migration of Swiss stone pine. These results emphasise the importance of integrating biotic interactions into ecological models to improve predictions of ecosystem responses to environmental changes.

Keywords: climate change, diplochory, mountains, range shift, synzoochory

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FINE-SCALE POPULATION GENETICS AND DISPERSAL OF *RATTUS NORVEGICUS* IN URBAN SINGAPORE REVEALED BY ddRAD-SEQ

Yan Zhuang[1]*, Denise Tan[1], Lee Ching Ng[1, 2, 3], Cheong Huat Tan[1]

[1] *Environmental Health Institute, National Environmental Agency, Singapore, Singapore*
[2] *Saw Swee Hock School of Public Health, National University of Singapore, Singapore*
[3] *School of Biological Sciences, Nanyang Technological University, Singapore, Singapore*
* *Corresponding author. Email: ZHUANG_Yan@nea.gov.sg*

Urban rats, including *Rattus norvegicus*, are commensal species that depend on humans for food and harbourage, posing significant urban management and public health challenges in densely populated cities such as Singapore [1]. Understanding rat population structure and dispersal patterns is critical for predicting pathogen transmission and implementing targeted control strategies [2]. We used double-digest restriction-site associated DNA sequencing (ddRAD-seq) to assess genetic relatedness and infer fine-scale dispersal pattens of *R. norvegicus within an urban site in Singapore.* Genome-wide single nucleotide polymorphisms (SNPs) revealed population substructure among individuals captured at nearby locations within the study site. Kinship analysis revealed extensive first- to fourth-degree relationships, familial connections were identified between individuals separated by distances ranging from 188 to 474 metres, suggesting potential movement across these distances. Admixture analysis supported a K = 4 ancestral population model, revealing genetic intermixing. This suggests the location may serve as a genetic hub where rats from distinct ancestral lineages converge and interbreed. Furthermore, fineRADstructure analysis demonstrated population stratification, showing genetic substructures that potentially reflect distinct breeding colonies to gene flow within the urban environment. These findings demonstrate that rat populations exhibit complex genetic structure even at fine spatial scales within urban environments. The coexistence of genetic clustering and gene flow suggests that whilst rats maintain some population structure, dispersal and breeding across the study area still occur. Our finding provides a foundation for understanding how urban landscape influence commensal rat population dynamics, which can inform the development of spatially targeted control strategies in Singapore's urban context.

Keywords: SNPs, genetic relatedness, population structure, movement

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ASSOCIATION BETWEEN RODENTICIDE RESIDUES AND POTENTIALLY ZOONOTIC PATHOGENS AND PARASITES IN URBAN BROWN RATS (*RATTUS NORVEGICUS*) IN HELSINKI, FINLAND

Viktor Zöldi[1]*, Suvi Sallinen[1], Rebekka Kukowski[1], Pertti Koivisto[2], Sanna Koivisto[3], Tuomas Aivelo[1, 4]

[1] *Organismal and Evolutionary Biology Research Programme, Faculty of Biological and Environmental Sciences, University of Helsinki, Helsinki, Finland*

[2] *Finnish Food Authority (Ruokavirasto), Helsinki, Finland*

[3] *Finnish Safety and Chemicals Agency (Tukes), Helsinki, Finland*

[4] *Science Communication & Society, Institute of Biology, University of Leiden, Leiden, The Netherlands*

* *Corresponding author. Email: viktor.zoldi@helsinki.fi*

Rodenticides have the potential to affect species other than their intended targets, whether through primary or secondary poisoning. Sublethal effects include weakened immune function, leading to greater vulnerability to pathogens [1–3]. Rat control primarily aims to protect human health, yet rodenticides may unintentionally increase pathogen and parasite transmission, emphasising the need for a disease-ecology perspective. Helsinki rats host a diverse assemblage of zoonotic organisms [4], including intestinal parasites, bacteria, and viruses. In Helsinki, application of rodenticide baits – mostly involving anticoagulant active ingredients – is undertaken mainly by pest management companies. To examine whether rodent control has wider ecosystem impacts, including potential effects on disease occurrence, we analysed the association between rodenticide exposure and infectious agents' prevalence.

To examine the two jointly, we sourced 54 fresh carcasses from 13 addresses across ten different postal code areas of Helsinki between June 2022 and May 2023, through a pest management company. We surveyed pathogens and parasites and analysed rodenticide residues, using the previously described methodology [4–5]. We used Bayesian generalised linear mixed-effects models to test whether rodenticide occurrence was associated with rat sex and weight, and to assess its relationship with parasite and pathogen prevalence.

Over half of the rats were rodenticide-exposed, one-third tested positive for infectious agents, whilst twelve individuals, originating from eight sample sites, were positive for both. Coumatetralyl was the most common residue (37% of the rats), and jeilongvirus the most prevalent infectious agent (15%). Difenacoum was detected significantly less often in males (male–female ratio 1:4), and difenacoum-exposed rats were less likely to carry parasites and bacterial infections. Our findings indicate that sublethally rodenticide-exposed, free-ranging rats represent a substantial secondary-poisoning risk in Helsinki. The relationship between rodenticide exposure and parasite or pathogen carriage, however, warrants further study.

Keywords: zoonoses, jeilongvirus, anticoagulant rodenticides, difenacoum, liver

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SEED DEFENCES ALTER DENSITY-DEPENDENT FORAGING AND SEED FATE IN SCATTERHOARDING RODENTS

Rafał Zwolak[1]*, Ligia Marcinkowa

[1] Department of Systematic Zoology, Adam Mickiewicz University, Poznań, Poland

** Corresponding author. Email: rzwolak@amu.edu.pl*

Predator satiation is a key mechanism linking pulsed seed production with consumer dynamics, yet it is typically treated as a function of seed abundance alone [1]. At the same time, a large body of work shows that seed traits influence foraging decisions of scatterhoarding rodents [2–3], but these effects are usually considered independent of seed density. We tested whether seed defenses modify satiation dynamics by combining a density-manipulation experiment with measurements of post-dispersal seed fate.

We conducted field experiments with yellow-necked mice (*Apodemus flavicollis*) foraging on acorns of two oak species (*Quercus robur* and *Q. rubra*) that differ strongly in shell mechanical resistance. Acorns were presented at five density levels and in two spatial arrangements (clumped vs. dispersed), and their fate (removal, consumption, caching, abandonment, and dispersal distance) was tracked over three-day sessions.

In the well-defended species (*Q. rubra*), seed removal declined markedly with increasing density, indicating rapid satiation. At the same time, consumption decreased, dispersal distance shortened, and a growing proportion of seeds was abandoned on the surface after dispersal.

In contrast, in the less defended species (*Q. robur*), removal remained consistently high across densities, and post-dispersal fate showed little change. Spatial distribution of seeds had only limited effects and did not alter the main species-specific patterns.

These results show that predator satiation is not determined by seed abundance alone. Instead, seed defenses modify how rodents respond to increasing resource availability, effectively shifting satiation dynamics. Our findings suggest that the influence of seed traits on rodent foraging is density-dependent, and that integrating seed defenses with masting theory may improve our understanding of plant–granivore interactions and seed dispersal processes in temperate forests.

Keywords: masting, predator satiation, seed dispersal, seed predation, synzoochory

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Poster presentations

FROM VALLEY TO TIMBERLINE: HOW ELEVATION AND YEAR SHAPE SMALL MAMMAL POPULATIONS

Alexandra Alecsa[1]*, Alexandra Mărginean[2], Ana Maria Benedek[2]

[1] Doctoral School in Ecology, Faculty of Biology, University of Bucharest, Bucharest, Romania

[2] Faculty of Sciences, Lucian Blaga University of Sibiu, Sibiu, Romania

** Corresponding author. Email: marcela-alexandra.sandu@s.unibuc.ro*

Small mammals are key components of terrestrial ecosystems, contributing to trophic interactions, vegetation dynamics, and soil processes [1]. Due to their short life cycles and sensitivity to environmental conditions, they are widely used to investigate demographic and morphological responses along environmental gradients [2]. Elevation is known to influence mammalian community composition and dynamics [3] and may also affect morphological traits. We examined elevational and interannual patterns of small mammal populations in the Cindrel Mountains (Romania), between approximately 500 and 1850 m a.s.l., across four forest types: oak, beech, spruce, and timberline. Sampling was conducted each September between 2021 and 2025 using two trapping grids of 64 live traps in each forest type, operated for three consecutive nights. Individuals were classified by sex and assigned to three age groups (juvenile, subadult, adult). We focused on three common species (*Clethrionomys glareolus*, *Apodemus flavicollis*, *Sorex araneus*) and explored variation in species representation, sex ratio, age structure, body size, and body mass across elevation and years. Four main predictions underpin this study: (1) dominant species change in relative abundance along elevation, (2) these patterns vary among years, (3) population structure (sex ratio and age structure) varies with elevation, (4) within species, body size and body mass vary across elevation and years and sexual dimorphism may be detectable. Ordination analyses suggest a joint structuring effect of elevation and year on species composition. Results indicate species-specific elevational patterns and interannual variation in population structure and body size metrics, whereas elevational trends are limited and non-linear. By integrating demographic and biometric perspectives across space and time, this study provides a structured baseline for understanding how environmental gradients shape small mammal populations and their dynamics.

Keywords: population dynamics, body size variation, age classes, sex ratio, temperate forest gradients

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DETECTION OF *BARTONELLA* AND *RICKETTSIA* SPECIES IN LICE COLLECTED FROM SMALL RODENTS

Asta Aleksandravičienė[1]*, Jana Radzijevskaja[1], Loreta Griciuvienė[1], Michal Stanko[2], Algimantas Paulauskas[1]

[1] Vytautas Magnus University, Kaunas, Lithuania

[2] Institute of Parasitology, Slovak Academy of Sciences, Košice, Slovak Republic

** Corresponding author. Email: asta.aleksandraviciene@vdu.lt*

Small rodents are known reservoirs of several zoonotic pathogens and host a variety of ectoparasites, including sucking lice. Bacteria of the genera *Bartonella* and *Rickettsia* circulate in rodent populations and may cause disease in humans. However, the occurrence of these pathogens in rodent-associated lice has been only rarely investigated [1–3]. The aim of this study was to determine the prevalence of *Bartonella* and *Rickettsia* species in lice collected from rodents in Slovakia.

Small rodents were captured alive at four sampling localities in eastern Slovakia. In total, 216 rodents representing six species were examined: *Apodemus agrarius*, *Apodemus flavicollis*, *Microtus arvalis*, *Microtus subterraneus*, *Clethrionomys glareolus*, and *Rattus norvegicus*. From these hosts, 1074 lice belonging to seven species were collected, including *Hoplopleura acanthopus*, *Hoplopleura affinis*, *Hoplopleura edentula*, *Hoplopleura* sp., *Polyplax serrata*, *Polyplax spinulosa*, and *Polyplax* sp. Ectoparasites obtained from each host were pooled according to louse species, developmental stage, and sex. Lice pools were screened using real-time PCR for *Bartonella* spp. and *Rickettsia* spp., followed by species identification through sequence analysis.

Bartonella spp. were detected in *H. affinis* lice collected from *A. agrarius*, *A. flavicollis*, and *C. glareolus*, as well as in a single *P. serrata* specimen obtained from *A. agrarius*. Sequence analysis revealed the presence of *Bartonella coopersplainsensis*, *Bartonella tribocorum*, and *Bartonella taylorii* genogroups.

Rickettsia spp. were identified in *H. affinis* and *P. serrata* specimens collected from *A. agrarius*, as well as in one *P. serrata* louse collected from *A. flavicollis*. Sequence analysis revealed the presence of *Rickettsia helvetica* and another *Rickettsia* spp.

The results of this study demonstrate that rodent-associated lice may harbor *Bartonella* and *Rickettsia* species, including potential zoonotic pathogens. These findings suggest that lice could play a role in the maintenance and circulation of these bacteria in rodent populations.

Keywords: small rodents, sucking lice, *Bartonella*, *Rickettsia*, Slovakia

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SEASONAL VARIATIONS OF MITE AND TICK INFESTATION OF SMALL MAMMALS IN LITHUANIA WITH PREDICTIONS ON CLIMATE CHANGE

Laima Baltrūnaitė*, Neringa Kitrytė
State Scientific Research Institute Nature Research Centre, Vilnius, Lithuania
** Corresponding author. Email: laima.baltrunaite@gamtc.lt*

Small mammals and their ectoparasites are known as reservoir hosts and/or vectors of various pathogens. Lithuania is among highly endemic countries for Lyme borreliosis and tick-born encephalitis in Europe with growth of new cases every year [1–2]. New data about various pathogens in reservoir host or vector species and its probable impact on human and animal health indicate need of further detailed investigation on ectoparasites ecology.

The aim of this research was to analyse seasonal changes in mite (Trombidiformes, Trombiculidae; Mesostigmata, Lelapidae) and tick (Ixodida, Ixodidae) infestation of small mammals.

The study was performed from May 2019 to May 2020 in Lithuania, Vilnius district. Small mammals were trapped once a month using snap-traps in three different habitats (mixed forest, natural meadow, and arable land). In total, 650 small mammal specimens belonging to ten species were trapped, and 10,031 ectoparasites were collected. The prevalence and mean intensity were calculated for each month.

The prevalence varied significantly across months in all three ectoparasite groups. The most extreme changes in prevalence were typical to ixodid ticks with total absence during winter months. In contrary, low prevalence of chigger mites was registered in summer. The mean intensity showed significant variation for chigger mites and ixodid ticks, reaching lowest values in summer and winter, respectively. During the study, an extremely warm and snowless winter was registered, but ixodid ticks were not found on small mammals. Global warming might affect parasite communities by altering species composition and abundance, as well as facilitating the emergence of new pathogens and diseases. It indicates the need of continuous multiannual monitoring of reservoir hosts, vectors, and pathogens throughout different seasons and geographic regions.

Keywords: small mammals, mites, ticks, seasonal variation

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DEMOGRAPHIC DATA ON THE EUROPEAN SNOW VOLE IN THE GRAN SASSO AND MONTI DELLA LAGA NATIONAL PARK

Alessia Breccia[1, 2*], Stefania Gasperini[1], Paola Bartolommei[1], Andrea Bonacchi[1], Emiliano Manzo[1], Roberto Cozzolino[1]

[1] Ethoikos Fondation, Convento dell'Osservanza snc, Siena, Italy

[2] University of Siena – Department of Life Sciences, Siena, Italy

** Corresponding author. Email: alessia.breccia6@gmail.com*

The European snow vole (*Chionomys nivalis*) is a South European–Turanian species predominantly living in rocky mountain habitats. The species is poorly known and characterised by a fragmented range. In Italy, its distribution includes the Alps and some areas of the central-northern Apennines, where reference information is still based on sporadic records [1]. Knowledge on the ecology of the European snow vole remains limited, a critical gap given the potential sensitivity of this mountain species to climate and environmental changes [2].

In 2025, a long-term monitoring study on the European snow voles was initiated in the Gran Sasso and Monti della Laga National Park to collect data on the species' ecology and biology. Demographic data were collected at the Campo Imperatore area using a capture–mark–recapture protocol. Two trapping grids were settled and two sampling sessions were carried out during the year, at the beginning of July and at the end of August. Traps were checked twice daily over five consecutive days in each grid and session. Overall, 67 individuals were captured and individually marked in the study area. Preliminary results from the first year of sampling, derived from spatially explicit capture–recapture analyses, yielded a density estimate of approximately 11 individuals per hectare. During the August session, around 50% of previously marked individuals were recaptured. The age structure of the population showed a prevalence of adults (87%) over juveniles (13%). Females were more frequently captured than males, and a high proportion of adults were in reproductive condition in both sessions, although a decrease was observed over the summer (76% in July and 43% in August).

Overall, this project will provide valuable information, improving knowledge on the ecology of the European snow vole and enabling evaluation of its potential role as a sentinel species for monitoring changes in alpine and Apennine ecosystems.

Keywords: European snow vole, population density, sentinel species, capture-mark-recapture

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SPEEDING UP IMAGE ANNOTATION AND OBJECT-DETECTION MODEL TRAINING: AN INTEGRATED PIPELINE FOR WILDLIFE ECOLOGISTS

Bolduc David[1]*, Fauteux Dominique[1, 2], Legagneux Pierre[1]
[1] *Biology Department and Northern Studies Center, Laval University, Canada*
[2] *Center for Arctic Knowledge and Exploration, Canadian Museum of Nature, Ottawa, Ontario, Canada*
* *Corresponding author. Email: david21bolduc@hotmail.com*

The field of ecological research greatly benefits from the recent technological advances and their increasing accessibility. Camera traps are a prime example of a technology that is now embraced by a diversity of research teams to tackle a wide spectrum of questions [1]. The reasons are simple: they allow us to keep an eye on our study subjects with minimal effort and almost no disturbance, and to do so in many places simultaneously. The saved field effort is, however, counterbalanced by the difficulty of extracting analysis-ready data from images. This can be done manually, which is extremely tedious and poorly repeatable, or we can develop and trust custom machine learning algorithms [2], a complex endeavour that may yield disappointing performance if data are limited or unbalanced. Here we present an end-to-end pipeline that starts with raw, unannotated images and ends with a custom object-detection or instance segmentation model. This pipeline has the major advantage of leveraging available object-detection and instance segmentation models to rapidly assemble a large dataset of annotated images. More precisely, we use Timelapse to manually classify images by species, speeding up the process with a handheld controller, MegaDetector and the Segment Anything Model to obtain object coordinates and contours, and the You Only Look Once (YOLO) model architecture to train our models, all these steps being linked with R and Python code. Additionally, we provide efficient techniques to tackle issues often present in wildlife image datasets (e.g. class imbalance). Following this pipeline, we obtained a performant model recognising and segmenting more than 15 species and allowing the extraction of morphological information on individuals.

Keywords: camera-traps, image analysis, object detection, classification

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EXPECTED ROLE OF SCATTERHOARDING RODENTS IN CLIMATE-DRIVEN *FAGUS SYLVATICA* MIGRATION TO A HIGHER ALTITUDE *PINUS CEMBRA* FOREST

Janina Dzięciołowska[1]*, Aleksandra Wróbel[2]

[1] *Student Society of Naturalists, Adam Mickiewicz University, Poznań, Poland*

[2] *Mammal Research Institute, Polish Academy of Sciences, Białowieża, Poland*

* *Corresponding author. Email: jandzi2@st.amu.edu.pl*

Climate change causes shifts in species ranges [1]. These shifts are strictly dependent on species dispersal abilities, but also on the character of recently formed biotic interactions in a new environment [2]. For synzoochoric plants, interactions with animals are one of the most crucial. Animals may act as seed predators or dispersers, being the key factor for final plant range [3]. Models suggest that climatically suitable habitat for beech will move upwards [1], but tree ability to follow these changes depends on rodents' behaviour. We compared how scatterhoarding rodents affect the recruitment of Swiss stone pine (*Pinus cembra*) and European beech (*Fagus sylvatica*) in stone pine forests in the Swiss Alps. We conducted seed-tracking experiments with camera traps to track the fate of individual seeds and identify the species responsible for their removal. Among the removed, found seeds, rodents consumed 88% of the pine seeds and 72% of the beech seeds. A more pronounced difference was observed in caching behaviour: 26% of beech seeds but only 6% of pine seeds were cached. These caching and consumption proportions varied significantly between rodent species. For example, red squirrels (*Sciurus vulgaris*) cached the majority of seeds of both tree species, while bank voles (*Clethrionomys glareolus*) ate all the beech seeds they had removed, showing no caching behaviour for this tree species. We also noted numerous cases of seed removal done by yellow-necked mice (*Apodemus* spp.) and garden dormice (*Eliomys quercinus*). They tended to eat more seeds than squirrels but still cached some – especially beech seeds. Our results indicate that rodent community may act as mutualists for beech, but as antagonists for stone pine. However, fluctuations in their number and food abundance will probably change the outcome of that phenomenon. Therefore, our study will be continued to fully explore this interaction across different ecological contexts.

Keywords: climate change, mountains, range shift, synzoochory

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INTEGRATING POPULATION GENETICS AND LANDSCAPE ANALYSES TO UNDERSTAND *LEPTOSPIRA* TRANSMISSION IN *MYOCASTOR COYPUS*

Blanchet Julie[1*], Loiseau Anne[2], Castel Guillaume[2], Pradel Julien[2], Tatard Caroline[2], Piry Sylvain[2], Cesari Lily[2], Galan Maxime[2], Berthier Karine[2, 3‡], Charbonnel Nathalie[2‡]

[1] University of Montpellier, CBGP, Montpellier, France

[2] CBGP, INRAE, IRD, CIRAD, Institut Agro, University of Montpellier, Montpellier, France

[3] INRAE, Plant Pathology, Montfavet, France

** Corresponding author. Email: julie.blanchet@umontpellier.fr*

‡Equal contribution of coauthors

Pathogens often exhibit heterogeneous spatial distributions, reflecting complex ecological and evolutionary processes. Understanding their transmission dynamics therefore requires integrating host population genetics and social organisation. The coypu (*Myocastor coypus*), an invasive species in the wetlands of France, is a relevant model in this regard. It contributes to the circulation of *Leptospira*, the bacteria responsible for leptospirosis, a still neglected zoonotic disease. Nevertheless, knowledge of the structure of the coypu population and its links to landscape features and pathogen transmission remains limited.

In this study, conducted in two watersheds in southern France, we applied landscape genetics to analyse how environmental heterogeneity and coypu ecology influence the zoonotic hazard from *Leptospira*. Genetic analyses of the coypu population were performed using individual genotyping data obtained from 20 microsatellite markers. Genetic indices (coefficient of relatedness, measure of genetic differentiation) were calculated and analysed in relation with landscape metrics, using the MAPI method [1]. This approach allowed us to identify environmental factors that shape the spatial patterns of genetic structure and gene flow of coypu populations.

Combining landscape genetic analyses with forthcoming analyses of the social organisation as well as *Leptospira* distribution data will allow us to investigate whether transmission is more likely to occur within family groups. *In fine*, our results will contribute to a better understanding of how the spatial and social dynamics of coypus modulate the circulation of *Leptospira* in these southern French watershed regions.

Keywords: *Myocastor coypus*, *Leptospira*, population genetics, rodent-borne zoonoses, spatial analyses

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LAELAPIDAE MITE DIVERSITY IN SMALL RODENTS FROM SUBURBAN HABITATS OF LITHUANIA

Evelina Kaminskienė[1]*, Violeta Šataitytė[1], Michal Stanko[2], Linas Balčiauskas[3], Algimantas Paulauskas[1], Jana Radzijevskaja[1]

[1] *Vytautas Magnus University, Kaunas, Lithuania*

[2] *Institute of Parasitology and Institute of Zoology, Slovak Academy of Sciences, Slovakia*

[3] *Nature Research CentreVilnius, Lithuania*

* *Corresponding author. Email: evelina.kaminskiene@vdu.lt*

Small rodents play an important role in maintaining the natural cycles of arthropod-borne pathogens and serve as key hosts for numerous ectoparasites [1]. Among these ectoparasites, mites of the family Laelapidae are frequently associated with small rodents and may act as potential vectors of microorganisms relevant to animal and human health [2–3]. However, the diversity and infestation patterns of these mites on small rodents remain insufficiently studied in Lithuania, particularly in suburban environments where interactions between wildlife and humans are more frequent. Therefore, the aim of this study was to evaluate the species diversity of Laelapidae mites and to assess their prevalence and mean intensity of infestation in small rodents inhabiting suburban areas of Lithuania. A total of 934 small rodents representing eight different species (*Apodemus agrarius*, *A. flavicollis*, *Clethrionomys glareolus*, *Microtus agrestis*, *M. arvalis M. oeconomus*, *Micromys minutus* and *Mus musculus*) were captured across 20 suburban locations in Lithuania. From these hosts, 14 species of Laelapidae mites, belonging to eight genera (*Androlaelaps*, *Cyrtolaelaps*, *Eulaelaps*, *Haemogamasus*, *Hirstionyssus*, *Hyperlaelaps*, *Laelaps*, and *Myonyssus*), were identified based on morphological characteristics. The prevalence and average intensity of infestation differed depending on the host species and collection site. Among all collected laelapid mite specimens, *Laelaps agilis* was the most prevalent species, occurring on 15.5% of rodents, with *Apodemus flavicollis* harboring the highest number of individuals. Two additional species, *Laelaps hilaris* and *Haemogamasus nidi*, were also common. Notably, this study reports the first record of *Cyrtolaelaps mucronatus* in Lithuania, thereby expanding current knowledge of Mesostigmata mite diversity in suburban habitats and providing a foundation for future studies on host–parasite relationships and pathogen-associated processes.

Keywords: Laelapidae, rodents, suburban habitats

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ECTOPARASITIC ACARID INFESTATIONS OF RODENTS IN OPEN HABITATS ACROSS THE ANTHROPOGENIC STRESS GRADIENT

Neringa Kitrytė*, **Laima Baltrūnaitė**
State Scientific Research Institute Nature Research Centre, Vilnius, Lithuania
** Corresponding author. Email: neringa.kitryte@gamtc.lt*

Rodents are important reservoir hosts of multiple zoonotic parasites and pathogens. The ectoparasitic acarids act as vectors for many pathogens in rodent populations while ixodid ticks are the main pathogen carriers between rodents and other species, including humans. Human-caused habitat changes disrupt environmental conditions that might also alter the patterns of ectoparasite infestations. The aim of this study is to investigate the infestation patterns of ectoparasitic acarids of rodents in open habitats with different levels of anthropogenic pressure.

The research was conducted in Lithuania between 2017 and 2024. Rodents were trapped using snap-traps set in six open habitats: bogs, shrubby meadows, natural meadows, pastures, arable lands, and farmlands (from the least changed to the most changed by the human). We chose to investigate two vole species – bank vole (*Clethrionomys glareolus*) and common vole (*Microtus arvalis*) – due to their differing habitat predilections [1] and importance as reservoir hosts of *Borrelia burgdorferi* sensu lato [2]. Mites of the families Trombiculidae (Trombidiformes) and Laelapidae (Mesostigmata), as well as ticks of the family Ixodidae (Ixodida) were collected.

In total, 221 bank vole and 513 common vole specimens were examined for ectoparasite infestations. Both vole species were infested at an overall similar rate: 81.9% of bank voles and 79.1% of common voles. Overall intensity of infestation was much higher in bank voles, with 26.7 acarids per infested host, while infested common vole on average carried 8.0 acarids. Three acarid groups showed different patterns of infestation considering both host identity and habitats. Concerningly, results indicated aggregation patterns of ticks on bank voles in farmlands – perfect conditions for pathogen spread in the habitat most actively used by human.

Keywords: rodents, ticks, mites, anthropogenic stress

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EVOLUTIONARY HISTORY AND ECOLOGICAL DIVERGENCE DRIVE GUT MICROBIOTA DIFFERENTIATION IN MAMMALIAN RADIATIONS: INSIGHTS FROM NEW GUINEA RODENTS

Jakub Kreisinger[1*], Daniel Okena[1, 2, 3], Frantisek Vejmelka[1, 2, 3], Halil Solak[1], Nona Moradpoor[4, 5], Alexis Ribas[6, 7], Srisupaph Poonlaphdecha[6, 7], Vojtech Novotny[3], Dagmar Čizkova[4]

[1] Department of Zoology, Faculty of Science, Charles University, Prague, Czech Republic

[2] Faculty of Science, University of South Bohemia in České Budějovice, Czech Republic

[3] Biology Centre of the Czech Academy of Sciences, České Budějovice, Czech Republic

[4] Institute of Vertebrate Biology of the Czech Academy of Sciences, Brno, Czech Republic

[5] Faculty of Science, Masaryk University, Brno, Czech Republic

[6] Parasitology Section, Department of Biology, Healthcare and Environment, Faculty of Pharmacy and Food Science, University of Barcelona, Barcelona, Spain

[7] Biodiversity Research Institute (IRBio), University of Barcelona, Barcelona, Spain

** Corresponding author. Email: jakubkreisinger@seznam.cz*

The extant rodent fauna of Papua New Guinea (PNG) stems from two colonisation events followed by rapid radiations: the Miocene Hydromyini and the Pleistocene native Rattini. Consequently, PNG rodents offer a unique opportunity to study microbiota assembly during mammalian adaptive radiation.

We conducted an extensive survey across elevational gradients (200–3700 m a.s.l.) in the Mt Wilhelm and Finisterre ranges [1]. We analysed gut microbiota (16S rRNA) and host phylogeny (ddRAD) in 835 individuals representing 39 species from the Hydromyini lineage, three from the endemic Rattini lineage, and three invasive *Rattus* species.

Within Hydromyini, phylogenetic relatedness and ecological differentiation strongly predicted microbiota structure. Carnivory was associated with reduced alpha diversity, while diet, locomotion, and body mass significantly shaped composition. Host ecology and phylogeny outweighed environmental filtering across altitudes.

We observed consistent differences between lineages. Unexpectedly, invasive *Rattus* microbiota resembled the distantly related Hydromyini more than the endemic Rattini. The uniqueness of endemic Rattini was driven by prevalent *Helicobacter*, Prevotellaceae, and Desulfovibrionaceae ASVs, which were nearly absent in other lineages.

Source-tracking analyses suggested asymmetric transmission: Hydromyini acted as a microbial source for both native Rattini and invasive *Rattus*. In contrast, transmission from invaders to endemic species was negligible. This, combined with the absence of prevalent putative pathogen-associated taxa in invasive *Rattus*, indicates a limited risk of microbial spillover from invasive to native rodents.

Keywords: microbime, metagenome, metabarcoding, symbiosis, adaptive radiation

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WHEN HABITAT MATTERS: RODENT COMMUNITIES ALONG A FUTURE MOTORWAY CORRIDOR IN TRANSYLVANIA

Anamaria Lazăr[1]*, Alexandra Sandu[2, 3], Alexandra Mărginean[2],
Niculina Cic[2], Anamaria Benedek[2]
[1] Transilvania University of Brașov, Brașov, Romania
[2] Lucian Blaga University of Sibiu, Sibiu, Romania
[3] Faculty of Biology, University of Bucharest, Bucharest, Romania
** Corresponding author. Email: anamaria.gurzau@unitbv.ro*

Rodents are important species in many terrestrial ecosystems, playing critical roles in their functioning [1–3]. In turn, rodent communities respond to several biotic and abiotic factors [1–2]. Habitat characteristics influence rodent diversity and abundance by providing food resources, shelter from weather, and protection from predators. Understanding species-habitat relationships is important not only for the advancement of the ecological theory, but also for practical reasons, allowing for the development of management measures aimed at conservation, especially in changing landscapes [3–4]. We evaluated rodent responses to habitat and climate, which directly affects rodent survival and indirectly influences population growth rates by affecting availability of food resources. The field survey was conducted in Southern Transylvania, Romania, prior to the construction of a motorway in the Făgăraș foothills. Thus, this study also aimed to provide a baseline for the future assessment of the infrastucture impact on rodent communities. Rodents were live-trapped monthly between June and September 2024, along the entire Făgăraș foothills sector of the future motorway. Explanatory variables were recorded for each surveyed habitat. Thirteen rodent species were captured in 2,178 trap nights. *Apodemus agrarius* was the dominant species throughout the study period, more abundant in autumn, when it was often the only captured species. Species richness and abundance were influenced by habitat type, seasonality, soil type, and vegetation structure. In general, both species richness and abundance were higher in uncultivated land and groves and significantly lower in agricultural crops.

Keywords: *Apodemus agrarius*, species-habitat relationships, infrastructure development, impact assessment, Transylvania

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MINERAL POLLUTION AND RODENT–HELMINTH PATHOSYSTEMS ACROSS URBAN NEIGHBORHOODS IN SENEGAL

Romane Lux[1], Nadia Crini[2], Caroline Amiot[2], Johannes Tavoillot[1], Hugo Sentenac[2], Renaud Scheifler[2], Christophe Diagne[1]*

[1] CBGP, IRD, INRAE, CIRAD, Montpellier SupAgro, Univ Montpellier, Montferrier/Lez, France

[2] Marie et Louis Pasteur University, CNRS, Chrono-environnement (UMR 6249), Besançon, France

** Corresponding author. Email: christophe.diagne@ird.fr*

Urbanisation in Africa is a rapid process that often promotes precarious environments, where interactions between humans and rodents – major reservoirs of zoonotic pathogens – are intensified [1]. These areas are also characterised by increasing chemical pollution from anthropogenic activities. Such pollutants can accumulate in reservoir rodents and disrupt immune function through toxic physiological effects when concentrations exceed or fall below critical thresholds, potentially affecting susceptibility to parasitic infections and amplifying pathogen transmission risks [2]. However, studies jointly addressing chemical pollution and parasite or pathogen dynamics within urban ecosystems remain scarce, particularly in urbanising African areas. Here, we explored the associations between mineral elements (ME, often referred to as trace or metal elements) and gastrointestinal helminth parasitism in house mouse (*Mus musculus domesticus*) populations. Helminths represent a focal parasitic group due to their strong influence on rodent population dynamics, their potential zoonotic nature, and their role in modulating host immune responses, thereby affecting co-infections with viral and bacterial pathogens [3]. Mice were sampled across multiple sites representing contrasting urbanisation profiles within the city of Dakar, Senegal [4]. Helminth communities were characterised using morphological and molecular approaches (CO1 gene), and concentrations of 27 mineral elements were measured in liver tissues using inductively coupled plasma techniques. Multivariate analyses and generalised linear mixed models were used to assess associations between mineral contamination and helminth infestation patterns. Our results revealed marked spatial variation in both helminth infestation and mineral contamination among mouse populations. Although no strong overall relationship between contamination levels and parasitism emerged, specific associations were detected between certain mineral elements and the probability of helminth infestation. Beyond their ecological and health implications, these findings highlight important methodological and conceptual challenges while stressing the need for further interdisciplinary efforts for a better understanding and management of zoonotic risks in rapidly urbanising environments in West Africa [5].

Keywords: ecotoxicology, one health, pathobiome, small mammals, West Africa

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RODENT CONTROL STRATEGIES AND LASSA VIRUS: UNEXPECTED EFFECTS IN GUINEA, WEST AFRICA

Joachim Mariën[1, 2], Mickaël Sage[3], Umaru Bangura[4], Alicia Lamé[3], Michel Koropogui[5], Toni Rieger[6], Barré Soropogui[5], Moussa Douno[5], N'Faly Magassouba[5], Elisabeth Fichet-Calvet[4]*

[1] *Evolutionary Ecology Group, Department of Biology, University of Antwerp, Belgium*

[2] *Virus Ecology Unit, Department of Biomedical Sciences, Institute of Tropical Medicine, Antwerp, Belgium*

[3] *Wildlife INNOVATION Research and Development Company, Besançon, France*

[4] *Zoonoses Control Unit, Bernhard Nocht Institute for Tropical Medicine, Hamburg, Germany*

[5] *Haemorrhagic Fever Unit, Virology Laboratory, Conakry, Guinea*

[6] *Department of Virology, Bernhard Nocht Institute for Tropical Medicine, Hamburg, Germany*

* *Corresponding author. Email: fichet-calvet@bnitm.de*

The Natal multimammate mouse (*Mastomys natalensis*) is the host of Lassa mammarenavirus, causing Lassa haemorrhagic fever in West Africa [1–3]. As there is currently no operational vaccine and therapeutic drugs are limited, we explored rodent control as an alternative to prevent Lassa virus spillover in Upper Guinea, where the disease is highly endemic in rural areas [4–5]. In a seven-year experiment, we distributed rodenticides for 10–30 days once a year and, in the last year, added intensive snap trapping for three months in all the houses of one village. We also captured rodents both before and after the intervention period to assess their effectiveness by examining alterations in trapping success and infection rates (Lassa virus RNA and IgG antibodies). We found that both interventions reduced the rodent population by 74–92% but swiftly rebounded to pre-treatment levels, even six months after the last snap-trapping control. Furthermore, while we observed that chemical control modestly decreased Lassa virus infection rates annually (a reduction of 5% in seroprevalence per year), the intensive trapping unexpectedly led to a significantly higher infection rate (from a seroprevalence of 25% before to 60% after snap trapping control). After six years, we conclude that annual chemical control, alone or with intensive trapping, is ineffective and sometimes counterproductive in preventing Lassa virus spillover in rural villages. These unexpected findings may result from density-dependent breeding compensation following culling and the survival of a small percentage of chronically infected rodents that may spread the virus to a new susceptible generation of mice.

Keywords: Lassa virus, *Mastomys natalensis*, rodent culling, rodenticide, snap trapping

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HOST ASSOCIATIONS OF IXODID TICKS PARASITISING RODENTS IN LITHUANIA

Dalytė Mardosaitė-Busaitienė*, Evelina Kaminskienė, Justina Snegiriovaitė, Algimantas Paulauskas, Jana Radzijevskaja
Vytautas Magnus University, Kaunas, Lithuania
** Corresponding author. Email: dalyte.mardosaite-busaitiene@vdu.lt*

Rodents (Muridae, Cricetidae) play an important role in the ecosystem, as they are hosts for ectoparasites, particularly the immature stages of ixodid ticks [1]. The aim of this study was to determine the host associations of ixodid ticks parasitising rodents in Lithuania. Using live traps, rodents were trapped in the Curonian Spit and the central part of Lithuania. A total of 188 rodents representing eight species (*Apodemus agrarius*, *Apodemus flavicollis*, *Micromys minutus*, *Mus musculus*, *Cletronomys glareolus*, *Microtus oeconomus*, *Microtus agrestis*, *Microtus arvalis*) were captured. Tick infestation was detected in 132 rodents. In total, 857 ticks were collected, including *Ixodes ricinus* (n = 731) and *Dermacentor reticulatus* (n = 126), comprising larvae (n = 665) and nymphs (n = 192). Tick infestation with *I. ricinus* was detected in all rodent species, with larvae being the dominant stage, whereas *D. reticulatus* infestation was recorded in five species and was dominated by nymphs. The highest prevalence of *I. ricinus* infestation was recorded in *M. oeconomus* and *A. flavicollis*, followed by *M. minutus*, *A. agrarius*, and *M. musculus*. *D. reticulatus* was most prevalent in *M. oeconomus*, while infestation levels in *M. minutus* and *A. flavicollis* were lower and similar. The mean abundance of *I. ricinus* ranged from 0.50 ± 0.27 ticks per host in *A. agrarius* to 4.40 ± 0.74 in *M. oeconomus*. For *D. reticulatus*, mean abundance was generally lower, varying between 0.11 ± 0.04 in *A. flavicollis* and 3.93 ± 0.93 in *M. oeconomus*. Mice and voles represent the main hosts for *I. ricinus*, while *D. reticulatus* is more associated with voles of the genus *Microtus*.

Keywords: mice, voles, ticks, *Ixodes ricinus*, *Dermacentor reticulatus*

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RODENTS AS INTERMEDIATE HOSTS OF CARNIVORE CESTODES IN LITHUANIA

Bastien Mullard*, Neringa Kitrytė, Laima Baltrūnaitė
State Scientific Research Institute Nature Research Centre, Vilnius, Lithuania
** Corresponding author. Email: Bastien.mullard@gamtc.lt*

Rodents are found everywhere and live constantly in contact with human populations [1]. They act as intermediate hosts for cestodes found in carnivores [2]. Moreover, most of these cestode species are zoonotic parasites, e.g. *Ecchinococcus multilocularis*, *Taenia* spp., *Mesocestoides* spp. [3]. The aim of this study was to investigate small rodent infestations with the intermediate stages of carnivore tapeworms and to analyse the differences between host species and habitats.

The research was done in Lithuania from 2017 to 2025. Rodents were trapped using snaps traps set in different habitats: forests, bogs, pastures, and farms. In total, more than 2800 rodents belonging to ten species were examined. We determined the prevalence and intensity of infestation in the liver and body cavity of rodents.

Overall, 10.4% of rodents were infested with intermediate stages of cestodes. We observed a significant variance in prevalence of infestation among species ($G = 36.8$, $p < 0.001$), ranging from 2.5% in *Apodemus agrarius* to 22.4% in *Microtus agrestis*. The prevalence of infestation in habitats was less widespread, but significant, ranging from 3.1% in bogs to 13.8% in deciduous forests ($G = 79.8$, $p < 0.001$).

The overall intensity of infestation reached 25.5 parasites per infested host, but it did not vary significantly either between species ($F = 2.5$, $p = 0.06$) or habitat ($F = 0.9$, $p = 0.44$). While some individuals were over-parasitised (up to 1000 immature cestode specimens), most of the infested individuals carried one parasite.

To conclude, our results suggest that both host species and habitat types have a significant influence on the risk of infestation, whereas intensity is more driven by individual host traits.

Keywords: ecology, Cestoda, intermediate host, rodents

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VIRAL PATHOGENS IN URBAN RATS ACROSS EUROPE: A SYSTEMATIC REVIEW FROM A ONE HEALTH PERSPECTIVE

Bartosz Mundt, Maciej Grzybek*
Institute of Maritime and Tropical Medicine, Medical University of Gdańsk
** Corresponding author. Email: maciej.grzybek@gumed.edu.pl*

Commensal rats (*Rattus norvegicus* and *Rattus rattus*) are common in European cities, where their close proximity to humans and ability to harbour zoonotic pathogens make them relevant indicators of urban environmental health [1–2]. Despite increasing interest in their role within One Health frameworks, the diversity, distribution, and epidemiological relevance of viral infections in European rat populations remain insufficiently characterised.

This systematic review was conducted according to PRISMA 2020 guidelines. Inclusion and exclusion criteria were applied to identify studies focused on urban rats and associated viral pathogens. Literature searches were performed using PubMed (MEDLINE), Embase, Web of Science Core Collection, Scopus and WILDbase to ensure broad coverage of relevant publications.

Numerous studies reported zoonotic viruses such as Hepatitis E virus and Seoul virus in urban rat populations. Prevalence varied widely across Europe, with notable differences between countries and cities. Evidence was unevenly distributed geographically, highlighting substantial gaps in surveillance and limited data from many regions. Overall, 71 studies met inclusion criteria and were further analysed.

Across Europe, *R. norvegicus* and *R. rattus* harbour a range of viral and parasitic agents of known or suspected zoonotic relevance. Research efforts remain geographically biased and methodologically heterogeneous, often based on short-term, single-pathogen studies, limiting comparability and interpretation of absence data. Integrating routine rat surveillance into European One Health systems, alongside environmental, wastewater and clinical monitoring, could improve early detection of public health threats and support targeted interventions

Keywords: rats, urban, viruses, zoonosis

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REGIONAL LASSA VIRUS LINEAGES SELECT FOR DIVERGENT MHC-I REPERTOIRES IN RODENTS

Ayodeji Olayemi[1, 2*], Jan Sarapak[3], Kerstin Wilhelm[3], Stephan Günther[4], Simone Sommer[3], Elisabeth Fichet-Calvet[2], Dominik Werner Melville[3]

[1] Natural History Museum, Obafemi Awolowo University, Ile Ife, Osun State, Nigeria

[2] Zoonoses Control Research Group, Bernhard Nocht Institute for Tropical Medicine, Hamburg, Germany

[3] Institute of Evolutionary Ecology and Conservation Genomics, University of Ulm, Ulm, Germany

[4] Department of Virology, Bernhard Nocht Institute for Tropical Medicine, Hamburg, Germany

** Corresponding author. Email: aolayemi@oauife.edu.ng*

Identifying genes under local adaptation is an essential step to understand the mechanisms of adaptive evolution. Pathogen-mediated selection is expected to enhance host fitness by favouring resistance to locally prevalent pathogens [1]. However, such pathogen-driven adaptation has been documented in only a few natural systems. Here, we sequenced the Major Histocompatibility Complex Class I region (MHC-I) of 739 *Mastomys natalensis* captured in Guinea and Nigeria, where the rodent is reservoir to two distinct Lassa virus (LASV) lineages [2]. As predicted, the MHC-I profiles of the two countries, while showing overlap, did not cluster together. Moreover, different MHC-I alleles were associated with active or past infection measured as PCR-positive or IgG-positive, respectively, in each population. MHC-I allele ManaMHC-I*017 showed a diametric response, with individuals carrying this allele less likely to be found with an ongoing LASV infection in Guinea while more likely in Nigeria. Similarly, individuals with ManaMHC-I*069 were less likely to have a positive antibody test in Guinea but the same allele had little effect on IgG detection in Nigeria, suggesting that an individual's fitness depends on its immunogenetic repertoire. Together, these findings encapsulate a genetically characterised case of local adaptation in a wild virus–rodent system. Moreover, we hypothesise that aside from differences in virus diversity, genetic variation within regional LASV lineages contributes to the marked differences in host immunogenetic diversity.

Keywords: Lassa virus, Major Histocompatibility Complex (MHC), *Mastomys natalensis*, adaptive evolution, fluctuating selection, local adaptation

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YELLOW-NECKED MICE (*APODEMUS FLAVICOLLIS*) AS RESERVOIRS OF *BORRELIA BURGDORFERI* S.L. IN FRAGMENTED FOREST HABITATS OF BELGRADE, SERBIA

Marija Rajičić[1], Milan Miljević[1], Branka Bajić[1], Ivana Budinski[1], Aleksa Rončević[1], Dunja Dragićević[2], Anja Šišković[2], Ivana Đurić Maslovara[2], OliveraVukićević Radić[2], Jelena Blagojević[1]*

[1] *Department of Genetic Research, Institute for Biological Research 'Siniša Stanković' – National Institute of the Republic of Serbia, University of Belgrade. Belgrade, Serbia*

[2] *Ecology and Environmental Improvement Sector, Public Utility Company 'Gradska čistoća', Belgrade, Serbia*

* *Corresponding author. Email: jelena.blagojevic@ibiss.bg.ac.rs*

Caused by tick-transmitted spirochetes of the *Borrelia burgdorferi* sensu lato (s.l.) complex, Lyme disease is a widespread zoonosis and an important public health concern in Europe[1], where at least five genospecies are recognised as human pathogens [2]. In the Belgrade area, *Borrelia afzelii*, commonly associated with small mammal reservoirs, is the predominant genospecies detected in tick vectors [3]. The yellow-necked mouse (*Apodemus flavicollis*), one of the most abundant small mammals in local forests, represents an important reservoir host.

This study assessed the prevalence of *B. burgdorferi* s.l. in heart and liver tissues of *A. flavicollis* collected from four urban forests in Belgrade and Mt Avala between 2019 and 2022 ($n = 112$). DNA extracted from both tissues was analysed using nested PCR and real-time PCR, and positive samples were further characterised by sequencing of the *ospA* gene.

Only one genospecies, *B. afzelii*, was detected, with varying prevalence among localities (6.25–24%). Minor differences in tissue-specific detection were observed between heart and liver samples.

Our results confirm the circulation of *B afzelii* in urban and peri-urban forest habitats in Serbia and highlight the role of *A. flavicollis* as a key reservoir species. These findings contribute to the understanding of the distribution of *B. burgdorferi* s.l. in a key reservoir species and provide insight into potential Lyme disease risk areas in the Belgrade region.

Keywords: *Apodemus flavicollis*, *Borrelia burgdorferi* sensu lato (s.l.), *Borrelia afzelii*

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EUROPEAN REFORESTATION AGENCY: ARE RODENTS AT OUR SERVICE FOR SUSTAINABLE POST-FIRE FOREST RECOVERY?

Konstantinos Raptis*, **Aleksandra Wróbel**
Mammal Research Institute, Polish Academy of Sciences, Białowieża, Poland
** Corresponding author. Email: k.raptis@ibs.bialowieza.pl*

Forest fires is a consistently occurring phenomenon in Europe as climate is shifting to higher temperatures and extended dry periods [1]. Animal-mediated seed dispersal is proving to be a natural process at our service for cost-free, heterogeneous forest regeneration [2]. This study investigates how seed dispersal agents such as granivorous rodents affect post-fire forest recovery in a Scots pine (*Pinus sylvestris*) monoculture. It provides insights on probable increase of oaks (*Querus* spp.) in this post-fire setting, by comparing the indirect interactions of the pedunculate oak (*Quercus robur*) and the invasive red oak (*Quercus rubra*). To assess these, rodent live-trapping and seed tracking experiments were conducted on three sites: burned, unburned, and one set along the fire-control trench ('the edge'). The experiments were located at the southern periphery of Białowieża forest in Poland where a low-intensity surface fire occurred, affecting a Scots pine monoculture. Seed removal and post dispersal fate were monitored to evaluate the degree of seed dispersal by rodents. We captured mice *Apodemus* sp. and bank voles (*Clethrionomys glareolus*) at the unburned site, whereas only mice were captured at the burned site. However, we found that mice were the only removers of experimental seeds. Out of all seeds removed and found, rodents cached 61.1%, while the remainder were mostly consumed. From these seeds, 55.4% was found in the burned site, 24.7% at the edge, and 19.9% in the unburned site. The average caching distance from the seed stations was 12.31 m. Furthermore, 67.1% of red oak acorns were removed with 41.4% of them being cached. For the native oak acorns, these amounts accounted for 63.8% and 36.9%, respectively. These results indicate rodents' contribution to the possible expansion of both oak species into disturbed habitats and therefore to their transformation into biodiverse self-sustaining ecosystems.

Keywords: synzoochory, seed dispersal, forest recovery, natural disturbances

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DIETARY NICHE DIVERSIFICATION ACROSS TWO MURINE RADIATIONS AND RECENT *RATTUS* INVASIONS ON THE ISLAND OF NEW GUINEA

Halil Mert Solak[1], Frantisek Vejmelka[1, 2, 3], Daniel Okena[1, 2, 3], Dagmar Cizkova[4*], Anna Bryjova[4], Vojtech Novotny[3], Alexis Ribas[5, 6], Srisupaph Poonlaphdecha[5, 6], Jakub Kreisinger[1]

[1] Department of Zoology, Faculty of Science, Charles University in Prague, Czech Republic

[2] Faculty of Science, University of South Bohemia in Ceske Budejovice, Czech Republic

[3] Biology Centre of the Czech Academy of Sciences, Ceske Budejovice, Czech Republic

[4] Institute of Vertebrate Biology of the Czech Academy of Sciences, Brno, Czech Republic

[5] Parasitology Section, Department of Biology, Healthcare and Environment, Faculty of Pharmacy and Food Science, University of Barcelona, Spain

[6] Biodiversity Research Institute (IRBio), University of Barcelona, Spain

** Corresponding author. Email: dejsha@seznam.cz*

Radiations following colonisation of competitor-free, resource-diverse environments are often driven by ecological opportunity, producing rapid diversification into vacant niches, including dietary niches. Later colonisers, however, must adopt alternative strategies to persist where the ecological space is already occupied by incumbents, potentially leading to different patterns of niche use and specialisation [1].

New Guinea provides an exceptional system to test these ideas: the island experienced two temporally separated rodent colonisations followed by rapid radiations – Hydromyini (~8.5 Ma) and Rattini (~2 Ma) – and more recently received invasive *Rattus* species through human-mediated dispersal [2]. We characterised diets of 819 individuals sampled along two elevational transects (200–3,700 m a.s.l.) using 18S rRNA metabarcoding of caecal contents and assigned specimens to 44 species-level taxa using a ddRAD phylogeny.

Ancestral dietary reconstructions show that some Hydromyini lineages retained herbivory while others diversified into fungivory, carnivory, and omnivory. In the later Rattini radiation, two native lineages were omnivorous and one specialised on fungi. Omnivorous Rattini exhibited high inter-individual dietary heterogeneity, whereas the fungivorous lineage was highly uniform. Compared to Hydromyini, native Rattini displayed narrower individual dietary niche breadths, suggesting that later colonisers can persist through individual-level specialisation or pronounced dietary opportunism. Recently invasive *Rattus* species remained strictly herbivorous and occupied divergent dietary niche, likely reflecting reliance on resources typical of synanthropic habitats.

Overall, our results indicate limited trophic overlap between later-arriving rodents and earlier-established radiations, highlighting how colonisation timing shapes dietary strategies and niche dynamics during insular radiations.

Keywords: dietary niche, metabarcoding, radiation, invasion, New Guinea

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REFUGE OR FILTER? SMALL MAMMAL COMMUNITIES ALONG AN ORCHARD INTENSIFICATION GRADIENT

Vitalijus Stirkė*, Linas Balčiauskas, Laima Balčiauskienė
State Scientific Research Institute Nature Research Centre, Vilnius, Lithuania
** Corresponding author. Email: vitalijus.stirke@gamtc.lt*

Due to frequent disturbance and chemical inputs, commercial orchards are often considered biodiversity-poor components of intensive agricultural landscapes. However, perennial structure gives them the potential to function as wildlife refuges. We examined how small mammal communities respond to management intensity and crop type in commercial orchards and berry plantations across Lithuania that span a gradient of agricultural intensification. From 2018 to 2025, snap-trapping at 19 sites recorded 13 small mammal species, with *Microtus arvalis* and *Apodemus flavicollis* dominating, followed by *A. agrarius* and *Clethrionomys glareolus*. The species' composition, abundance, and diversity varied across years, seasons, and habitats. The highest values were typically observed in autumn, and no population outbreaks were detected. Management intensity was the primary driver of community structure. Diversity and abundance declined sharply with increasing intensification. Small mammals were absent from the most intensively managed orchards, which were characterised by frequent mowing, soil disturbance, and heavy pesticide or rodenticide use. In contrast, low-intensity orchards with understory vegetation and habitat heterogeneity consistently supported diverse, stable small mammal communities [1–3]. These eight-year results demonstrate that commercial orchards can act as effective biodiversity refuges within intensive farmland but only below a critical management threshold. Therefore, reduction of chemical inputs and maintenance of structural heterogeneity are essential for sustaining small mammals and the ecosystem functions they support in perennial cropping systems.

Keywords: small mammals, commercial orchards, agroecology, agricultural practices, rodent diversity

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COMPARISON OF *LEPTOSPIRA* SPP. PREVALENCE IN BANK VOLES (*MYODES GLAREOLUS*) FROM NORTH-WESTERN GERMANY IN 2023–2024 WITH A PREVIOUS STUDY FROM 2018 TO 2020

Elisabeth Striese[1]*, Birke A. Tews[1], Marion Saathoff[2], Jona Freise[2], Lutz Fischer[2], Martin Pfeffer[3], Rainer G. Ulrich[1], Anna Obiegala[1]

[1] Friedrich-Loeffler-Institute, Federal Research Institute for Animal Health, Greifswald-Insel Riems, Germany

[2] Lower Saxony State Office for Consumer Protection and Food Safety, Wardenburg, Germany

[3] Institute of Animal Hygiene and Veterinary Public Health, University of Leipzig, Leipzig, Germany

** Corresponding author. Email: elisabeth.striese@fli.de*

Leptospirosis, the most widespread zoonosis worldwide, is transmitted through direct contact with infected wildlife such as rodents or through indirect contact with their excrements. Since *Leptospira* spp. can cause severe infections in humans, including kidney failure and multiple organ dysfunction, it is important to understand the transmission dynamics and to identify risk factors for zoonotic transmission.

A previous study conducted between 2018 and 2020 in north-western Germany demonstrated that season, population density, and individual host characteristics significantly influenced *Leptospira* prevalence in bank voles (*Myodes glareolus*) [1]. This current study aims to record the prevalence of *Leptospira* spp. in bank voles from the same study region and trapping sites in 2023–2024 as well as to compare seasonal patterns with previously published data.

In 2023 and 2024, 710 bank voles were caught at seven already established trapping sites in forest plots near Osnabrück in north-western Germany. Kidney samples were screened using quantitative PCR targeting the *lipl32* gene of pathogenic *Leptospira* spp. [2]. Subsequently, a PCR targeting the *secY* gene was performed to identify *Leptospira* species [3]. To further determine the sequence types, multilocus sequence typing was performed using a combination of seven different genes [4].

Associations between infection status and host characteristics (sex, body mass, reproductive status) as well as seasonal and annual variation are investigated and compared with the data and results from the previous study.

The results of our study underscore the importance of long-term monitoring and help to better understand the ecological and demographic factors of zoonotic risk. These findings help raise awareness of leptospirosis among physicians and public health authorities and enable the development of effective preventive measures.

Keywords: bank vole, Germany, zoonoses, leptospirosis

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THE DARK SIDE OF AFFORESTATION: 16 YEARS OF DEMOGRAPHIC COLLAPSE IN A GENERALIST RODENT

Marc Vilella[1]*, Lídia Freixas[1], Alfons Raspall[2], Aurelio F. Malo[3, 4]*, Ignasi Torre[1]

[1] *Bibio Research Group, Natural Sciences Museum of Granollers, Granollers, Spain*

[2] *Consorci del Parc Natural de la Serra de Collserola, Barcelona, Spain*

[3] *GloCEE Global Change Ecology and Evolution Research Group, Department of Life Sciences, Universidad de Alcalá, Madrid, Spain*

[4] *Department of Life Sciences at Imperial College London, Silwood Park, Ascot, Berkshire, United Kingdom*

* *Corresponding authors. Email: aurelio.malo@uah.es*

Afforestation and shrub encroachment are dramatically altering Mediterranean forest landscapes [1], raising concerns about the ecological- consequences for biodiversity. This study focuses on the wood mouse (*Apodemus sylvaticus*), a key species in Mediterranean food webs [2], to characterise its responses to long-term habitat transformations. We analysed population trends, occupancy, and body condition from 2008 to 2023 across 18 sampling plots in Barcelona province (Catalonia, Spain). By integrating fine-scale microhabitat data (LiDAR-derived vegetation structure) with landscape-level land cover factors, we demonstrated a clear gradient of habitat favourability along forest succession. Open scrublands consistently served as high-quality habitats, supporting larger populations, greater breeding activity, and significantly higher individual body weight (approximately 10% heavier) than in mature, low-quality wooded habitats. Multi-season occupancy models revealed higher colonisation probabilities and lower turnover rates in scrubland, whereas forests exhibited higher extinction rates. Additionally, density-dependent population growth was stronger in scrubland, suggesting more tightly regulated populations [3]. Despite these spatial differences, we observed a significant long-term population decline of 60–70% in abundance and a moderate spatial retraction of 12–26% across all habitat types over the 16-year period. These habitat-driven effects, likely influenced by increased predation risk and competition in dense forests, indicate an overall loss of habitat suitability for the wood mouse as afforestation progresses. Although the species remains widely distributed, the magnitude of the observed (and predicted [4]) decline suggests that its conservation status and its pivotal role in Mediterranean ecosystems should be reconsidered. Ongoing vegetation changes driven by global change factors may continue to intensify these negative trends, potentially leading to cascading effects on forest-dwelling predators [5].

Keywords: *Apodemus sylvaticus*, afforestation, shrub encroachment, population dynamics, Mediterranean forest

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