



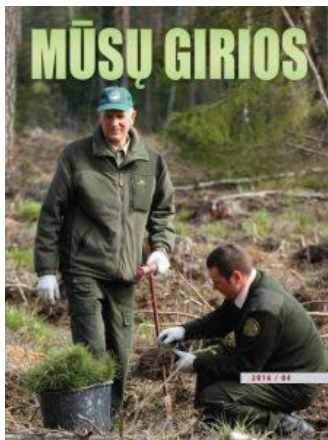
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ABSTRACT BOOK

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FULL PRESENTATIONS

STORY OF A SINGLE MEADOW: LONG TERM CHANGES IN A SMALL MAMMAL COMMUNITY UNDER HUMAN INFLUENCE

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Abstract

In 2008–2020, we snap-trapped small mammals in a 7.05 ha flooded meadow near Rusnė island (55°19'26.23"N, 21°20'24.15"E). During the course of the study, the habitat transitioned from a near-natural flooded meadow in 2008–2012 to a mowed and pastured area in 2020 (reed beds remaining only at the very edges), i.e. a reverse succession of the meadow-to-forest was observed. The anthropogenic influence grew mostly after 2018 and was best expressed in 2020. In this area, we recorded 11 small mammal species and trapped 1917 individuals with a total effort of 9466 trap nights. The dominating species were: harvest mouse in 2008, root vole in 2009 and 2012, and striped field mouse in 2010 and 2013–2020. These accounted for 41.4–92.9% of all small mammals (Figure 1). The average relative density of small mammals was 20.25 individuals per 100 trap nights (range 7.56–40.67), with a four-year-long cycle observed, this mainly being dependent on striped field mice. Species richness was 4–9 and the range of Shannon's diversity index 0.46–2.19. Results of changes in the community structure are analysed according to the hypotheses that: (i) community formation, especially changes in the dominant species, were flood-driven, (ii) herbi-, grani-, insecti- and omnivorous species were separated in time (dominant in different years) according to "favoured states" theory, and (iii) changes in the community structure were related to recent anthropogenic activity. The first two of these hypotheses were confirmed by our previous publications. The possibility of virus influence on decreasing abundances of root voles is still unclear.

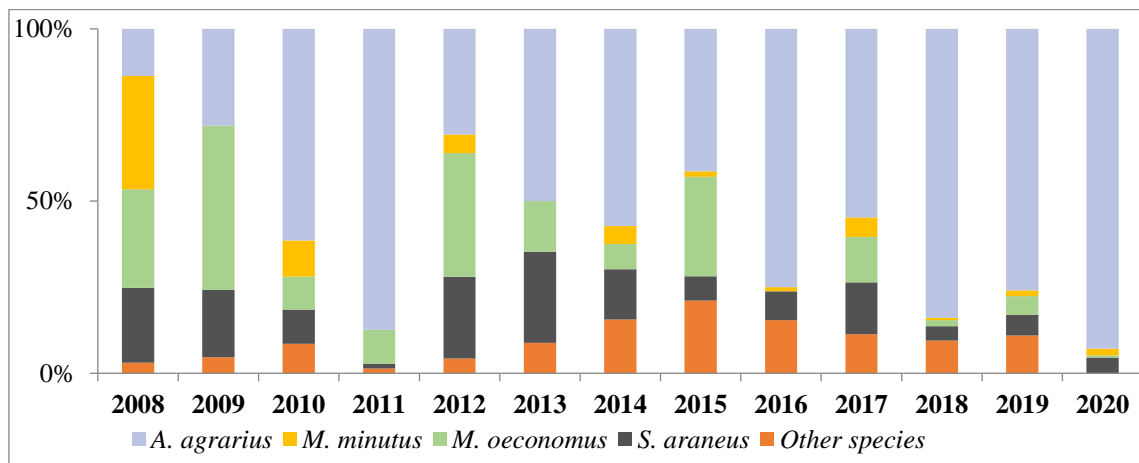


Figure 1. Changes in composition of the small mammal community, 2008–2020.

Keywords: flooded meadow, Rusnė, small mammals, community structure

NEST BOXES VS NOCTURNAL ACOUSTIC SURVEYS FOR ESTIMATION OF HABITAT PARAMETERS OF THE EDIBLE DORMOUSE (*GLIS GLIS*)

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Abstract

The edible dormouse (*Glis glis*) is a rather well investigated rodent species in Europe. Living in arboreal habitats, these dormice willingly occupy nest boxes set up specially for them. Over the years, recording of habitat parameters around nest boxes occupied by dormice was considered to be the most efficient method to collect information about their habitat preferences. Only a few researchers used nocturnal acoustic surveys for the same goal when dormouse presence/absence was estimated according to the sounds of their activity. So far nobody has compared these two methods with each other and did not evaluate their advantages and disadvantages. In this presentation for the first time, we will compare the two methods mentioned above for estimation of habitat parameters of the edible dormouse in Lithuania. In spring 2018, 50 nestboxes were set up in the Dūkštos forest. These nest boxes were inspected in autumn 2018–2020, and presence/absence of dormice or signs of their activity were recorded. In June 2020, nocturnal acoustic surveys were conducted in the same forest. Dormouse presence/absence was estimated according to night calls of edible dormice recorded in 93 points spaced across the forest. The results from these two studies as well as pros and cons of two methods used for estimation of habitat parameters will be presented.

Keywords: edible dormouse, nest boxes, nocturnal surveys, habitat parameters, Lithuania

REVIEW OF CAMERA TRAP FEATURES FOR SUCCESSFUL LYNX IDENTIFICATION

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Abstract

Eurasian lynx (*Lynx lynx*) individuals have unique coat patterns that enables researchers to identify individuals from photographs. This feature is useful in numerous ecological studies and camera traps became one of the most important tools for lynx research and monitoring. The aim of this study was to analyze how the choice of the camera trap model and its spatial-temporal arrangement affect the quality of lynx photographs for identification of individual animals. Research was conducted on 789 photographs that were taken in lynx natural habitat in Croatia and Slovenia in the period from 2007 to 2020. Twelve different camera trap models were used. Photographs were classified into three categories in terms of quality for identification. The following features were recorded for each photograph: photo trap manufacturer and model, date and time, location of camera trap (marking site, forest roads), flash type and whether it is used, focal length, ISO (sensitivity of digital camera sensor to light), resolution, speed trigger, aperture, length and width of the animal's body and body position (lateral or other position) on the photo, how much and what proportion of the body was photographed (length of the animal divided by the width of the photo in pixels), photo quality and color of the photo (color or black-white). Our analysis showed that photos taken at lynx marking sites had significantly better quality than those at forest roads, as it was possible to identify lynxes on 97.6% of the photos taken at marking sites ($p < 0,001$). Also, we confirmed that for animals in motion on forest roads there is a statistically significant difference in the quality of the photographs with respect to flash activity. On daytime photographs from forest roads identification was not possible in 8.1% of cases, while on night photographs it rises to 35.2%. The success of lynx identification can be improved by using camera models that have resolution higher than 1270 pixels. Also, if the lynx is present on more than 50% of the photo surface, identification will be even more successful. Considering all the parameters of camera traps that were included in this research, the best models for lynx identification are Cuddeback's C1, C2, C3, E1 and E2 models and Sunplus SPCA553 model.

Keywords: camera traps, camera features, identification, Eurasian lynx, *Lynx lynx*

SPECIES, NUMBERS OR SEX RATIO? EVALUATION OF UNGULATE DAMAGES TO YOUNG FOREST STANDS IN LATVIA

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Abstract

Moose (*Alces alces*) and red deer (*Cervus elaphus*) can inflict serious losses to forestry especially during winter, when access to alternative feed sources is limited. The extent of damages depends both on the species involved and population density. However, there are conflicting studies published, that females and calves of ungulates choose higher quality biotopes than males, and vice versa - males are more selective than females with calves. Within a regular grid of the National forest monitoring system, we selected ca. 600 young pine, spruce and aspen stands based on Forest inventory data from the years 2018–2020. In selected forest stands, number of ungulate pellet groups (pellet group index per hectare – PGI) and percentage of heavily damaged and entirely destroyed seedlings was compared using evenly distributed sample plots that cover 5% of the surveyed area. The pellet counts (pellet group index per hectare – PGI) characterize the species composition of ungulates present in area, sex and age groups as well as time spent in each forest stand. We categorised the forest stands according soil fertility and dominant tree species. Pine stands on rich soils were more damaged, with more trees destroyed (broken main stem and/or bark stripping of full perimeter) and there was significantly higher PGI for moose cows and calves compared to bulls. However, cows with calves also predominate in pine stands on poor soils and the difference between PGI of females and that of the males is even more pronounced. We also found that there is a positive relationship between PGI of moose cows and calves, and the number of damaged and destroyed trees per hectare in all 3 stand groups ($Sig.\alpha < 0.05$). There were statistically significant differences between PGI of red deer cows and calves and the percentage of damaged and destroyed trees in spruce stands. Assuming there are differences in damages made by the ungulates of different species, age and sex, we suggest that assessment of animal numbers and population structure should be done before the winter period, not after. Utilising new animal census technologies such as trail cameras, acoustic recorders, drones etc. should enable quick responses to predicted forest damages and facilitate appropriate population management decisions to avoid conflict situations between game and forest management.

Keywords: moose, red deer, forestry, winter browsing, pellet counts

SEQUENCING *DE NOVO* Y CHROMOSOME REFERENCE GENOME OF THE DOG

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Abstract

Y chromosome fulfills several important functions that have been understudied outside of model organisms. Due to inherent assembly difficulties, such as high repeat content, and large ampliconic regions, mammalian Y chromosomes are rarely included in the genomic analysis and in case of canids, the lack of a high-quality dog Y chromosome genome prevents our complete understanding of canid genome function and evolution. Our goal was to use a novel methodology to produce a *de novo* dog Y chromosome reference genome. Reference Y chromosome sequence for dog will prove most valuable in the future in various research areas connected to canids such as (i) importance of paternal lineages in the domestication process of dog, (ii) development of genetic markers used to study male-specific dispersal and population genetics in canids and (iii) evaluation of sex bias during hybridization in natural populations.

Keywords: dog, genomics, Y-chromosome, de novo sequencing, flow-sorting

A MOTHER'S STORY – THE PHYLOGENETIC RELATIONSHIP IN CHAMOIS

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Abstract

The chamois, genus *Rupicapra*, is the most abundant mountain-dwelling ungulate in Europe and the Near East and is currently recognized to be divided into two species: *R. rupicapra* (Northern chamois) and *R. pyrenaica* (Southern chamois) further divided into seven and three subspecies, respectively. While neither of the species is of conservation concern, some subspecies are protected at the national level in (part of) their distribution ranges. However, for most subspecies and populations the information necessary to assess the conservation status are lacking and several populations were subject to translocations and reintroductions, further complicating their general taxonomic picture. Here we combine nine newly sequenced mitochondrial genomes (mitogenomes) of four subspecies with previously published mitogenomes of *Rupicapra* (5) and related (sub)species in the Caprini, Ovibovini and Pantilopini families (39). The Bayesian and maximum likelihood phylogenetic analyses concordantly confirmed the monophyly of the genus *Rupicapra* and its positioning within the Caprini tribe. Both analyses identified the subdivision of the subspecies into three lineages in accordance with their geographical distributions (Eastern, Central and Western). The Central and Western lineages were more closely related, confirming previously reported results based on partial mitochondrial DNA regions. Within the Eastern lineage, *R. r. balcanica* was the most differentiated and included all individuals coming from the northern part of the Dinaric Karst mountain range, Mt. Velebit (Croatia), a known human-caused contact zone between *R. r. rupicapra* and *R. r. balcanica*, whereas *R. r. tatica* and *R. r. rupicapra* showed a sister group relationship. Overall, our results, while providing an increased resolution, confirmed the phylogeny previously reconstructed using both whole and partial mitochondrial DNA sequences. The discrepancy among nuclear, mitochondrial and Y-chromosome markers in phylogenetic reconstruction of the genus thus remains. Further studies combining multiple markers and possibly including archeological remains are therefore warranted to solve the controversy.

Keywords: chamois, mitogenome, phylogeny, *Rupicapra*

EUROPEAN LEVELS OF WILD BOAR HYBRIDIZATION

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Abstract

After a strong demographic decline before World War II, wild boar (*Sus scrofa*) populations are expanding and the species is now the second-most abundant ungulate in Europe. This increase raises concerns due to wild boar impact on agriculture and natural ecosystems and as potential vector of disease transmissions. The population expansion is the result of multiple factors, among them, it has been hypothesized that hybridization with the domestic pig (*Sus scrofa domesticus*) has led to modifications of life history traits, including fertility and litter size. We compared a literature review with results from the analysis of 47 148 Single Nucleotide Polymorphisms (SNP) in wild boar from Europe (292) and the Near East (16), and commercial (44) and local (255) pig breeds, to discern patterns of hybridization across Europe. The literature review showed that, over time and using a combination of genetic markers, wild boar x domestic pig hybridization has been reported in most European countries. Principal Component and maximum likelihood analyses performed on the SNP dataset showed a much more geographically confined distribution of hybridization. Observed values varied greatly for both datasets, ranging from absent to very high frequency of hybrids. However, the difference in geographic distribution of hybrids highlights the importance of large-scale investigations and the need to combine multiple markers (slow and fast evolving) for hybrid detection.

Keywords: Hybridization, genetic markers, Europe, *Sus scrofa*

UNEXPECTED INTERACTION BETWEEN REINTRODUCED BEAVERS AND INVASIVE WOODY SPECIES IN EUROPEAN FLOODPLAINS

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Abstract

The Eurasian beaver (*Castor fiber*) has already re-colonised its historical distribution area. However, floodplain habitats were considerably altered during the last two centuries by the river regulations, the spread of invasive species and other anthropogenic disturbances. In this environment, new interactions can develop between a reintroduced ecosystem engineer and the non-native, but also rapidly spreading species.

At the first time in Europe, the beaver's impact on the invasion of woody species was examined in the Danube water catchment area, Hungary. We selected 20 study sites for a forage selection survey. The supply and utilization of thin branches were examined in 100 sampling circles per site with a 2-metre in radius. Half of the sampling circles were situated directly along the water bank (water bank transect, WBT), and the others ten meters further from the water (outer transect, OT). Differences in the utilization between the softwood species group (SWS: *Salix* spp. and *Populus* spp.) and invasive alien species group (IAS: *Acer negundo*, *Fraxinus pennsylvanica* and *Amorpha fruticosa*) were examined by performing Mann-Whitney U test for all transects, separately.

The beaver utilized both the SWS and IAS group, but the within group utilization ratio was always lower in the case of the IAS, than that of the SWS. Statistically significant differences were gained in the case of 13 WBTs and 4 OTs. By selective foraging, the beaver might indirectly accelerate the further spread of invasive woody species.

The protection of European floodplain habitats (Annex I of the EU Habitats Directive) and the protection of the Eurasian beaver (Annexes II and IV of the EU Habitats Directive) might result in conservation conflict. The only good solution for mitigating this conflict would be the reconstruction and active management of floodplain habitats.

Keywords: ecosystem engineer species, biological invasion, conservation conflict, forage preference, selective foraging

LONG-TERM ABUNDANCE DYNAMICS IN FOUR DORMOUSE (GLIRIDE) POPULATIONS IN LITHUANIA

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Abstract

Long-term studies in four populations of hazel, edible and forest dormice were carried out in Lithuania. All populations investigated experienced declines of abundance, and consequences of these declines were very different – from total restoration and increase of abundance to extinction of a local population. In the edible dormouse population investigated during 1990–2014, significantly decreased dormouse abundance was restored over five-year period. Small local population of the forest dormouse, a part of metapopulation, was studied during 1999–2020. This local population became extinct after none of the males survived hibernation in 2013/2014, and only few females left. In one hazel dormouse population investigated during 1984–1993, decrease of abundance in 1987 was restored already next year, but another decrease was recorded during three last years of the studies. Abundance of another hazel dormouse population investigated during 1984–1990 and 1999–2020, was rather stable for many years, but dropped unexpectedly in 2014 and reached the lowest level in 2020. Increased winter and summer mortality, unfavourable sex ratio and unbalanced population age structure resulted in low reproduction success. When population abundance decreases below some critical threshold, restoration of decreased population abundance may last for many years. In small dormouse populations, such long-lasting decrease of abundance together with unfavourable sex ratio can determine extinction of these populations.

Keywords: abundance dynamics, dormouse populations, Gliridae, Lithuania

TEMPORAL PATTERNS OF UNGULATE-VEHICLE COLLISIONS IN LITHUANIA

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Abstract

Wildlife mortality caused by vehicles is a serious conservation and economic problem as collisions with large mammals are global, pervasive and increasing. We analysed 14,989 reports of ungulate-vehicle collisions (UVC) that occurred in Lithuania from 2002 to 2017. We analysed UVC data for four major ungulate species (roe deer, red deer, moose and wild boar) and checked for potential seasonal or daily trends. The temporal distribution of collisions was species-dependent. UVC analysis showed strong monthly and hourly pattern. Most occurrences took place before or during sunrise (dawn) and after or during sunset (dusk) during the year. In spring, the highest UVC peaks occurred early in the morning and late in the evening, while in winter these peaks occurred in late mornings and early evenings. With most UVC occurring on Fridays, daily variations were weak. We conclude that temporal variations of UVC distributions are result of a complex interaction of phenological factors and animal behaviour. The information provided in this study reinforces the knowledge on the dynamics and patterns of UVC and represents an important element for the identification of mitigation measures. Our findings suggest that efforts to reduce UVC should also focus on driver attitudes considering the seasonal and daily variations in UVC.

Keywords: Road safety; Roadkill; Collision patterns; Seasonal variability; Day/night cycle; Mitigation measures

NEW BAT SITE IN THE STONE MINES OF MOLOVATA NOUA, REPUBLIC OF MOLDOVA

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Abstract

In September 2020 a new bat site was found in the limestone mines near Molovata Noua, Republic of Moldova, located on the left bank of Nistru river, at 47.326 N and 29.089 E. The mine has 8 entrances placed at 20–50 m from each other, of which 6 were accessible for study. The bats were studied directly by visual observations, all observed individuals were identified. The distance from the entrance, crowding of individuals (single or in groups), the number of individuals of each species were noted. A total of 396 individuals from 9 species were registered: *Rhinolophus hipposideros*, *Myotis myotis*, *M. blythii*, *M. daubentonii*, *M. dasycneme*, *M. mystacinus*, *Plecotus austriacus*, *P. auritus* and *Eptesicus serotinus*. The bat diversity was rather high, being registered 9 of 21 species occurring on territory of R. Moldova. The most abundant was *M. daubentonii* with 43.94%, followed by *E. serotinus* with 25.25% and *M. mystacinus* with 23.99%. Other species had a low share of less than 4%. Most of the individuals were located near the entrances, at 1–30 m, and were found in cracks solitarily. Only the species *E. serotinus*, *M. myotis* and *M. daubentonii* formed small groups of 2–5 individuals. All bat species, except *E. serotinus*, are rare, listed in the Red Book of Moldova (2015). At European level all species are listed in Appendix II of Bern Convention and in Annex II of Convention on the Protection of Migratory Species. We have to mention the recording of *M. myotis* (12 individuals), critically endangered species, that was not registered in the last 40 years. The Molovata Noua site is an important place for bat diversity conservation in the central zone of Moldova and the monitoring of bat fauna will continue.

The studies were performed within the State Program project 20.80009.7007.02.

Keywords: Bat species, diversity, abundance, Molovata Noua, rare species

TAXONOMIC STATUS OF *ERINACEUS ROUMANICUS* (MAMMALIA: ERINACEOMRPHA) IN THE REPUBLIC OF MOLDOVA

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Abstract

In previous studies the hedgehog species from the territory of the Republic of Moldova was considered as *Erinaceus europaeus*. In the last years (2009–2019) a detailed study of the hedgehogs from Moldova was performed and new data on their occurrence, spreading and morphology were revealed. The aim of the paper is to establish the taxonomic status of hedgehog in the Republic of Moldova according to external and cranial morphology in order to determine the exact species. In the study 15 linear measurements and 3 indexes of skull were used on 36 individuals. The skull is quite massive and changes significantly with age and the most obvious features are the development of crest, especially of sagittal and supra-occipital ones. The angular process of the mandible is long and narrow, and its upper edge is formed by the crest that moves along its medial side. The mandibular foramen is shifted towards the lower end of the mandible. The articular condyle has the shape of elongated drop. The temporal-mandibular joint is almost flat, the mandibular coronary process is high and heavily curved, and there is a well-pronounced recess between the angular process and the horizontal ramus of the mandible. The cranial parameters varies in low range thorough the territory of Moldova. The variation coefficient is higher in condylobasal length and brain case breadth and in other cranial measurements it lies between 0.16 and 3.85. The length of naso-maxillary suture vary between 3.74–6.39 mm, which is particular for *E. roumanicus* that has a long naso-maxillary suture, while in *E. concolor* this suture is very short or absent. Thus, according to the morphology of mandibular, maxilar and nasal indexes, as well as naso-maxillary suture length, the territory of the Republic of Moldova is inhabited by the species *E. roumanicus*.

The studies were performed within the State Program project 20.80009.7007.02.

Keywords: *Erinaceus roumanicus*, cranial morphology, mandible, naso-maxillary suture

WOOD LEMMING (*MYOPUS SCHISTICOLOR*) – A NEW SPECIES IN THE BALTIC STATES

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Abstract

The wood lemming (*Myopus schisticolor*, Lilljeborg 1844) is the only extant species of *Myopus* and its most close relatives are found in genus of the brown lemmings (*Lemmus*). It is considered to be a monotypic species and its range extends from Fennoscandian Peninsula across Northern and Central Russia to Pacific Coast of Russian Far East. Until 2019 there was no records of wood lemmings in the Baltic states. Recent findings of several lemmings in Estonia, in 2019–2020, suggest that it is not only a new species for Estonian fauna but has surprisingly wide spread in the country. This study summarises the results of mtDNA analysis of six out of nine known wood lemming finds in Estonia, compares the results to previously analysed lemmings across their distribution area and investigates their relatedness to the nearest individuals.

Keywords: Wood lemming, *Myopus schisticolor*, mtDNA

GENETIC VARIABILITY OF THE EUROPEAN BISON (*BISON BONASUS* L.) POPULATION IN LITHUANIA

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Abstract

The European bison (*Bison bonasus* Linnaeus, 1758) is the largest herbivore mammal surviving in Europe. Since 1973, Lithuania has been one of few European countries with the first free ranging herd. The species is still included in the country's Red Data Book. The knowledge about population genetic diversity of this species is limited. This study aimed to estimate genetic structure in the European bison using mitochondrial DNA (mtDNA) control region. We conducted a study of genetic diversity of 50 individuals collected from a free-living Lithuania population. Variable sites, nucleotide (π) and haplotype diversity (H_d) values were estimated in the studied *B. bonasus* population in Lithuania and compared results with other studies. Current genetic diversity study indicated low mtDNA control-region sequence variation in the European bison population from Lithuania.

Keywords: Bison bonasus, mtDNA, genetic variability

CONSERVATION STATUS ASSESSMENT FOR MAMMALS IN LATVIA – HOW SUCCESSFUL WE WERE IN REPORTING UNDER ARTICLE 17 OF THE HABITATS DIRECTIVE

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Abstract

Almost half of the mammal species inhabiting Latvia (28 of 64) are listed on the annexes of the EU Habitats Directive. Article 17 of the Directive obligates the EU Member States to report on the conservation status of these species. The determination of overall conservation status demands to assess parameters that characterize the conservation status: range, population, habitat for the species and future prospects. Besides, it is necessary to define favourable reference values for the range and population size of species. The presentation will focus on the knowledge on mammal species in Latvia needed to perform the Article 17 report for the period 2013–2018. For most species conservation status assessment was based on national monitoring programmes. Monitoring of 19 protected non-game species is coordinated by Nature Conservation Agency, monitoring of 6 protected game species – by State Forest Service. An additional information source were studies performed to develop species action plans for 9 mammal species and site management plans for Natura 2000. In some cases, the only source of information on distribution of species were data available in the nature observation portal *dabasdati.lv*. Several knowledge gaps were identified. For 4 species the state of range including favourable reference range is unknown. For 10 species the state of population is unknown. Among them are not only rare bat species but also widespread game species – Eurasian beaver. For most of them, favourable reference population is unknown or defined at the assumption level. Sufficiency of area and quality of occupied habitat were unknown in 7 cases. Some more knowledge gaps were identified when assessing the short-term trend direction of parameters. Setting favourable reference values for the species listed in the annexes of the EU Habitats Directive, including mammals, will be done within the recently commenced LIFE-IP *LatViaNature* project (2020–2028).

Keywords: protected mammal species, monitoring, knowledge gaps, Latvia

ZOOARCHAEOLOGICAL COLLECTION AND RECENT ZOOARCHAEOLOGICAL RESEARCH IN VILNIUS UNIVERSITY

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Abstract

Zooarchaeology is the study of animal remains from archaeological sites. It is interdisciplinary field of sciences with the goal to gain a better understanding of the relationship between humans and their environment, especially between humans and other animals. However, the other aim of the animal remains research is to gain better understanding about the animals and their environment. Animal remains are the direct source investigating human and animal paleodiet, paleomigrations and spread or extinct of the species. Zooarchaeology in Lithuania is facing an increasing number of animal remains together with growing interest and better acknowledgement in zooarchaeological research, especially among archaeologist. Zooarchaeological collection of Vilnius University Faculty of History contains *ca* 6 000 kg animal remains dated from the 7 000 cal BC – to the modern times, that were collected from many archaeological sites all over Lithuania. All these skeletal remains of domestic and wild mammal species can be used to investigate diet, migration, origin or evolution of the local fauna, environment and climate. Animal bones from our collection quite often are used by Scandinavian, Polish and other European scientists, however Lithuanian zooarchaeological remains still lack of interest of local Baltic zoologists or other nature scientists. In this presentation, I give a short overview of the research topics and faunal collection stored in Vilnius University with an objective to open up the possible collaboration and discussion on archaeological, zooarchaeological and zoological research in the Baltic.

Keywords: zooarchaeology, research collection, animal remains, Vilnius University

EFFECT OF WILD BOAR (*SUS SCROFA*) ROOTING IN AN ERODED AND SEDIMENTED FOREST IN HUNGARY

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Abstract

Wild boar (*Sus scrofa*) rooting can change physical characteristics in the habitat by overturning extensive areas of soil, impacting natural or man-made processes of erosion and sedimentation in the forest. To analyze these effects, an evaluation of the volume of soil removed in the Babat Valley (Gödöllő, Hungary) was performed for over 8 months. The compaction and moisture content of 10 deep (51.6 ± 13 cm) rootings (5 sedimented/5 non-sedimented soil) were measured. The majority of rootings were in the upper (0–30 cm) layer of the soil with an average $90 \text{ m}^3/\text{ha}\cdot\text{month}$ of soil disturbance. However, the results for the compaction analyses change depending on the depth, therefore there are significant differences in the upper 20 cm layer of the rootings, with a higher compaction in sedimented rootings (avg. 1.3 MPa) compared to control samples (0.9 MPa). These results are related to the mixing of soil layers' organic matter, moisture and the consequent changes in texture. The higher compaction on sedimented areas can be the effect of the sedimentation and the waterflow that brought the sediment to the area. There were no significant differences in the moisture content in different types of soil; that can be due to the dry weather. The rooting activity can be beneficial for amphibians, earthworms and insects by using the created humid depressions in the soil as hiding places or micro-habitats. The combined effect of the sediment and the rooting activities of the wild boar can provide new information for the evaluation of the infiltration of surface water into the soil that changes the rate of water erosion processes. This can be used as a new input in such strictly protected micro-regions where soil protection is vital for nature conservation.

Keywords: water erosion, soil compaction, soil moisture, soil disturbance, soil-wild boar relation

ENETWILD – HARMONIZED APPROACH TO DATA COLLECTION AND ITS IMPLICATIONS FOR CONSERVATION AND WILDLIFE MANAGEMENT IN EUROPE

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Abstract

The ENETWILD consortium (www.enetwild.com) was constituted in 2017 on behalf of EFSA (European Food Safety Authority), that funded the project. Leading research organizations with expertise in the various areas of wildlife studies were invited to develop a harmonized approach to collecting, modelling and sharing data on wildlife populations transmitting animal disease agents. Due to the growing concern for the spread of African swine fever in Europe, its first objective was to focus on the wild boar population throughout Europe. More than 100 institutions from 33 countries expressed their interests in participating in the consortium activities. Organized data collection combined the review of scientific literature, “grey data” and different European datasets, allow high quality studies at the scale that is effectively useful for real-life management. Different data models were developed and published as an output of the project. The collated data have made it possible, among the others, to perform an analysis of wild boar-domestic pig interface in Europe.

Following successes in the field of wild boar data collection, the project was extended to wild ruminants and carnivores. Additionally, guidance on estimation of abundance and density of targeted species were produced and shared online to provide insights on how to obtain reliable estimations by using different methods. Complementary sources of data are also being explored in the context of the brother project MammalNet.

It is essential to further enhance the European network supporting the data collection and to provide insights on the utilization of the data in wildlife management activities. The project will make it possible to develop a deeper understanding of the practical implementation of harmonized protocols for wildlife disease and population surveillance.

Keywords: data collection, EFSA, harmonization, geographical distribution, spatial modelling, wildlife disease monitoring, wildlife population monitoring

ROE DEER PHYLOGEOGRAPHY IN EUROPE. UNCOMMON PATTERNS IN THE COMMON SPECIES.

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Abstract

Roe deer are one of the most important species of ungulate in Europe. Due to their wide range, many genetic studies were performed in various areas of Europe. Interestingly, most of the studies on roe deer phylogeography were done in western and southern part of the species range, while omitting big parts of Central and Eastern Europe. In our study we aimed to reconstruct the phylogeny of roe deer based on intensive sampling, which covered the whole European range of the species, including many areas which have not been studied before. We collected and sequenced 1469 roe deer samples from 20 European countries and pooled them with 1541 sequences derived from GenBank. Obtained phylogenetic trees and networks indicated the presence of two separate roe deer phylogenetic lineages corresponding to two closely related species: the European (*Capreolus capreolus*) and the Siberian roe deer (*C. pygargus*). Among the European lineage, we confirmed the presence of three major clades: Central, East and West. We did not detect any new clades at the eastern edge of the species range. The Central clade was the most widespread and had the highest number of haplotypes. Western clade was the least numerous with a scattered and patchy distribution. Mismatch distribution indicated that the central and eastern clades were under expansion during the Weichselian glacial period, while expansion of the Western clade overlaps with Eemian interglacial stage. Distribution of the lineages and clades are important predictors of the historical changes in roe deer populations. As our data were not always concordant with previous findings on the distribution and origin of the European roe deer clades, we provided possible explanations for the indicated picture.

Keywords: quaternary history, refugia, ungulates

DO MICROTUS VOLES SHARE THE SAME TROPHIC NICHE IN COMMERCIAL ORCHARDS?

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Abstract

We found three *Microtus* vole species sharing physical and trophic space in commercial orchards. We analysed the isotopic niche of the common vole (*Microtus arvalis*), comparing it to field vole (*M. agrestis*) and root vole (*M. oeconomus*), seeking to understand the trophic niche and trophic ecology of these species living in human-influenced habitats. The isotopic niche is not equal to the trophic niche of the community but is similar in many respects. We measured carbon ($\delta^{13}\text{C}$) and nitrogen ($\delta^{15}\text{N}$) stable isotope signatures in voles trapped in orchards and neighboring control meadows in 2018–2019. *M. arvalis* accounted for 30.1%, *M. agrestis* 2.1% and *M. oeconomus* 2.9% of all trapped individuals. Stable isotope ratios were measured in the vole hair using an elemental analyzer (EA) (*Flash EA1112*) coupled to an isotope ratio mass spectrometer (IRMS) (*Thermo Delta V Advantage*) via a ConFlo III interface (EA-IRMS). The widest trophic niche was held by the dominant *M. arvalis* ($\delta^{13}\text{C} = -27.1 \pm 0.04\text{‰}$, range $-28.6 - -24.6\text{‰}$, $\delta^{15}\text{N} = 4.9 \pm 0.1\text{‰}$, range $0.5 - 14.5\text{‰}$), exceeding that of *M. agrestis* ($\delta^{13}\text{C} = -27.5 \pm 0.1\text{‰}$, range $-29.0 - -26.5\text{‰}$, $\delta^{15}\text{N} = 5.1 \pm 0.3\text{‰}$, range $1.9 - 9.1\text{‰}$) and *M. oeconomus* ($\delta^{13}\text{C} = -27.4 \pm 0.1\text{‰}$, range $-28.5 - -26.4\text{‰}$, $\delta^{15}\text{N} = 5.4 \pm 0.3\text{‰}$, range $2.2 - 8.4\text{‰}$). The difference between average $\delta^{13}\text{C}$ values in vole species was 1.6%, while between average $\delta^{15}\text{N}$ values 7.9%. The three analysed *Microtus* species shared the same trophic space to some extent in all habitats according to $\delta^{15}\text{N}$ but were separated according to $\delta^{13}\text{C}$ in orchards and control habitats (ANOVA). Age related differences of $\delta^{13}\text{C}$ values were found in *M. arvalis* (lowest in juveniles), while gender-related differences of $\delta^{15}\text{N}$ values in *M. oeconomus* (females > males).

Keywords: $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ stable isotopes, trophic niche, voles, commercial orchards

THE INFLUENCE OF THE TYPE OF HUNTING GROUND ON THE AGE STRUCTURE AND THE SHARE OF YOUNG HARE (*LEPUS EUROPAEUS L.*)

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Abstract

The objective of this research was to study the impact of the type of hunting ground on the age structure of hares shot. The analysis included 157 hares shot in 2019. In hunting grounds in lowland region of Serbia (Zemun area) 65 hares were shot while in hunting grounds in Central Serbia which belong to a mountainous type of hunting grounds 92 hares were shot. The hypothesis about a proportion of two main independent sets by means of chi-squared test within the SAS PROC FREQ procedure was tested. In both types of hunting grounds, a dominant share in population constitute hares aged from 6 to 12 months (lowland 34%, Central Serbia 23%). In addition, a low share of hares younger than 3 months was determined, being below 1% in both cases. The greatest difference in age structure was determined in hares old between 3 and 6 months. In Zemun area this share accounted for 14% while in Central Serbia the share of this group accounted for 31%. Chi-squared test showed high statistical significance ($p < 0.01$), what supports the thesis that type of hunting ground can have a high statistical impact on the age structure of hares in hunting grounds.

Keywords: hare, type of hunting ground, age structure, hi square test

Acknowledgment

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COMMON VOLE FEELS COMFORTABLE IN ORCHARDS

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Abstract

Small mammals are an important part of biological diversity and providers of ecosystem functions. Although biodiversity is declining in agricultural areas in Europe, the diversity of small mammal species can be high. Of this diversity, only a few species of mice of the genus *Apodemus* and voles of the genus *Microtus*, in particular the common vole (*Microtus arvalis*), are considered to be the largest pests. At the same time, common vole is a reference species for risk assessment of plant protection products in many EU countries. In the pilot study, we evaluated species composition, abundance and diversity of small mammal communities in 18 commercial orchards and berry plantations in Lithuania in 2018–2020, representing other Baltic countries with similar climate and agricultural traditions, testing the influence of crop type and intensity of agricultural practices. In total, 1449 individuals (11 species) were trapped. In the orchards, dominant species was common vole, 38 % of all trapped individuals, while in the control habitats dominant was striped field mouse (*Apodemus agrarius*) with the share of 30 %. Common vole was detected in 12 of the 18 orchards and plantations (66.7%) and 14 of the 18 control habitats (77.8%). The average abundance of common vole was 3.91 ± 0.54 per 100 traps per day, in summer 3.96 ± 0.55 , in autumn 3.91 ± 0.54 per 100 traps per day. The abundance of animals in the gardens and control habitats did not differ. In lightly and moderately intensively maintained gardens, the share of common vole in the small mammal community was higher than in control habitats. Intensive maintenance (frequent mowing or loosening of rows and application of plant protection products and use of rodenticides) makes gardens and berry habitats unsuitable not only for common vole but also for other species of small mammals.

Keywords: *Microtus arvalis*, commercial orchards, abundance, dominance

ROOTING DYNAMICS OF THE WILD BOAR ACCORDING TO ACORN AVAILABILITY

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Abstract

The continuous population growth of the wild boars (*Sus scrofa*) in the recent decades has been noticed worldwide. Energy-rich components such as oak acorns are fundamental in their diet. Meanwhile the regeneration of the temperate oak forests has become increasingly difficult and slow, and wild boars are often marked as one of the main impeding agents in this phenomenon. Therefore, we should have better understanding of the wild boar rooting - which is the most obvious sign of feeding behavior of the species - and its spatiotemporal relationship with the acorn density. Thus, we monthly measured the acorn density and the presence of the wild boar rooting in an oak forest between 2016 October and 2019 April. The study site was divided to 20x20m grid cells to investigate the spatiotemporal patterns of the rooting activity. Comparing the acorn densities, we identified the first two years as mast years unlike the third one. Aligned with that, within the acorn-rich periods (October to April), we found that the study site was rooted in significantly higher proportions in the two mast years than in the non-mast year. We revealed that 9.12% of the cells stayed undisturbed throughout the study. On average, 12.59% of the cells contained newly formed rooted patches, and 15.6% of cells was repeatedly disturbed. Rooting were usually shallow, mainly affecting the litter layer (in 71.75% of the cases). According to our findings, wild boars indeed have a great effect on the whole system by rooting almost the entire forest stand at least once and therefore probably have an effect on the acorn density too. But the masting of the oaks also has an essential role in dynamics of the rooting.

Keywords: Wild boar, *Sus scrofa*, Acorn, Forest regeneration, Oak, Game damage

SAMPLES FROM HUNTING BAGS MODELLED WITH THE HYPERGEOMETRIC DISTRIBUTION REVEAL TRENDS IN AGE STRUCTURE OF WOLF AND LYNX POPULATIONS

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Abstract

The population structure of wolves and lynx in Latvia has been monitored during the last two decades by randomly sampling culled individuals from the hunting bags and taking teeth samples for precise age determination of the animals. The outcome of such sampling without replacement (i.e. number of individuals from the sample belonging to a particular age class) can be modelled using a hypergeometric process. We applied a logit-linear model with hypergeometric error to study temporal trends in the proportions of certain age classes within the harvest from 1999 to 2020 for wolves and 2003 to 2020 for lynx. The models were fitted using maximum likelihood. The results indicated no significant temporal trend for the youngest age classes (juveniles, yearlings), but slow decline was estimated to be likely for older age classes, indicating structural changes in growing wolf and lynx populations. This study has been conducted as part of a postdoctoral research project "Sub-population dynamics of grey wolf *Canis lupus* and Eurasian lynx *Lynx lynx* in Latvia and identification of depredation risk on livestock" (No. 1.1.1.2/VIAA/3/19/511) funded by European Regional Development Fund.

Keywords: age structure, demography, hypergeometric distribution, wolf, lynx

TEMPORALITY OF COAT PATTERNS IN ENDANGERED EURASIAN LYNX POPULATION IN CROATIA

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Abstract

Phenotypic traits in felids show a great diversity of coat pattern and marking. In Eurasian lynx (*Lynx lynx*), four types of coat pattern had been identified: big spots, small spots, rosettes and coat with no spots. The present study aimed to track frequencies of coat patterns over time in endangered Eurasian lynx in Croatia. A total of 195 photographs of lynx individuals from Croatia, collected in the 1978–2019 period was used. Individuals shown in photographs were assigned to one of the four coat patterns by two researchers working independently. Discrepancies were resolved by a third researcher in 20 (10.26%) cases when the first two researchers disagreed. Later, the frequencies of each of the four patterns were compared between images taken in 1980–1994 and 2011–2019 using chi-squared test. Frequencies of all four coat patterns differed significantly between individuals photographed in 1978–1999 and those photographed in 2000–2019 ($p < 0.05$). The frequency of coats without spots fell from 14% to zero, coats of rosettes dropped from 23% to 9%, coats of small spots dropped from 16.5% to 11.5%, while the frequency of big spots increased from 46% to 80%. The change in the frequency of all coat patterns may be attributed to the small population size with limited gene flow. Dinaric lynx population was established by a reintroduction of six individuals into Slovenia in 1973 from the Slovakian Carpathian Mountains. Offspring of those animals successfully dispersed to Croatia, Italy, Austria as well as Bosnia and Herzegovina, but the population remained isolated. Forty years later, significant inbreeding and low effective population size were proven by genetic analysis in Dinaric lynx population. Therefore, the phenotypic population profile could be used as an indicator of potential genetic-based conservation problems. Nevertheless, to be sure that inbreeding plays the key role in the observed phenotypic change, genetic analyses should always be conducted.

Keywords: Eurasian lynx, *Lynx lynx*, endangered populations, coat patterns, phenotypic population profile

ENDOPARASITE PREVALENCE AND INFECTION RISK FACTORS AMONG CATS IN AN ANIMAL SHELTER IN ESTONIA

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Abstract

Cats are important hosts for different zoonotic parasites that can be hazardous to human health. To date, few studies have attempted to identify the factors affecting parasitic infections in shelter animals. This study aims to analyse the presence of endoparasites in shelter cats in Tartu, Estonia, and identify factors affecting endoparasite prevalence and intensity. The risk factors considered were age, location (urban vs rural cats) and time spent in shelter. In total, 290 faecal samples were collected from cats at an animal shelter in 2015–2016 and investigated for endoparasites using the concentration flotation technique. In total, 138 shelter cats (47.6%) were infected with endoparasites and their overall prevalence was: *Toxocara cati* (36.6%), *Cystoisospora* spp. (12.4%), Taeniidae (4.1%), *Toxoplasma gondii*/*Hammondia hammondi* (3.4%), *Eucoleus aerophilus* (2.1%), *Cryptosporidium* spp. (2.1%), *Ancylostoma* sp. (0.7%) and *Giardia* sp. (0.7%). Coinfections occurred in 38 cats (13.1%); most frequently of *T. cati* and *Cystoisospora* spp. (4.5%), *Cystoisospora* spp. and *T. gondii*/*H. hammondi* (2.1%). Where species identification of cestode and nematode samples was not possible according to morphology, genetic analysis of the mitochondrial *cox1* gene was carried out. DNA was successfully analysed for 6 (46.2%) out of 13 samples that required genetic identification, revealing *Ancylostoma tubaeforme* in one nematode sample and *Hydatigera taeniaeformis* in five cestode samples. Cats from rural areas had significantly higher endoparasite prevalence than cats from urban areas. Helminth prevalence decreased due to anthelmintic treatment in cats available for adoption (held ≥ 15 days in the shelter), whereas the protozoa prevalence increased significantly in these animals. It is important to note that the analysis revealed lower infection intensity for quarantine cats (held 1–14 days in the shelter) compared with cats available for adoption. The relatively high prevalence of endoparasites (including zoonotic) in shelter cats ready for adoption suggests that current anthelmintic procedures require improvements.

DETECTION AND LOCALIZATION OF ADULT MALE RED DEER *CERVUS ELAPHUS* DURING THE MATING SEASON USING PASSIVE ACOUSTIC RECORDERS

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Abstract

The monitoring of wild animal populations is important for wildlife conservation, damage management and sustainability. Although large in size red deer (*Cervus elaphus*) can be elusive and hard to detect, so population abundance and trends are often hard to estimate. Passive acoustic recorders are frequently used to study highly vocal species, like birds, bats, whales and dolphins. During mating season adult red deer males emit loud calls, which allows them to be effectively detected using acoustic recorders. Acoustic recorders are capable of detecting and recognizing animals in a large area and without the presence of an observer, but since it is very difficult to differentiate between multiple individuals, metrics like call activity are often used instead of a count or density estimations when dealing with aural observations. This study aimed to automatize the detection and localization of red deer calls in audio data. The experimental setup contained three passive recording units *Sound Meter SM4* from *Wildlife Acoustics Inc.* with GPS-synchronization capabilities deployed in Rāmuļi, Latvia during red deer mating season in September 2020. Machine learning algorithms like unsupervised K-means, support vector machines, K-nearest neighbours and decision trees were benchmarked for automated red deer call detection and counting from acoustic records. Hyperbolic localization of sound source using near-field assumption was applied to time-synchronized acoustic records from tree microphones. Additional tests were performed on sound sources with known locations showing detection error of ± 25 meters. In total, 1750 hours of acoustic data were recorded between late August and early October 2020 resulting in more than 10 000 red deer calls detected using initial unsupervised K-means analysis.

Keywords: red deer, deer mating calls, passive acoustic monitoring, acoustic localization, machine learning

SOME NEW DATA ABOUT MAMMALS BIOFLUORESCENCE

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Abstract

Biofluorescence is widespread in nature. A similar phenomenon was found among marine invertebrates, fishes, amphibians, and some birds. Studies of mammalian fluorescence have been carried out too. So, the phenomenon was previously found in opossums, American flying squirrels. In 2020, biofluorescence of the pelage was described in the platypus. Also patches of fur glowing in ultraviolet light were found in the wombat, the Tasmanian devil. We irradiated with ultraviolet light with a wavelength of 365 some samples of skins and stuffed mammals kept in the collection of the Udmurt State University and the National Museum of the Udmurt Republic (Izhevsk, Udmurt Republic, Russia). We observed the light green glow of stoat (*Mustela erminea*) fur. In total, 5 samples, 4 stuffed animals and 1 skin, were examined. All the stoats were in winter fur. Under ultraviolet rays, a pronounced light green glow was noted on the underside of the body, legs and tail. The upside and head were not glow. Also, down hairs were not glow too. Studies on live animals and fresh samples were not carried out, but since the glow zones coincide, it is unlikely that the phenomenon is associated with the features of the manufacture and storage of samples. We are currently planning further study of this phenomenon.

Keywords: Biofluorescence, mammals, stoat, *Mustela erminea*

MINI PRESENTATIONS

BABESIA SPP. IN TICKS COLLECTED FROM EUROPEAN BISON

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Abstract

Babesia are hard tick-transmitted protozoan hemoparasites, of great economic, veterinary and medical impact worldwide and have a wide host range, including hundreds of mammal species. All species of *Babesia* are naturally transmitted by the bite of infected ticks. The aim of the present study was to investigate the prevalence of *Babesia* pathogen in ticks collected from European bison (*Bison bonasus*). For that purpose, we used nested-PCR for *Babesia* spp. detection. A total of 242 ticks belonged to two species (*Ixodes ricinus* and *Dermacentor reticulatus*) were tested. *Babesia* DNA were found in 17.7% *I. ricinus* ticks and 5.4% *D. reticulatus* ticks. Sequence analysis of the 18S rRNR gene fragment showed that ticks were infected with *Babesia divergens*, *Babesia venatorum* and *Babesia microti*. The present study is the first report of *Babesia* spp. in ticks collected from European bison in Lithuania. Tick-borne pathogens can influence health and cause deaths of European bison.

BACTERIAL PATHOGENS IN LICE COLLECTED FROM SMALL RODENTS

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Abstract

Wild rodents are important hosts of *Bartonella* and *Rickettsia* species and some species of these bacteria are considered to be pathogenic for humans. Although rodent ectoparasites, such as fleas and ticks, are known as vectors of *Bartonella* spp. and *Rickettsia* spp., there are limited data on the prevalence of these bacteria in other rodent ectoparasites – lice. More than half of described blood-sucking lice species are found on rodents. 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 live-captured between 2010 and 2015 at four different sites in eastern Slovakia. A total of 1074 lice belonging to seven species (28 *Hoplopleura acanthopus*, 732 *Hoplopleura affinis*, 1 *Hoplopleura edentula*, 7 *Hoplopleura* sp., 225 *Polyplax serrata*, 79 *Polyplax spinulosa*, and 2 *Polyplax* sp.) were collected from 216 small rodents representing six species (*Apodemus agrarius* n=151, *Apodemus flavicollis* n=35, *Microtus arvalis* n=13, *Microtus subterraneus* n=2, *Myodes glareolus* n=11 and *Rattus norvegicus* n=4). Lice were tested for *Bartonella* and *Rickettsia* pathogens by real-time PCR targeting the *ssrA* and *gltA* gene respectively. *Bartonella* spp. were found in *H. affinis* lice species collected from *A. agrarius*, *A. flavicollis*, *M. glareolus* rodent species and in one *P. serrata* louse collected from *A. agrarius*. Sequence analysis revealed that the *Bartonella* strains belonged to the *B. coopersplainsensis*, *B. tribocorum*, *B. taylorii* genogroups. *Rickettsia* DNR were detected in *H. affinis* and *P. serrata* lice collected from *A. agrarius* and in *P. serrata* collected from *A. flavicollis*. Sequence analysis revealed the presence of *Rickettsia helvetica* and *Rickettsia* sp. To the best of authors knowledge, this study is the first investigation of rodent-associated bacterial pathogens *Rickettsia* and *Bartonella* in lice parasitizing rodents in Europe.

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

DIFFERENCES IN UNGULATE POPULATION USE IN DIFFERENT HUNTING GROUND UNITS IN LITHUANIA

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Abstract

Abundant ungulate populations are considered ecosystem drivers that affect forestry and agriculture. Their management is ecologically and economically based on game density regulations, considering the balance between density and carrying capacity of the territory, population status and dynamics, as well as hunting needs.

Although the population status and dynamics are not new questions, it is still unclear how to manage populations properly depending on the hunting intensity. We aimed to analyse and compare the ungulate population status like moose, red deer, roe deer and wild boar in the Punia pine forest, where the commercial hunting is conducted, and in the hunting grounds managed by hunter clubs in Prienai forest. We performed the study during four hunting seasons of 2009–2010, 2010–2011, 2011–2012, and 2012–2013. The data on harvesting and abundance were obtained from the field works and using the official statistics of the Ministry of Environment.

The moose local populations are not abundant, or animals occur occasionally, and their density does not reach the minimum permissible rate. At the same time within the study area, moose hunting is remained to be insufficient. The red deer population is rather stable in the hunting grounds used by hunter clubs while hardly reaches the minimum density rate. On the commercial hunting area, the population density 2–3 times exceeds the permissible density rate. The red deer population should be harvested more intensively. The wild boar is used intensively in the grounds of hunter clubs, while animal density is close to the permissible rate. Unfortunately, on the areas of commercial hunting, wild boar is not actively managed that is why their density exceeds permissible rate even four times.

The main harvested species are red deer and wild boar in both hunting grounds. Their abundant populations stay close to permissible density rate. However, gamekeepers keep the larger animal numbers on the areas of commercial hunting. As the main aim is the trophy hunting, the stags and boars are most used when compared to females and young. Therefore, on the areas of commercial hunting, use of wild boar and red deer is unreasonable and their density exceeds permissible rate several times.

Keywords: commercial hunting, hunting clubs, population, status, ungulate

HABITAT SELECTION BY SMALL MAMMALS IN MOUNTAIN FORESTS IS INFLUENCED BY POPULATION DENSITY AND ALTITUDE

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Abstract

For seven years we conducted surveys in the Retezat Mountains of the Romanian Carpathians, aiming to assess the dynamics of small mammals in relation to habitat characteristics along the altitudinal gradient. Abundance of dominant rodents *Apodemus flavicollis* and *Myodes glareolus* fluctuated significantly from year to year, with lower densities in odd years. Based on the theory of source-sink habitats, we expected the habitat selection by these species to be more intense at low densities. Because *A. flavicollis* is more thermophilous than *M. glareolus*, we hypothesized that the intensity of habitat selection by this species is greater at high altitudes. In addition, because both rodents are typical forest species with reduced temporal segregation of their activity, we expected that (micro)habitat segregation would facilitate their coexistence as dominant species in this continuous and relatively homogenous landscape. Thus, we predicted that the two species would have opposite responses to the significant habitat characteristics. To evaluate intensity of habitat selection we used Poisson generalised linear models (GLMs) including capture effort as offset, or negative binomial GLMs to account for significant overdispersion, for each species and partial dataset (odd – even years and low – high altitudes) and we standardized the regression coefficients to make them comparable. As predicted, the two dominant rodent species were affected mostly by different factors, or showed opposite responses to the same variable. The only exception was the cover of the tree layer, which had a positive effect on both species, typical forest rodents, but weaker and only temporary in *A. flavicollis*. Habitat selection was more intense during periods of low density, which was in accordance with our expectation. Habitat selection was overall weaker in *M. glareolus*, which was least constrained by habitat characteristics at high altitudes, suggesting that its optimal habitats are high altitude forests.

Keywords: rodents, altitudinal gradient, source-sink habitats, *Apodemus flavicollis*, *Myodes glareolus*

GENETICS AS A USEFUL TOOL FOR UNDERSTANDING RELATEDNESS, MOVEMENTS AND SOCIAL BEHAVIOUR IN WILD BOAR

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Abstract

Wild boar (*Sus scrofa*) is a globally widely distributed species that has recently increased in population size and distribution causing more socio-economic and ecological concern than any other ungulate species. Therefore, a comprehensive understanding of the species needs is urgently needed. The wild boar has long been considered a polygynous species with strong social bonds in female-based groups. However, recent molecular studies have proved that the species is actually polygamous and the composition of social groups can vary depending on ecological and predation/hunting pressures. By combining the harvest coordinates with the genotype of each individual, we can provide additional insights into the mating and social behaviour of the species under different environmental and hunting conditions. Here we present a fine scale spatial distribution of allelic diversity and relatedness of wild boar in a 2 600 ha large typical hunting ground of central Slovenia. We genotyped 58 individuals (of both sexes and all age classes) harvested from 2017 to 2020 at 13 neutral microsatellite loci. The relatedness data was combined with exact harvest location (coordinates) to provide insight into behavioural features (e.g. seasonal dispersions and social grouping). Analysis of high-probability relatedness (>0.90) revealed one potential father, seven potential mothers and their 17 offspring (either piglets, yearlings or younger adults), and additional 19 close, but non-parental relations (i.e., full-siblings and half-siblings of both sexes and all age classes). We found many genetic relations and high degree of relatedness among the studied individuals, indicating existence of only few main maternal groups and high matrilineal effect with high side-fidelity of females and prevalence of only short dispersal of piglets in this rather small study area. Moreover, we detected a frequent multiple paternity in the studied population as we found six litters (with majority of siblings within a particular litter shot together) with different fathers.

Keywords: microsatellite, relatedness, spatial behaviour, social structure, wild boar

INFERRING POPULATION HISTORY AND DEMOGRAPHY USING MICROSATELLITES AND MAJOR HISTOCOMPATIBILITY COMPLEX GENES IN EUROPEAN ROE DEER

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Abstract

Microsatellites have traditionally been used in population genetics because of their variability and presumed neutrality, while major histocompatibility complex (MHC) genes are of increasing interest as strong selective pressures shape their standing variation. Despite the potential of MHC genes and microsatellites to complement each other in deciphering population history and demography, the two have been so far rarely used in tandem.

We studied MHC and microsatellite variability in a population of European roe deer (*Capreolus capreolus*), the most abundant large mammal in Slovenia. Our aim was to study the spatial distribution of neutral genetic diversity using 13 microsatellite loci and the allelic diversity at exon 2 of the MHC class II DRB locus using the next-generation approach (Ion Torrent S5, Thermo Fisher) in 173 individuals hunted in the period 2013–2019.

Spatial differences based on the neutral, microsatellite, genetic diversity of roe deer in Slovenia revealed separation of the population into three groups from the following areas: (i) southwestern sub-Mediterranean and Karst region, (ii) Central Slovenia, and (iii) the Sub-Pannonian region in the north-east. We identified ten MHC alleles, seven of which had previously been found in roe deer in Europe, while the remaining three alleles were newly identified. Global estimates of dN/dS averaged across all codon sites and did not show positive selection. Both neutral and genetic MHC variability were higher in the central part of the country and lower in areas with an environment unsuitable for roe deer (i.e., dense old Dinaric forests in the southeast, and a harsh alpine environment in the north). This pattern can be explained by population history, different approaches to population management and/or different connectivity between subpopulations. Data on genetic variation, which are important for understanding the demographic history and life-history traits of the species, are needed to better predict population dynamics, which would improve science-based population management.

Keywords: microsatellites, major histocompatibility complex, next-generation sequencing, spatial genetic diversity, roe deer

OTTER POPULATION STRUCTURE AND ROLE IN ECOSYSTEMS

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Abstract

The otter (*Lutra lutra* L.), a predatory mammal of the family Mustelidae, is widespread in North Africa, Europe and Asia, with the exception of the most northern regions and the Arabian peninsula. The otter is a protected species in Europe, the otter was included in the Lithuanian Red Data Book in 1989, and in 2000 it was classified as a preserved species. According to the research carried out in Lithuania in 2009, otters were found in 78.4% of the inspected sites, but currently the abundance of the otter population in Lithuania has greatly increased. This study aims to assess the abundance and structure of the otter population in Lithuania. The abundance of the otter population is highly dependent on the state of the food chains, the study explains the impact of the growing otter population on existing ecosystems and assesses the impact of climate change on the otter population in Lithuania.

Keywords: otter, population, structure, food chains, Lithuania

***BARTONELLA* SPP. PREVALENCE IN DOMESTIC CATS AND THEIR ECTOPARASITES IN LITHUANIA**

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Abstract

Climate change and human migration with companion animals have an impact on the spreading of vectors and associated pathogens, which causes a growing risk of zoonoses. *Bartonella* spp. are abundant zoonotic vector-borne pathogens that are found in domestic cats. Infection of cats with bartonellal agents results in a wide spectrum of disease that ranges from subclinical, inapparent infection to severe, potentially fatal illness. One of the most common being – Cat scratch disease, caused by *B. henselae* and *B. clarridgeiae*. When infection results in disease, affected animals usually develop fever, lethargy, myalgia, and, in the most severe cases – death. *Ixodes ricinus*, *Dermacentor reticulatus* ticks or cat flea *Ctenocephalides felis*, which are widespread in Europe can be vectors of *Bartonella* spp. Humans can be infected via a scratch or bite of the cat, also bite of the infected cat flea or tick. The aim of this study was to investigate *Bartonella* spp. prevalence in domestic cats, their ticks and fleas in Lithuania. A total of 105 of *I. ricinus* and *D. reticulatus* ticks and 102 *Ct. felis* and *Ct. canis* fleas were collected from cats and tested for pathogens by using nested PCR methods. Blood samples were collected from 163 cats presented in pet clinics and animal shelter. *Bartonella* spp. DNA in samples was detected using a nested-PCR of the ITS region. *Bartonella* species were detected in 3 (2.9%) out of 105 ticks, 8 (4.9%) out of 163 cats and 21 (20.6%) out of 102 fleas. Positive tick samples were 33.3 % of engorged ticks and 66.7 % of unfed ticks. All ticks from positive *Bartonella* spp. samples were *I. ricinus*. *Bartonella* spp. were detected in 16 out of 92 of *Ct. felis* flea species, and 5 out of 10 *Ct. canis* flea species. The ITS region sequences showed that both, *B. henselae* and *B. clarridgeiae* were detected in cats and fleas. *B. henselae* was more common than *B. clarridgeiae*. Three *B. henselae* strains were identified. This study is the first report on prevalence and molecular characterization of *B. henselae* and *B. clarridgeiae* in cats and cat fleas in Lithuania. It is essential for animal and human health to make studies on these pathogens and to make sure that prevention means are applied.

Keywords: *Bartonella*, cats, detection and molecular characterization, Lithuania

EFFECT OF HUNTING METHOD ON CORTISOL CONCENTRATIONS IN THE WILD BOAR SERUM

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Abstract

The objective of this study was to determine cortisol concentration in the serum of hunted wild boar in Croatia. Blood samples were collected during regular hunting season in the period between November 2018 and January 2020. Blood samples were taken from wild boar hunted using two most common methods: driven (n=139) and individual hunt (n=61) from high seats. Additionally, animals obtained by driven hunt were divided on those hunted in the unfenced areas (n=83) and fenced area (N=56). Fencing was considered as possible source of additional stress. Serum cortisol was determined using an enzyme immunoassay kit (Cortisol ELISA kit, Enzo Life Sciences, Inc.). Differences in cortisol concentration were observed between analysed hunting methods. As potential stress-related indicator, mean cortisol concentration was the highest in serum of wild boar culled during fenced driven hunt (327.18±46.53 nmol/l). In unfenced driven hunt mean cortisol concentration was slightly lower (312.57±35.57 nmol/L). Individual hunt from high-seats had the lowest (p<0.0001) determined cortisol levels (33.70±4.28 nmol/L). Driven hunt with dogs is a hunting method with the highest hunting pressure and it is obviously relevant for higher pre-culling stress. Individual hunting resulted in cortisol concentrations that could be considered as the one closest to the baseline levels for wild boar. To strengthen our findings and obtain more insights into the influence of different hunting methods on stress in wild boar we need to investigate the cortisol of more animals under different circumstances and longer period.

Keywords: stress, *Sus scrofa*, hunting

IMPACT OF HABITAT FRAGMENTATION ON GENETIC DIVERSITY AND STRUCTURE OF WILD BOAR (*SUS SCROFA*) POPULATION IN LITHUANIA

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Abstract

The wild boar (*Sus scrofa*) is one of the most widespread mammal species in Europe. Today wild boar populations are increasing, in both size and distribution range, across most parts of Europe. This species is one of the most popular game animals in Lithuania.

The data on genetic diversity and population structure of the wild boar in the Baltic states are still scarce. To characterize the amount of genetic variation and population structure of wild boar, and to assess the impact of habitat fragmentation on the formation of population structure in Lithuania, we genotyped and analyzed 15 microsatellite loci for a total of 96 wild boar specimens from 35 locations. The microsatellite analysis of wild boar indicated high levels of genetic diversity within the population. The Bayesian clustering analysis in STRUCTURE identified 4 genetic clusters among sampled wild boar that could not reveal a clear separation between subpopulations. The Mantel test based on correlation between the pairwise geographic and genetic distances observed across all collection localities revealed a weak but significant correlation.

Keywords: *Sus scrofa*, microsatellite loci, genetic diversity, Lithuania

ACTIVITY AND SPREAD OF FALLOW DEER (*DAMA DAMA L.*) AFTER RELEASE TO THE WILD

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Abstract

In Lithuania, there is an abundance of cases when fallow deer, living in enclosures, in smaller or larger groups are released to the wild on purpose. However, the released fallow deer are not methodically observed, thus science research and data analysis on such fallow deer migration, distribution, adaptation and reproduction are not practically carried out.

In this study, GPS collar marked fallow deer have been released to the wild. There were 5 in all fallow deer collar marked (2 male deer and 1 female deer in Pakarklė forest, Kaunas district as well as 1 male deer and 1 female deer in Pašušvis forest, Radviliškis district). The collar marked deer, along with others, marked with ear tags, were released in the forests of two municipalities (Kaunas and Radviliškis districts). Fallow deer GPS collar mark were set to send a signal to the server with coordinates of the animal location. The coordinates of the marked fallow deer locations allowed the calculation of the distance, covered in one hour, how far the animal has moved from the release site, what area the animal used. Data on habitat selection priorities were analyzed: the number of points, registered in the forest area, what stands were selected, how far away they were from the forest edge. The distance between the co-released fallow deer during the whole research period was analyzed.

In order to have information on how far the released animals move from the release site, the distance from the point of release site of fallow deer to the points where the animal was registered on other days, were calculated (by calculating the point of the center of stay of each day). On average, on a daily basis fallow deer kept a distance of 1 km distance from the release site: the average distance of males was 1.3 km and 0.5 km, and that of females was 1,1 km (pic.2.5 in Pakarklė forest, Kaunas district), the distance of a male was 3.4 km, whereas the distance of a female deer was 0.9 km.

The distance covered and the area occupied is also dependent on the sex of the animal. The average area occupied by one animal during the study period was 42.2 ha. Males maintained an average of 60.2–60.3 ha, while females maintained only 10.7 ha.

Males used to cover the distance an average of 3.6–4.1 km per day, while the female covered the distance – 2.2 km. The males covered an average of 25.5 km and 28.5 km per week, and females – 15.4 km respectively.

Keywords: Fallow deer, GPS collars, distribution, activity

PHYLOGEOGRAPHY OF THE SIBERIAN FLYING SQUIRREL (*PTEROMYS VOLANS* L., 1785): NEW DATA FROM CONTINENTAL AND ISLAND POPULATIONS

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Abstract

Siberian flying squirrel inhabits boreal forests from Finland to Eastern Siberia, Korean Peninsula, Sakhalin and Hokkaido Islands. The ecological specificity and widespread suggest close relation of the species genetic diversity to the dynamics of forest zone formation in the Quaternary. Phylogeography of *P. volans* throughout the range has been studied using cyt b. However, a number of geographic regions important for verifying the obtained results remain unstudied.

We present the data on complete cyt b sequences (1140 bp) of *P. volans* from 7 previously unstudied localities in the Urals (14 individuals), Western Siberia (4 individuals), the Russian Far East (Primorye – one individual) and Sakhalin (one individual). Eight haplotypes are identified, five of which are new. Phylogenetic reconstructions (BI-tree, MJ-network) including new data confirm the differentiation of phylogroups "Hokkaido", "Far East", and "Northern Eurasia" with the subgroup "Northwestern Eurasia" distributed from Europe to the south-east of West Siberia. The haplotype from Primorye is included in the "Far East" group, the Ural and West Siberian haplotypes are included in the "Northwestern Eurasia" subgroup. The only haplotype found in West Siberia (previously identified in the north-east of European Russia) is widespread in the Urals and is basal for all Uralian haplotypes.

To reconstruct the history of the island population of Hokkaido, the phylogenetic position of *P. volans* from Sakhalin is important. The only known haplotype sequenced by us belongs to the "Far East". The genetic distance between this haplotype and Hokkaido haplotypes is considerable and is comparable to the distances of other Far Eastern haplotypes.

The study provides new data on the genetic diversity of the flying squirrel in the central part of Northern Eurasia and do not confirm the hypothesis of the expansion to Hokkaido through Sakhalin during the last glacial maximum.

The study is supported by RFBR № 19-04-00966.

Keywords: phylogeography, genetic diversity, mitochondrial genome, species range, Siberian flying squirrel, Quaternary, forest zone formation

ANALYSIS OF LONG-TERM DYNAMICS OF THE ABUNDANCE OF MOUSE-LIKE RODENTS IN THE TAIGA ECOSYSTEMS OF EASTERN FENNOSCANDIA.

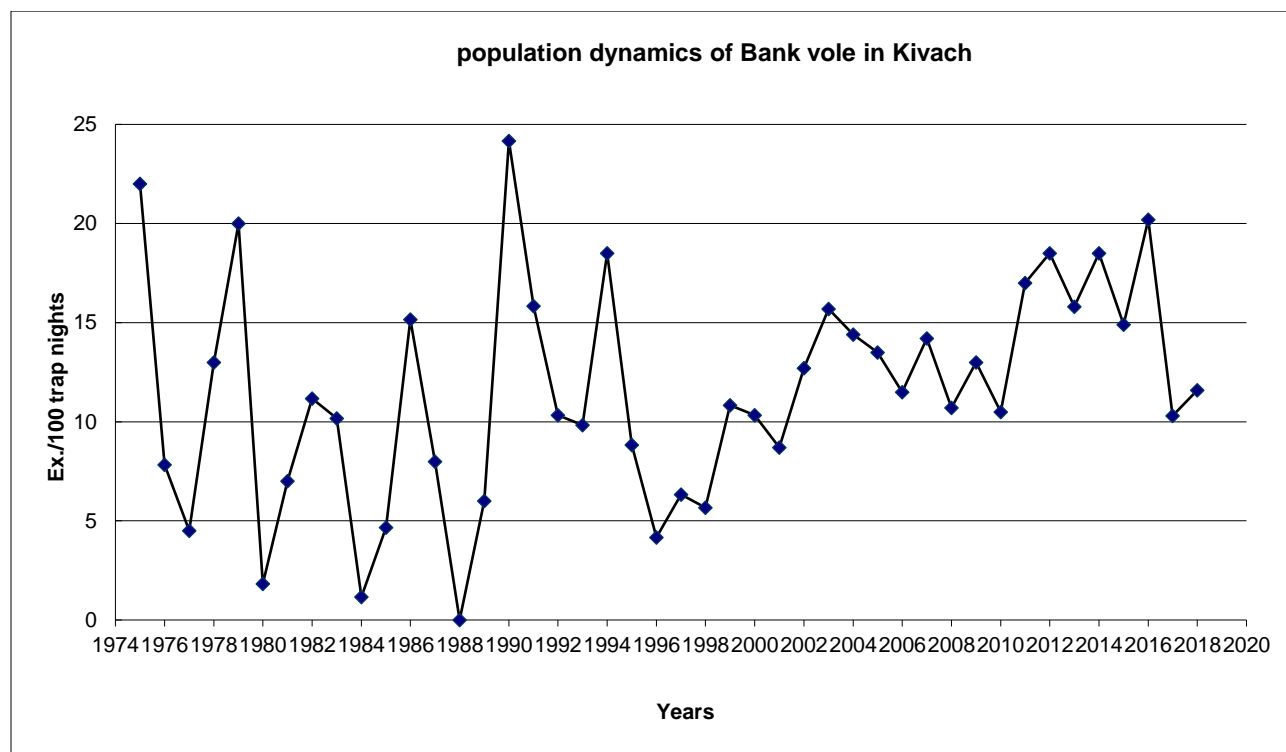
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Abstract

We analyze the results of long-term (45 years, 1975–2020) counts of the abundance of mouse-like rodents in the territory state nature reserve "Kivach", as well as in the adjacent territory (middle taiga, Karelia, Russia). Particular attention is paid to the trends in the dynamics of the abundance of small mammals in different periods of observation. The most significant changes occurred with the indicators of the population dynamics of the dominant species – bank vole (*Myodes glareolus* Schreber, 1780). The abundance of this species has changed dramatically: over the 2007–2016, it was on average 1.5 times higher than in the first 10 years of observations, and then underwent a sharp decline (picture). On the contrary, the coefficient of variation decreased significantly since 1997. We assume that the observed changes may be associated with climate change and, accordingly, environmental conditions in different seasons, which in turn affects the dynamics of rodent populations.



DISTRIBUTION OF EURASIAN BEAVER (*CASTOR FIBER*) IN UPPER TISA RIVER - AN OVERVIEW OF CONSERVATION PROBLEMS

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Abstract

Beavers are considered “engineers” of the environment due to their ability to modify river systems and their surrounding areas. Changes brought by the beaver activity create favorable or unfavorable habitats for other species, facilitating their appearance or disappearance. Thus, beavers are considered a keystone species for biodiversity, having a high impact on river ecosystems. Tisa River is one of the main rivers of Central and Eastern Europe contributing to about 13% of the total Danube flow and is part of the historical range of the Eurasian beaver (*Castor fiber*). In Romania, as in other European countries, during the 19th century, the Eurasian beaver was hunted to extinction. Between 1998 and 2003 181 beavers were reintroduced in the rivers Olt, Mureș and Ialomița. In the last 15–20 years, the beaver has regained its favorable habitats by advancing upstream the Tisa corridor from Hungary, where it was also reintroduced. Presently, the species is a common presence in Romanian part of Upper Tisa River and on its tributary rivers. Upper Tisa River is part of Natura 2000 Network as ROSCI 0251 Tisa Superioară, but the beaver was not included in the site’s standard data form. As a result, although studies on biodiversity and the effect of human impact are conducted across the site in order to elaborate the management plan, the beaver will not benefit from management measures and thus protection in this area. This work presents the distribution of the beaver on the upper course of the Tisa River, highlighting the main pressures and threats on this species in this area and proposes a series of conservation measures specific to the given situation.

Keywords: beaver, upper Tisa River, human impact, conservation measures, Natura 2000

DEVELOPMENT OF GOLDEN JACKAL (*CANIS AUREUS*) POPULATION IN ESTONIA

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Abstract

The occurrence of golden jackal was first confirmed in Estonia in late winter 2013 when a young specimen was occasionally hunted. Since then the local reproductions were registered every year and the population has been increased in numbers and in its distribution range. The biggest hunting bag was in 2018 when all together 76 specimens was shot. Currently, the main part of local population is distributed along the western coast of Baltic sea including the island Saaremaa and a small reproductive nucleus is settled in east near lake Peipus. Population is slowly expanding its range both in western and eastern side of the country. In recent years there has been some 10–20 annual reproductions that are the northernmost known in whole jackal range. The number is fluctuating in last years mainly due to various hunting pressure. Jackal is in the list of small game species with open season from September 1. to February 29. Monitoring of the species includes hunting bag analyses, registration of occasional observations, camera trapping and bioacoustic survey in permanent calling transects.

Keywords: golden jackal, expanding population, Estonia

PREVALENCE AND GENETIC DIVERSITY OF *BARTONELLA* SPECIES IN RODENTS (MURIDAE, CRICETIDAE) IN LITHUANIA

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Abstract

Rodents (Muridae, Cricetidae) represent an important group of mammalian hosts as considered reservoir host of *Bartonella* species. More than 20 *Bartonella* spp. are associated with rodents and several rodent-associated *Bartonella* species have been related to human diseases. The aim of the research was to investigate *Bartonella* spp. prevalence and genetic diversity in various species of rodents collected in Lithuania. A total of 580 rodents representing eighth species – *A. flavicollis* (n=201), *A. agrarius* (n=76), *M. musculus* (n=12), *M. minutus* (n=40), *M. glareolus* (n=165), *M. oeconomus* (n=58), *M. agrestis* (n=25) and *M. arvalis* (n=3) were captured with live or snap traps in 12 locations of Lithuania during 2015–2016. The presence of *Bartonella* DNA was examined by real-time PCR targeting the *ssrA* gene. The molecular characterization of the bacteria strains was based on sequence analysis of two housekeeping genes (*rpoB*, *groEL*) and the 16S–23S rRNA intergenic spacer region (ITS). The overall prevalence of *Bartonella* spp. was 54.8% and ranged from 8.3% in *M. musculus*, 15.8% in *A. agrarius*, 33.3% in *M. arvalis*, 42.4% in *M. glareolus*, 53.4% in *M. oeconomus*, 57.5% in *M. minutus*, 79.6% in *A. flavicollis* to 80% in *M. agrestis*. Phylogenetic analysis based on two housekeeping genes and ITS region demonstrated that rodents harbor multiple *Bartonella* species belonging to six clades associated with human pathogenic *B. grahamii*, *B. rochalimae* and *B. tribocorum* species, and other species *B. taylorii*, *B. coopersplainsensis* and *B. doshiae* which pathogenicity to humans is still unknown. *Bartonella* strains belonged to *B. grahamii* and *B. taylorii* clades were heterogenic. Phylogenetic analysis based on each of the targets demonstrated high variability of *B. taylorii* and *B. grahamii* strains between different and either same rodent species. The frequent distribution and high genetic diversity of *Bartonella* species in rodents suggests that rodents may play an important role as potential reservoir hosts and thus in the maintenance of this pathogen in Lithuania.

Keywords: rodents, *Bartonella*, distribution, genetic diversity, Lithuania

GENETIC MONITORING OF GREY WOLVES IN SERBIA

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Abstract

Genetic monitoring is a crucial aspect of an effective wildlife conservation strategy. Application of molecular markers in the study of natural populations of large mammals provides information about their genetic variability and indicates its potential for adaptation and survival. Continuous genetic monitoring provides insight into temporal changes in genetic diversity and highlights necessity for conservation actions in case of its decrease. As a major predator, grey wolf was a widespread species in the past; however, as is the case with other large mammals, wolves have faced a drastic decline in population size during the last two centuries. In Serbia, wolves play a key role in maintaining the structure and function of the ecosystems by regulating predator-prey relationship. The main goal of this study is to evaluate the genetic diversity of the Serbian grey wolf population, as well as to identify any changes in genetic variability level as compared to the results obtained for the same population over the last several years. Genomic DNA was extracted from 49 grey wolves muscle tissue samples collected across central Serbia during the regular hunts in 2020 and chosen microsatellites loci were amplified by PCR. Individuals were genotyped by panel of 22 microsatellites markers, 21 autosomal and amelogenin sex determination locus (Canine ISAG STR Parentage Kit). Genetic variability parameters were calculated in GenAlEx and GENEPOP. The number of alleles per locus varied between 16 in the case of AHT121 and 5 alleles for FH2848 locus, with the average number of alleles per locus of 8.286, and the number of effective alleles of 4.467. Overall expected heterozygosity (0.747) was higher than the observed heterozygosity (0.694), with an average coefficient of inbreeding (F_{IS}) over all loci of 0.082. Results of this study show that the genetic diversity of this population is high and that in comparison to previous studies of the same population conducted in the last couple of years, it can be concluded that the wolf population in Serbia is currently stable.

Keywords: grey wolf, genetic diversity, microsatellites

FIRST RECORD OF BEAVER (*CASTOR FIBER L.*) IN PRUTUL DE JOS RESERVE, REPUBLIC OF MOLDOVA

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Abstract

The beaver was found in the Miocene fauna and during the Anthropocene as a permanent component of the fauna on the Republic of Moldova territory. According to scientific information, the European beaver have disappeared in the middle of the second millennium AD (Lozan, 1970). The Prutul de Jos Reserve is located in the Prut river meadow, including Beleu Lake (628 ha), on an area of 1755.4 ha. The forest vegetation (326 ha) is formed mostly by different willows species, the reed and rush vegetation occupies 370 ha. In 2019, on the bank of the Prut River, a stump of freshly gnawed willow stalk was observed, with beaver traces around it. In October 2020, several stumps and traces of the beaver were found in the area with full protection, at distances of 100–300 m from the lake. Also, the species was recorded by camera trap. The beaver reached the reserve along Prut river from the Danube Delta, where it migrated naturally from the basins of the rivers Olt, Mureș and Ialomița, Romania. In 1998 a project has started to introduce the beaver in Romania's fauna by colonizing 182 animals brought from Germany. So, the process of dispersal and migration of the beaver was quite fast. In present climatic conditions, when the drought occurs more and more frequently and the water deficit is increasing, it is difficult to predict how the beaver would manifest its adaptive capacities in colonizing new territory. Some studies show that the beaver continues its activity in case of water drying, by deepening the water basin, if the food source is rich and available. The presence of predatory species (*Nyctereutes procyonoides*, *Vulpes vulpes*, *Canis aureus*) will slow down the colonization of the beaver, in particular, by attacking young animals, if the appropriate biotechnical measures are not implemented.

The studies were performed within the State Program project 20.80009.7007.02.

Keywords: Beaver, Prutul de Jos Reserve, willow, colonization, climatic conditions.

DEVELOPMENT OF SIMPLE DNA BARCODE-BASED APPROACH TO CARNIVORE DIETARY STUDIES BY USING FAECAL SAMPLES

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Abstract

Knowledge on a diet of carnivores is essential to assess the role of studied species in the ecosystem, the potential competition with other carnivores, and the impact on prey species. Therefore, dietary analyses have important implications for preparing and implementing appropriate conservation actions, and further management plans. However, the accuracy of prey identification based solely on the morphological determination of undigested food particles in the stomach or faeces is often unreliable, and the working process is time consuming. Furthermore, direct observations of feeding preferences of most carnivores are often impossible due to living in closed habitats, preferred nocturnal activity or specific feeding strategies and behaviour.

Genetic analysis of faecal samples can complement other methods used for studying diet or predatory behaviour in predators and provide an invaluable tool for determining ecological requirements even of rare, endangered or elusive species. Nevertheless, these techniques must be tailored to specific research objectives.

In this study, we aim to develop a simple molecular methodology to reliably determine prey species in grey wolf (*Canis lupus*) faeces. We intend to develop a metagenomic barcode-based approach for prey identification using next-generation sequencing technology. The barcode system is based on the amplification of short DNA segments that are sufficiently informative to distinguish even closely related species. Such fragments are labelled with an additional sequence (the barcode), allowing to pool and sequence several samples at the same time. In present study, we will use two mitochondrial regions widely employed for metabarcoding of vertebrates in combination with quencher primers to exclude amplification of the predator DNA. Metagenomic data from faecal samples, obtained in this study, will significantly contribute to more advanced and relevant dietary as well as ecological studies of this apex predator in the future.

Keywords: Dietary analysis, metagenomic, faeces, grey wolf

VECTOR-BORNE INFECTIONS IN FREE-RANGING RED DEER (*CERVUS ELAPHUS*) DURING THE WINTER SEASON IN NORWAY

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Abstract

Many emerging infectious diseases are of wildlife origin, are vector-borne, and present a growing health concern for both humans and livestock. Wild cervids are essential hosts for maintaining *Ixodes* ticks and deer keds and consequently, infection diseases vectored by these ectoparasites. The red deer is widely distributed game species in Europe, including Norway. The geographical and spatial distributions of some European vectors have been changing in recent decades. Expansion of vectors can affect the spread of related vector-borne pathogens such as *Anaplasma phagocytophilum*, *Babesia* spp. and *Bartonella* spp. In the present study, the presence and prevalence of these vector-borne pathogens in red deer were investigated during the winter season. Blood samples were analysed from 38 free-ranging adult red deer that had been chemically immobilised in January and February 2014–2016 in the counties of Telemark and Agder in Norway. The overall prevalence of *A. phagocytophilum* and *Babesia* spp. in the examined animals was 31.6 % and 47.4 % respectively. *Bartonella* DNA was detected in 53.3% of red deer. Seven animals were co-infected with two pathogens and four animals had triple infections. Sequence analysis revealed the presence of two *Babesia* species: *B. divergens* and *B. odocoilei*. The *Bartonella* strains were closely related to *B. bovis* and the clade associated with *B. schoenbuchensis*, *B. chomelii* and *B. capreoli*. Seven *msp4* sequence variants of *A. phagocytophilum* were identified. Detection of *Anaplasma*, *Babesia* and *Bartonella* DNA in red deer during the winter season, when ticks, deer keds and other blood-sucking arthropods are inactive, demonstrated the presence of persistent vector-borne infections in this animal host.

Keywords: *Anaplasma phagocytophilum*, *Babesia* spp., *Bartonella* spp., *Cervus elaphus*, Norway

UNGULATE IMPACTS ON THE VEGETATION OF A PERI-URBAN REPTILE HABITAT

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Abstract

Red deer and wild boar densities are increasing in Europe, and they are also more common in urban and peri-urban areas. Ungulates have numerous direct and indirect effects on faunal diversity, including the alteration of habitats available for reptiles. In our ongoing project we focus on investigating impacts of ungulates on a strictly protected reptile species (Caspian whipsnake, *Dolicophis caspius*) in Hungary. We assess ungulate browsing impacts and wild boar rooting intensities in relation to the ranging behavior of the snakes in a peri-urban study area, in Budapest. Using drone photography, we also follow the development of shrub encroachment processes to better understand the impact of ungulates on vegetation changes and indirectly on the availability of preferred patches for snakes. Our preliminary results show that snakes are widely distributed within the study area, but they are mostly localized at the edges of shrubby patches, and not in the open or entirely closed areas. A large part of the home range areas of snakes is rooted, which can mitigate shrub encroachment process. Relative to this, deer browsing does not seem to have huge impact on the vegetation cover. Adequate management and population control of ungulates, considering their negative and beneficial effects on the vegetation, are very important to maintain a stable habitat for that fragmented snake population.

Keywords: Caspian whipsnake, deer, wild boar, rooting, shrub encroachment

DOMESTIC CAT HYBRID IDENTIFICATION USING DIAGNOSTIC MOLECULAR METHODS

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Abstract

Every country has legislations at the national level specifically prohibiting or restricting the private possession of wild animals and their hybrids, by regulating certain species; a family or subfamily that animal belongs to; or rare or endangered species. As wildcat populations are foremost threatened by hybridization with the domestic cat. In Lithuania, private persons are prohibited from possessing protected wildlife, including members of Felidae family wild cats, except where the person owned such animal before the current wildlife protection law became effective in 2018. As the increasing awareness of wild-hybrids has led to a renewed interest in rapid diagnostic assays. During this research a suspected Asian Leopard Cat (*ALC-Felis bengalensis*) hybrid was tested to identify the lineage. Molecular identification characterized by PCR and sequence analysis of the ATP-8 mitochondrial gene. After comparing the obtained gene sequence variants of the ATP-8 gene fragment in the studied cat with the foreign sequences published in the Gene Bank between the domestic cat *Felis catus* and the Afroasis *Felis silvestris*, *Felis libyca*, we obtained genetic changes. The relative percentage of sequence changes was 1/3 between the tested cat and the domestic cat *F. catus* and the Afroasis *F. silvestris*, *F. libyca*, allowing the identification of the test object as a second-generation hybrid of Afroasis cat.

Keywords: *Felis libyca*, domestic cats, molecular detection, Lithuania

ANAPLASMA PHAGOCYTOPHILUM INFECTION IN CERVIDS AND THEIR TICKS IN LITHUANIA

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Abstract

Anaplasma phagocytophilum is a bacterial pathogen, which is a major cause of zoonotic disease – anaplasmosis. The main vectors of *A. phagocytophilum* are ticks of the *Ixodes ricinus* complex. The role of wildlife species in the circulation of *A. phagocytophilum* is yet to be clearly determined, but several species of wild ruminants are thought to be important reservoirs. Epidemiological studies in multiple countries have shown that the prevalence of *A. phagocytophilum* highly depends on the density of ticks and their potential hosts such as cervids which are one of the main sources of nutrition for *Ixodes* ticks. In Lithuania, cervids are important game animals but their contribution as reservoirs for *A. phagocytophilum* remains unknown. The objectives of the study were to investigate the prevalence of *A. phagocytophilum* infections in cervids and in ticks *feeding* on *cervids* and to characterize the *A. phagocytophilum* strains obtained from animals and ticks based on sequence analysis of *msp4* gene. Forty-four cervids representing three species roe deer *Capreolus capreolus*, red deer *Cervus elaphus* and moose *Alces alces* were sampled by hunters during hunting seasons 2010–2013 and 2016–2017 in Lithuania. A total of 187 ticks (178 *Ixodes ricinus* ir 9 *Dermacentor reticulatus*) were collected from these animals. Animal blood and spleen samples (collected from 27 roe deer and 2 red deer) and ticks were analysed for the presence of *A. phagocytophilum* DNA by nested PCR based on *msp4* gene. *A. phagocytophilum* DNA was identified in 10 (37.04%) of the 27 roe deer. The overall prevalence of *A. phagocytophilum* in *I. ricinus* and *D. reticulatus* ticks was 39.3% (70/178) and 22.2 % (2/9) respectively. The sequence analysis of the *msp4* gene of *A. phagocytophilum* revealed ten different sequence types: seven *msp4* sequence types were detected in roe deer and five in ticks. Four different *msp4* gene variants derived from roe deer had unique nucleotide polymorphisms and therefore differed from other *A. phagocytophilum* sequences previously deposited in the GenBank database.

Keywords: cervids, *Anaplasma phagocytophilum*, ticks, Lithuania

MOLECULAR DETECTION OF *MYCOPLASMA* SPP. IN BATS FROM LITHUANIA

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Abstract

The order Chiroptera is considered the second largest group of mammals in the world, hosting important zoonotic virus and bacteria. Hemotropic mycoplasmas (hemoplasmas) are worldwide distributed bacteria affecting domestic and wildlife animals besides human beings. Hemotropic mycoplasmas are the smallest free-living, self-replicating, gram-negative epicellular bacteria that parasitize red blood cells causing haemolytic anaemia, thrombocytopenia, fever, infertility, and poor weight gain. However, knowledge of hemoplasmas is limited in bats, and was poorly studied throughout the world and had never been investigated in bats of Lithuania. The aim of the present study was to detect and identify *Mycoplasma* species using molecular detection methods in bats from Lithuania. A total number of 20 dead bat were collected in Lithuania during 2017–2019. DNA was extracted from the spleen and lung samples. Detection of hemoplasmas was performed using conventional PCR targeting a 600-bp region of the 16S rRNA gene. *Mycoplasma* DNA were found in 0,5% (1/20) of bats. Positive sample sequence showed 92–96 % similarity with *Mycoplasma* sp. sequences from GenBank. This study is the first report of molecular detection of *Mycoplasma* spp. in bats in Lithuania.

Keywords: bats, mycoplasma, molecular detection

THE STATE OF THE COLONY OF POND BATS IN EARLY HIBERNATION IN TANECHKINA CAVE

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Abstract

Continuous and long-term observations of individual species at permanent sites of their residence allow us to reconstruct the processes and create a reasonable interpretation of the relationships and patterns behind the observed changes in the populations of these species. In during monitoring the number of bats on wintering grounds in the tunnels of the Leningrad region, an important role is played by assessing the state of bats, both at the beginning and middle of wintering, and at its end. This work is devoted to this assessment of the state. This material was collected during winter surveys in the Leningrad Region in the last week of November 2016, 2019, 2020 in Tanechkina cave, located on the left bank of the Volkhov river near the village of Staraya Ladoga. This tunnel for the extraction of quartz sand is abandoned and is the northernmost mass wintering of bats, in particular a rare species – pond bat, *Myotis dasycneme*. Within the framework of the work, the number, pattern of attachment and formation of groups of different numbers were taken into account. The results are presented in Table 1 and Figure 2.

Table 1. The ratio of the number of pond bats in early hibernation in the Tanechkina cave

Date	Open, %	In the crevice, %	Total
27.11.2016	75.6	24.4	1975
26.11.2019	69.2	30.8	1421
29.11.2020	64.6	35.4	1510

At the beginning of wintering, the predominance of bats outside various shelters is noticeable in the ratio of 1 to 1.8–3.1. In addition, it is worth saying that at this time the area of the underground lake, which floods the cave during periods of thaw and heavy rains, is significantly reduced.

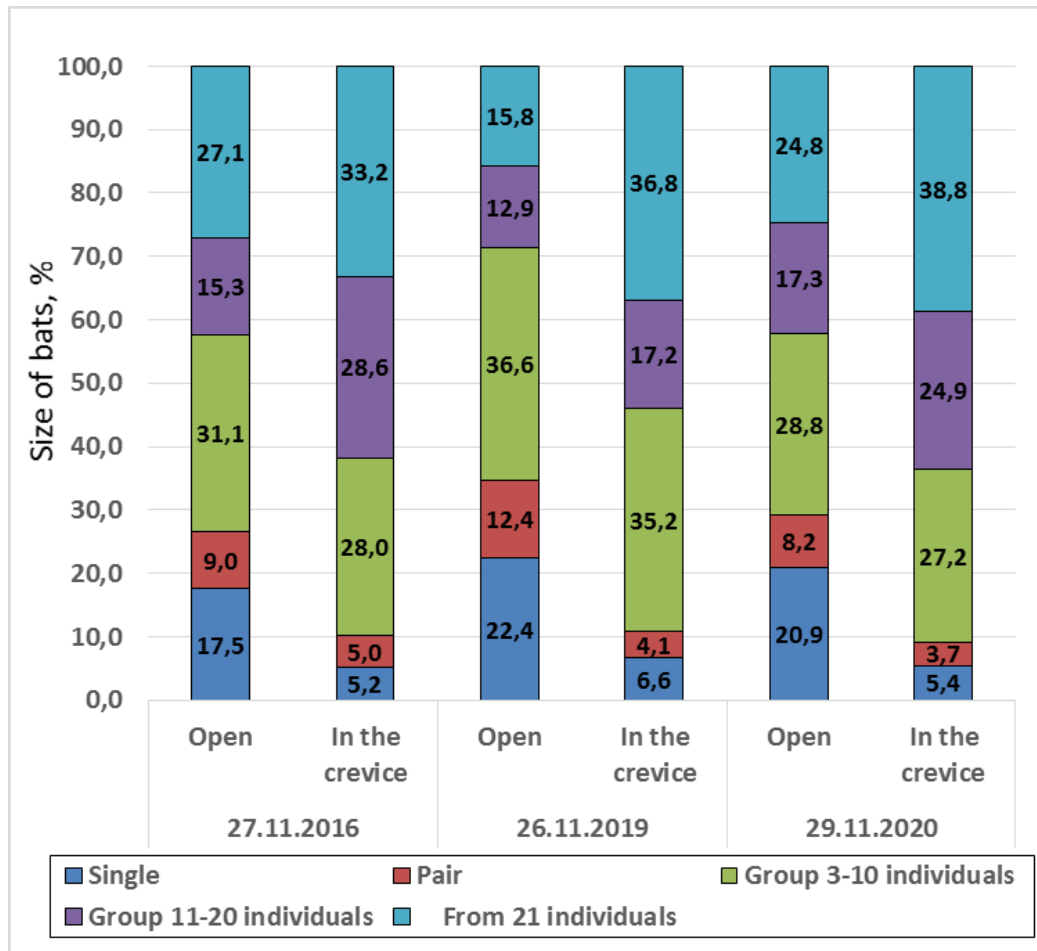


Fig. 1. The ratio of different groups and the number of pond bats

Assessing the state of the wintering colony of pond bats, we can say that at the beginning of wintering, the ratio of its various groups is quite stable. Most animals prefer to spend the winter openly (64.6–75.6%), rather than in various shelters (24.4–35.4%). Open-hanging animals prefer to spend the winter alone (up to 20.9%) or in groups of 3 to 10 individuals (up to 36.6%) and groups of more than 21 individuals (up to 27.1%). As for those who prefer hiding places, most of the animals were found here in groups. The largest number was in dense groups of more than 21 individuals (up to 38.8%), as well as in groups of 3 to 10 individuals (up to 35.2%).

SMALL RODENTS AND THEIR ECTOPARASITES IN DIFFERENT HABITAT TYPES IN LITHUANIA

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Abstract

Wild small rodents and their ectoparasites play a significant role in the maintenance of pathogenic microorganisms in the nature and in the transmission of zoonotic diseases to humans and animals. Nevertheless, rodent-ectoparasite associations are still poorly known. Rodents are widely distributed and well adapted to different ecosystems and climates and understanding rodent-ectoparasite associations in different habitats is important from a human public health perspective. The aim of this study was to investigate ectoparasites (ticks and mites) parasitizing small rodents and estimate infestation patterns in mice and voles inhabiting different habitat types in Lithuania. Seven different species of rodents (*Apodemus flavicollis*, *A. agrarius*, *Microtus arvalis*, *M. agrestis*, *M. oeconomus*, *Myodes glareolus* and *Micromys minutus*) were caught in natural (overgrown and flooded meadows, peatbog and swamp) and suburban (commercial apple orchard) habitats in 2015 and 2018. A total of 1108 ectoparasites, represented by two species of ticks identified as *Ixodes ricinus* (n=706) and *Dermacentor reticulatus*. (n=125), and six species of Laelapidae mites (n=277; *Laelaps agilis*, *L. hilaris*, *Hyperlaelaps microti*, *Haemogamassus nidi*, *Eulaelaps stabularis* and *Myonyssus gigas*) were collected from small rodents. The overall prevalence of infestation with different ectoparasites varied between species of hosts and sampling sites. The most frequently infested with *I. ricinus* ticks and Laelapidae mites were *A. flavicollis* mice (77.0% and 73.0% respectively), while the overall prevalence of infestation with *D. reticulatus* was significantly higher on *M. oeconomus* voles (48.0%). Rodents collected in natural habitats were significantly higher in both ticks and mites infestation, compared to rodents in suburban habitats. Our study provides new data on associations between different species of small rodents and their ectoparasites in natural and suburban habitats in Lithuania.

Keywords: small rodents, ticks, mites, infestation, different habitat

CHANGES IN WOLF (*CANIS LUPUS L.*) DIET COMPOSITION AFTER THE OUTBREAK OF AFRICAN SWINE FEVER IN LITHUANIA

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Abstract

Damage made by wolves (*Canis lupus L.*), namely the loss of livestock as well as competition to hunters, remains the point of most contention and thus an examination of diet remains actual. The aim of this study was to find out changes in wolf diet composition after the outbreak of African swine fever in Lithuania

The samples for wolves' diet were collected during 2019–2020 in various places of the country. It was examined 126 cases of wolves' food remains: prey remains in locations of kills and consumption (n=39), content of stomachs (n=18) and scats (n=69). Data from scats and stomachs were pooled together, but the data from prey kills remnants were analyzed separately to escape the increase of big prey part in wolf diet. Composition of wolf food was expressed in two ways: the percentage of scats, which contained different prey species relative to the total number of analyzed samples (frequency of occurrence F%) and the percentage of biomass of a particular food component relative to the total biomass consumed by wolves (B%). Collected samples were classified into two seasons for analysis: winter (October–March) and summer (April–September).

Studied examples were compared with research results from 2004–2012 period, when 225 samples were analysed. Wolf diet in this earlier research consisted mainly of Cervidae (roe deer and red deer) 43.4%, wild boar 33.0% and beaver 18.1%.

Keywords: wolf, diet, scat, stomach, Lithuania.

GENETIC STRUCTURE OF WILDCAT (*FELIS SILVESTRIS*) POPULATIONS IN THE AREA BETWEEN THE DINARIC AND SCARDO-PINDIC MOUNTAINS

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Abstract

The wildcat *Felis silvestris*, is widely distributed from Western Europe to Western China and throughout the African continent. Hundreds of years of synergy of negative factors including habitat loss have led to the extinction of the European wildcat from most of its historical range. In addition, transport networks, urban areas as well as agricultural landscapes divide natural habitats into small isolated patches and create barriers that restrict gene flow and ultimately leads to a hidden genetic structure within the European wildcat populations.

We studied the genetic makeup of the wildcats in a topographically diverse landscape between Dinaric Mts., Scardo-Pindic Mts. and Pannonian basin. Using microsatellite variations, we determined the genetic variability and population structure of the wildcat in the area of SE Europe, where data on the genetic prospects of this endangered felid are completely lacking. A total of 113 tissue samples of free-living putative European wildcats were taken from dead (natural, vehicle collisions, etc.) or from live-trapping individuals in telemetry studies. We investigated whether geographical isolation is reflected in the genetic architecture of the wildcat populations and how recent human management has influenced the population structure. Finally, we investigated introgressive hybridization between populations of wildcats and domestic cats (*Felis catus*).

The genetic structure of wildcat populations based on Bayesian Information Criterion divides populations into two genetic clusters, that distinguish individuals according to their geographical origin (north to south gradient). The apparent loss of the genetic integrity due to hybridization with domestic cats has been observed throughout the region, but it is of especial concern in Serbia.

Wildcat populations in the studied area are geographically structured, and management and conservation strategies should vary depending on the current status of the population, genetic diversity and the potential for long-term survival.

Keywords: endangered felid, genetic structure, hybridization, microsatellite

USING ION S5 SYSTEM FOR NEXT-GENERATION SEQUENCING OF LATE PLEISTOCENE AND HOLOCENE BISON SAMPLES

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Abstract

Species of the genus *Bison* constituted an important part of the Eurasian and North American Pleistocene megafauna. However, after the Quaternary extinction event, only the American bison (*Bison bison*) and the European bison or wisent (*Bison bonasus*) survived into modern times. While the traditional classification of fossils is based on the use of their morphological characteristics, new methods have been introduced in recent decades, such as the analysis of DNA, extracted from archaeological or palaeontological material (ancient DNA or aDNA). An invaluable tool in the analysis of ancient DNA is next-generation sequencing, due to its ability to sequence short fragments (<100bp).

In this study, we aim to develop and implement a simple methodology to amplify short fragments of the mitochondrial genome of ancient steppe bison and European bison using the Ion S5 System (ThermoFisher). We intend to develop a metagenomic barcode-based approach using next-generation sequencing technology for the successful amplification of aDNA, extracted from Late Pleistocene and Holocene *Bison* bone samples. The barcode system is based on the amplification of short DNA segments which are labelled with an additional barcode sequence. This allows us to create a library, by pooling and sequencing more fragments, from a single sample in one chip run. We designed the primers to amplify short fragments (106 bp to 198 bp) of the *Bison* mitochondrial genome.

PCR amplifications were performed on two Holocene samples, targeting different regions of the mitogenome (12S, 16S, BND1, BND2, COX1, COX3, BND3, BND4 and cytochrome b). The methodology developed in this study will significantly contribute to the analysis of bison aDNA with the Ion S5 System.

Keywords: *Bison bonasus*, *Bison priscus*, ancient DNA, next-generation sequencing

Summary of BTC 11

11th Baltic Theriological conference was held online in January 26-27th, 2021 in Lithuania. The aim of 11th Baltic Theriological conference was to show trends of the Baltic theriology in mammalian ecology, fauna and distribution, mammal conservation and management, mammalian genetics, taxonomy and philogeography, parasitology and investigation methods. **24 short** and **25 full** presentations were given by participants from **12 countries**: Lithuania, Latvia, Estonia, Respublic of Moldova, Russian Federation, Hungary, Romania, Slovenia, Croatia, Poland, Serbia and Finland. Coverage of the different mammalian groups in the presentations of BTC 11 is shown in the Fig. 1. Number of presentations according sections and the type of presentations is given in Fig. 2. New and inovative investigation methods were discussed nearly in all sections. Due to the online format, possibility to present their results in short oral presentation form was given to all young scientists for the first time. This conference opened up a new opportunities in different topics for colaboration and cooperation between not only for Baltic but also for Central European countries.

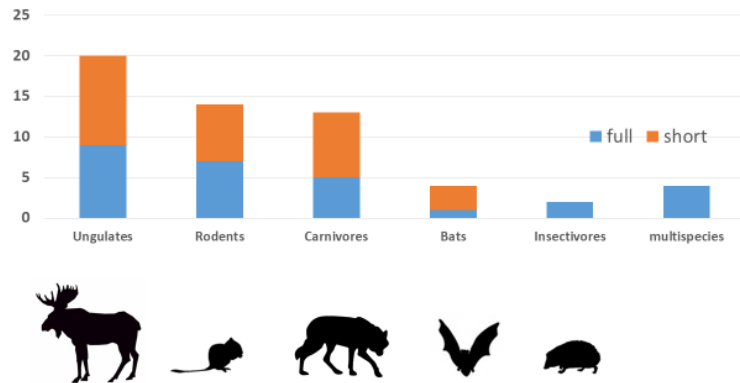


Figure 1. Taxonomic coverage in presentations of BTC 11.

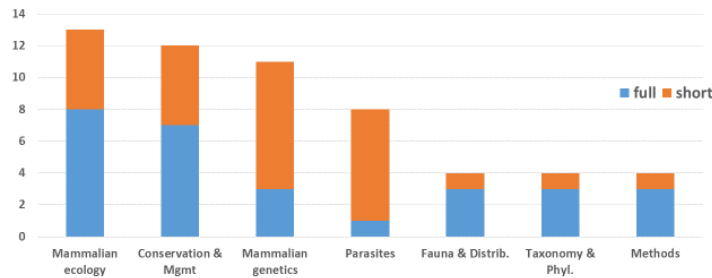


Figure 2. Number of presentations in the sections of BTC 11.

We would like to remind you that the results presented in this conferece can be published in the Special Issue of *Sustainability* (MDPI) journal. For publication possibilities please contact Ms. Queena Cui: queena.cui@mdpi.com.

Meet you in Latvia, 2023

Organizing Committee A. Paulauskas

Scientific Committee L. Balčiauskas

Information about presenters

No.	Name	Surname	E-mail	Institution	Degree	Presentation type	Presentation title	Page
1	Asta	Aleksandravičienė	asta.aleksandraviciene@vdu.lt	Vytautas Magnus University, Lithuania	PhD	Mini	<i>Babesia</i> spp. in ticks collected from European bison	37
							Bacterial Pathogens in Lice Collected from Small Rodents	38
2	Linus	Balčiauskas	linas.balciauskas@gamtc.lt	Nature Research Centre, Lithuania	PhD	Full	Story of a Single Meadow: Long Term Changes in a Small Mammal Community Under Human Influence	8
3	Tomas	Barkauskas	tomas.barkauskas40@gmail.com	Vytautas Magnus University, Lithuania	MSc	Mini	Differences in ungulate population use in different hunting ground units in Lithuania	39
4	Justyna	Baršėvskā	Justyna.barscevska@gamtc.lt	Nature Research Centre, Lithuania	PhD	Full	Nest Boxes vs Nocturnal Acoustic Surveys for Estimation of Habitat Parameters of the Edible Dormouse (<i>Glis glis</i>)	9
5	Ana Maria	Benedek	benedek_ana@yahoo.com	Lucian Blaga University of Sibiu, Romania	PhD	Mini	Habitat Selection by Small Mammals in Mountain Forests is Influenced by Population Density and Altitude	40
6	Silvia	Blašković	sblaskovic9@gmail.com	University of Zagreb, Croatia	PhD	Full	Review of camera trap features for successful lynx identification	10

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7	Aja	Bončina	boncina.aja@gmail.com	University of Primorska, Slovenia	MSc	Mini	Genetics as a Useful Tool for Understanding Relatedness, Movements and Social Behaviour in Wild Boar	41
8	Elena	Bužan	elena.buzan@upr.si	University of Primorska, Slovenia	Prof	Mini	Inferring Population History and Demography Using Microsatellites and Major Histocompatibility Complex Genes in European Roe Deer	42
9	Dalia	Černevičienė	dalia.cerneviciene@stud.vdu.lt	Vytautas Magnus University, Lithuania	PhD	Mini	Otter population structure and role in ecosystems	43
10	Natalia	Dibolskaia	dibolsckaya.natali@yandex.ru	Institute of Zoology, Republic of Moldova	PhD	Full	New Bat Site In The Stone Mines Of Molovata Noua, Republic Of Moldova	18
11	Gundega	Done	gundega.done@silava.lv	State Forest Research Institute Silava, Latvia	MSc	Full	Species, Numbers or Sex Ratio? Evaluation of Ungulate Damages to Young Forest Stands in Latvia	11
12	Paulė	Drigotaitė	paule.drigotaite@vdu.lt	Vytautas Magnus University, Lithuania	BSc	Mini	Bartonella spp. prevalence in domestic cats and their ectoparasites in Lithuania	44

No.	Name	Surname	E-mail	Institution	Degree	Presentation type	Presentation title	Page
13	Maris	Hindrikson	maris.hindrikson@ut.ee	University of Tartu, Estonia	PhD	Full	Sequencing <i>de novo</i> Y chromosome reference genome of the dog	12
14	Laura	Iacolina	laura.iacolina@famnit.upr.si	University of Primorska, Slovenia	PhD	Full	European Levels Of Wild Boar Hybridization	14
15	Žygimantas	Janeliūnas	zygimantasjaneliunas@gmail.com	Vytautas Magnus University, Lithuania	PhD	Mini	Impact Of Habitat Fragmentation On Genetic Diversity And Structure Of Wild Boar (<i>Sus Scrofa</i>) Population In Lithuania	46
16	Erika	Juhász	erikamaria.juhasz@gmail.com	Eötvös Loránd University, Hungary	PhD	Full	Unexpected Interaction Between Reintroduced Beavers and Invasive Woody Species in European Floodplains	15
17	Rimvydas	Juškaitis	rjuskaitis@gmail.com	Nature Research Centre, Lithuania	PhD	Full	Long-term Abundance Dynamics in Four Dormouse (Gliridae) Populations in Lithuania	16
18	Nikolina	Kelava Ugarković	nkelava@agr.hr	University of Zagreb, Croatia	PhD	Mini	Effect of Hunting Method on Cortisol Concentrations in The Wild Boar Serum	45
19	Artūras	Kibiša	arturas.kibisa@vdu.lt	Vytautas Magnus University, Lithuania	Prof	Mini	Activity and Spread of Fallow Deer (<i>Dama dama</i> L.) After Release to The Wild	47

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21	Andrius	Kučas	andrius.kucas@gamtc.lt	Nature Research Centre, Lithuania	PhD	Full	Temporal Patterns of Ungulate-Vehicle Collisions in Lithuania	17
22	Juri	Kurhinen	kurhinenj@gmail.com	University of Helsinki Finland	PhD	Mini	Analysis of Long-term Dynamics of the Abundance of Mouse-like Rodents in the Taiga Ecosystems of Eastern Fennoscandia.	49
23	Vukan	Lavadinović	vukan.lavadinovic@sfb.bg.ac.rs	University of Belgrade - Faculty of Forestry, Serbia	PhD	Full	The Influence of the Type of Hunting Ground on the Age Structure and the Share of Young Hare (<i>Lepus Europaeus</i> L.)	28
24	Anamaria	Lazăr	anagurzau@yahoo.co.uk	Transilvania University of Braşov, Romania	Prof	Mini	Distribution of Eurasian beaver (<i>Castor fiber</i>) in Upper Tisa River – an Overview of Conservation Problems	50
25	Peep	Männil	peep.mannil@envir.ee	Estonian Environment Agency, Estonia	MSc	Mini	Development of golden jackal (<i>Canis aureus</i>) population in Estonia	51
26	Dalytė	Mardosaitė-Busaitienė	dalyte.mardosaitė-busaitiene@vdu.lt	Vytautas Magnus University, Lithuania	PhD	Mini	Prevalence and Genetic diversity of <i>Bartonella</i> species in Rodents (Muridae, Cricetidae) in Lithuania	52

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28	Victoria	Nistreanu	vicnistreanu@gmail.com	Institute of Zoology, Republic of Moldova	PhD	Full	Taxonomic Status Of <i>Erinaceus Roumanicus</i> (Mammalia: Erinaceomrpha) In The Republic Of Moldova	19
29	Grete	Nummert	grete.nummert@tallinnzoo.ee	Species Conservation Research Centre, Tallinn Zoo, Estonia	MSc	Full	Wood lemming (<i>Myopus schisticolor</i>) – a new species in the Baltic states	20
30	Viorica	Paladi	vioricapaladi.c@gmail.com	Institute of Zoology, Republic of Moldova	PhD	Mini	First Record Of Beaver (<i>Castor Fiber L.</i>) In Prutul De Jos Reserve, Republic Of Moldova	54
31	Algimantas	Paulauskas	algimantas.paulauskas@vdu.lt	Vytautas Magnus University, Lithuania	Prof	Full	Genetic variability of the European bison (<i>Bison bonasus L.</i>) population in Lithuani	21
32	Valdis	Pilāts	valdis.pilats@daba.gov.lv	Nature Conservation Agency, Latvia	MSc	Full	Conservation Status Assessment for Mammals in Latvia – How Successful We Were in Reporting Under Article 17 of the Habitats Directive	22
33	Giedrė	Piličiauskienė	giedrepils@gmail.com	Bioarchaeology Research Centre, Vilnius University, Lithuania	PhD	Full	Zooarchaeological Collection and Recent Zooarchaeological Research in Vilnius University	23
34	Natalia	Pitta-Osses	nata.pitta@gmail.com	Szent István University	Prof	Full	Effect of Wild Boar (<i>Sus scrofa</i>) Rooting in an Eroded and Sedimented Forest in Hungary	24

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36	Sandra	Potušek	sandra.potusek@famnit.upr.si	University of Primorska, Slovenia	MSc	Mini	Development of Simple DNA Barcode-Based Approach to Carnivore Dietary Studies by Using Faecal Samples	55
37	Jana	Radzijeuskaja	jana.radzijeuskaja@vdu.lt	Vytautas Magnus University, Lithuania	Prof	Mini	Vector-borne infections in free-ranging red deer (<i>Cervus elaphus</i>) during the winter season in Norway	56
38	Thabang	Rainett Teffo	Teffo.Thabang@hallgato.uni-szie.hu	Szent Istvan University, Hungary	PhD	Mini	Ungulate impacts on the vegetation of a peri-urban reptile habitat	57
39	Miglė	Razgūnaitė	migle.razgunaitė@vdu.lt	Vytautas Magnus University, Lithuania	MSc	Mini	Domestic cat hybrid identification using diagnostic molecular methods	58
40	Irma	Ražanskė	irma.razanske@vdu.lt	Vytautas Magnus University	PhD	Mini	<i>Anaplasma phagocytophilum</i> infection in cervids and their ticks in Lithuania	59

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42	Povilas	Sakalauskas	povilas.sakalauskas@vdu.lt	Vytautas Magnus University, Lithuania	MSc	Mini	Molecular Detection of <i>Mycoplasma</i> spp. in Bats from Lithuania	60
43	Egor	Shchekhovskii	shchekhovskii@mail.ru	ITMO University	PhD	Mini	The state of the colony of pond bats in early hibernation in Tanechkina cave	61
44	Raminta	Skipitytė	raminta.skipityte@ftmc.lt	Nature Research Centre, Lithuania	PhD	Full	Do Microtus Voles Share The Same Trophic Niche In Commercial Orchards?	27
45	Justina	Snegiriovaite	justina.snegiriovaite@vdu.lt	Vytautas Magnus University, Lithuania	MSc	Mini	Small Rodents and Their Ectoparasites in Different Habitat Types in Lithuania	63
46	Vitalijus	Stirkė	vitalijus.stirke@gamtc.lt	Nature Research Centre, Lithuania	PhD	Full	Common Vole Feels Comfortable In Orchards	29
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49	Jurģis	Šuba	jurgis.suba@silava.lv	State Forest Research Institute Silava, Latvia	PhD	Full	Samples from Hunting Bags Modelled with the Hypergeometric Distribution Reveal Trends in Age Structure of Wolf and Lynx Populations	31
50	Ira	Topličanec	ira.toplicanec@gmail.com	University of Zagreb, Croatia	PhD	Full	Temporality of coat patterns in endangered Eurasian lynx population in Croatia	32
51	Ants	Tull	ants.tull@ut.ee	University of Tartu, Estonia	PhD	Full	Endoparasite prevalence and infection risk factors among cats in an animal shelter in Estonia	33
52	Felicita	Urzi	felicita.urzi@upr.si	University of Primorska, Slovenia	PhD	Mini	Genetic Structure of Wildcat (<i>Felis silvestris</i>) Populations in the Area Between the Dinaric and Scardo-Pindic Mountains	65
53	Alekss	Vecvanags	alekss.vecvanags@videsinstituts.lv	Institute for Environmental Solutions, Latvia	BSc	Full	Detection and localization of adult male red deer <i>Cervus elaphus</i> during the mating season using passive acoustic recorders	34

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