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BIOLOĢIJAS
FAKULTĀTE**



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LATVIJAS UNIVERSITĀTE
**BIOĻĪJAS
FAKULTĀTE**

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Latvijas Universitātes 80. zinātniskā konference
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Referātu tēzu krājums**

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Bioloģijas sekcija / Biology section

Zooloģijas un dzīvnieku ekoloģijas apakšsekcija / Zoology and animal ecology sub-section

Programma / Programme

3rd of February, 2022

Vadītājs/Chair: Asoc. prof. Ainārs Auniņš, Dr. biol. Gunita Deksnē		
10.00–9.05	Asoc. prof. Ainārs Auniņš <i>Faculty of Biology, University of Latvia</i>	Atklāšana <i>Opening</i>
Uzaicinātie ziņojumi / Plenary session		
10.05–10.40	Dr. Eduardas Budrys <i>Nature Research Center, Lithuania</i>	Kā atrast slēptās sugas? Baltijas lapsēnu gadījums <i>How to find a cryptic species? A case of Baltic wasp</i>
10.40–11.15	Dr. Mārtiņš Briedis <i>Swiss Ornithological Institute, Switzerland; University of Latvia, Institute of Biology, Latvia</i>	Klimata pārmaiņu ietekme uz pavasara iestāšanās fenoloģiju un to saistība ar izmaiņām Eiropas putnu populācijās <i>Ongoing changes in spring onset phenology are affecting long-term trends of European bird populations</i>
11.15–11.30	Virtuālā kafijas pauze, diskusijas, stenda referāti <i>Coffee break, discussions, posters</i>	
Mutiskie ziņojumi / Oral presentations		
11.30–11.45	Viesturs Vīgants	Tuvās distances migranta mājas strazda <i>Sturnus vulgaris</i> migrācijas stratēģiju noteikšana, izmantojot atmosfēras spiedienu <i>Using barometric pressure for tracing migration patterns of a short-distance migrant, the common starling <i>Sturnus vulgaris</i></i>
11.45–12.00	Ivo Dinsbergs	Mājas strazda <i>Sturnus vulgaris</i> pavasara atlidošanas fenoloģijas izmaiņas Ziemeļaustrumeiropā laika posmā no 1922. līdz 2017. gadam <i>Changes in spring arrival phenology of Common Starling <i>Sturnus vulgaris</i> in Northeastern Europe from 1922 to 2017</i>
12.00–12.15	Oskars Keišs	Zosis Latvijā 2021. gadā: pētījuma mēģinājums <i>Geese in Latvia 2021: pilot-project</i>

12:30-12:35	Stenda referātu prezentācijas (1 min) <i>Short poster presentations (1 min)</i>	
	Antra Stīpniece	Invazīvo sugu plēsēju skaita samazināšana Engures ezera dabas parkā 2021. gadā <i>Control of invasive predator species at Engure Lake Nature Park in 2021</i>
	Larisa Kurenkova	Divu Hartinga strupastes pasugu <i>Microtus hartingi</i> (Rodentia: Arviocolinae) radniecīgo un neradniecīgo mātīšu komunālā vairošanās eksperimentālajos apstākļos <i>Communal reproduction of related and unrelated females of two subspecies of the harting's vole <i>Microtus hartingi</i> (Rodentia: Arviocolinae) under experimental conditions</i>
	Maira Mateusa	Zoonotiskie parazīti rudajās lapsās (<i>Vulpes vulpes</i>) un jenotsuņos (<i>Nyctereutes procyonoides</i>) <i>Zoonotic parasites in red foxes (<i>Vulpes vulpes</i>) and racoon dogs (<i>Nyctereutes procyonoides</i>)</i>
12.35-14.00	Virtuālā kafijas pauze, diskusijas, stenda referāti <i>Coffee break, discussions, posters</i>	
14.00-14.15	Indriķis Krams	Ārpuspāra paternitāte izskaidro melno mušķērāju (<i>Ficedula hypoleuca</i>) kooperatīvo uzvedību <i>Extra-pair paternity explains cooperation in the pied flycatcher (<i>Ficedula hypoleuca</i>)</i>
14.15-14.30	Elza Birbele	Latvijā reintroducētās <i>Hyla</i> ģints kokvārdes sugas diferenciācija: primārie rezultāti <i>Species identification of the reintroduced <i>Hyla</i> treefrog in Latvia: preliminary results</i>
14.30-14.45	Inese Cera	Kāpu vilkzirnekļa <i>Arctosa cinerea</i> sastopamība Latvijā <i>The distribution of Northern bear spider <i>Arctosa cinerea</i> in Latvia</i>
14.45-15.00	Iveta Jakubāne	<i>Arion ater</i> (Linnaeus, 1758) s.l. pasugas Latvijā <i>Subspecies of the terrestrial slugs <i>Arion ater</i> (Linnaeus, 1758) s.l. in Latvia</i>
15.00-15.15	Ronalds Krams	Priežu tīklapsenes (<i>Acantholyda posticalis</i> Matsumura, 1912) izplatības ietekme uz lielo zīlīšu (<i>Parus major</i> Linnaeus, 1758) vairošanās sekmēm <i>Outbreaks of the great web-spinning sawfly (<i>Acantholyda posticalis</i> Matsumura, 1912) effect on the reproductive success of great tits (<i>Parus major</i> Linnaeus, 1758)</i>
15.15-15.30	Virtuālā kafijas pauze, diskusijas, stenda referāti <i>Coffee break, discussions, posters</i>	

15.30–15.45	Jurgis Šuba	Vai Latvijā uzbrukumi mājlopiem saistīti ar vilku vecuma struktūras īpatnībām? <i>Are livestock depredation cases in Latvia associated with the age structure of wolves?</i>
15.45–16.00	Pēteris Daknis	LiDAR datu pielietojuma lietderības izvērtējums lielo ligzdu meklēšanā <i>Evaluation of LiDAR data utility in search for large nests</i>
16.00–16.15	Alekss Vecvanags	Savvaļas pārnadžu populācijas rādītāju noteikšana monitoringa nolūkiem izmantojot mašīnāpmācības pieeju <i>Inferring wild ungulate population metrics for monitoring purposes using a machine learning approach</i>
16.15-16.30	Alessandro Di Marzio	Rīgas Zooloģiskais dārzā izglābto pelēko roņu GPS monitoringa rezultāti <i>Results of GPS monitoring of grey seals rescued by Riga Zoo</i>
16.30-16.45	Kārlis Rudenko	Kalibrēta <i>Galleria mellonella</i> ēsmas testa aprobācija kvantitatīvai <i>Steinernema feltiae</i> (Filipiev, 1934) klātbūtnes novērtēšanai griezto ziedu rožu audzēšanai izmantotos kokosa šķiedras substrātos <i>Approbation of a calibrated <i>Galleria mellonella</i> bait test as a quantitative method of assessing the presence of <i>Steinernema feltiae</i> (Filipiev, 1934) in samples of coco coir substrates used in cut rose production</i>
16.45–17.--	Noslēgums, diskusijas <i>Conclusions, discussions</i>	

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PLENARY SESSION

PLENĀRIE ZIŅOJUMI

HOW TO FIND A CRYPTIC SPECIES? A CASE OF BALTIC WASP

Eduardas Budrys

Institute of Ecology, Nature Research Centre, Lithuania

E-mail: eduardas.budrys@gamtc.lt

Baltic region, being close to the centre of Europe, is relatively well studied from the aspect of taxonomy and faunistics of insects, however, there are still taxa where discovery of new, undescribed species is possible. The easiest way to find a new species in our region is a study of genetic diversity in cryptic species complexes.

There are four hypothetic evolutionary pathways leading to formation of cryptic, i.e. morphologically little differentiated species (Struck et al., 2018). Two of them, convergence and morphological stasis, result in weak differentiation of morphological traits and, at the same time, considerable distance between the DNA markers that are affected by the random genetic drift. The commonest tool for detection of such genetic differentiation is a study of haplotype diversity of the mitochondrial cytochrome oxidase c subunit 1 partial sequence (CO1-5'), the marker that is used in the taxonomic method of DNA barcoding in animal kingdom. This type of study is well standardised, relatively easy and cheap.

In our study of a common cavity nesting wasp *Ancistrocerus trifasciatus* (Muller, 1776) (Hymenoptera: Vespidae) we found that some samples differ much more than we might expect for the DNA variation among conspecific specimens. For testing the hypothesis that the divergent haplotypes represent a new cryptic species we (1) extracted DNA of multiple specimens reared from Hymenoptera trap-nests exposed in multiple localities and habitats; (2) sequenced their "barcoding" CO1-5' marker and assessed the diversity of haplotypes; (3) studied the other mitochondrial markers, namely, the mtDNA sequence from CO1 to ND3, including complete CO1, CO2, ATP8, ATP6, CO3 and ND3 genes, and the mtDNA sequence from ND6 to ND1, including complete ND6, CytB and partial ND1 genes, as well as the 12S mitochondrial rDNA; (4) studied the sequences of the nuclear rDNA operon, namely partial 18S, partial 28S, ITS1 and ITS2; and (5) studied selected protein-coding nuclear genes. All studied markers demonstrated tangible differences of the supposedly cryptic species from *A. trifasciatus*.

To confirm the status of the cryptic species, we applied three species delimitation methods, namely, the "Assemble Species by Automatic partitioning" (ASAP; Puillandre et al. 2021), the Bayesian implementation of Poisson tree process (bPTP; Zhang et al., 2013) and the generalized mixed Yule-coalescent (GMYC) model (Fujisawa and Barraclough, 2013) to the dataset of the "barcoding" CO1-5' DNA sequences that included all obtained haplotypes of the supposedly cryptic species and *A. trifasciatus*, as well as all CO1-5' sequences of *Ancistrocerus* species publicly available from the Barcode of Life Data System (BOLD; Ratnasingham and Hebert 2007, 2013). For the bPTP and GMYC analysis, where the phylogenetic tree is needed, we used the consensus trees, which were obtained applying the method of Bayesian inference, using MrBayes, version 3.2.3 (Ronquist and Huelsenbeck 2003) and the method of the maximum likelihood, implemented in MEGA 7 (Kumar et al. 2016). All three species delimitation methods demonstrated that the haplotypes of the cryptic species form a species level lineage in the genus *Ancistrocerus*.

The next step of the study was reconstruction of phylogenetic relationships of the Northern European *Ancistrocerus* species, using all available mitochondrial and nuclear DNA markers with a combined length approximately 19400 bp. The result demonstrated that the new cryptic wasp is actually a sister species of *A. trifasciatus*.

We also assessed the option of a possible role of *Wolbachia*-caused cytoplasmic incompatibility that has been demonstrated being important in some cases of speciation in arthropods and nematodes. The study of the bacterial 16S rRNA in flight muscle tissues revealed presence of *Wolbachia* in a part

of specimens of most of the studied *Ancistrocerus* species, including the new cryptic species. Further study of the variation of *Wolbachia* surface protein (wsp) marker in the samples with *Wolbachia* infection demonstrated presence of the same strain in both the new cryptic species and the widespread *A. trifasciatus*. Thus, *Wolbachia*-caused cytoplasmic incompatibility hardly could affect the speciation process of the new species.

Finally, we statistically assessed the differences in body size, sex ratio prey composition, habitat choice, nesting cavity choice, nest structure and a few other behavioural traits between the new cryptic species and *A. trifasciatus*. The new species was slightly smaller and had a little more female-biased sex ratio. It significantly more commonly than *A. trifasciatus* occurred in the mixed swamp woodlands (EUNIS habitat G4.1) and generally in the forests with deciduous tree species in the canopy layer. The new wasp species demonstrated stronger preference to the trunks of European spruce and stronger avoidance of Scots pine trunks as nesting substrate, comparing to *A. trifasciatus*. The prey spectrum of both species was wide and overlapping, with dominance of Tortricidae larvae.

A careful study revealed a few weak but stable morphological differences that allow at least a preliminary identification of females of the cryptic species with reasonable probability and including of it in an identification key. Hopefully, further studies will reveal various other features of this Baltic wasp.

ONGOING CHANGES IN SPRING ONSET PHENOLOGY ARE AFFECTING LONG-TERM TRENDS OF EUROPEAN BIRD POPULATIONS

Mārtiņš Briedis

Swiss Ornithological Institute, Department of Bird Migration, Switzerland
University of Latvia, Institute of Biology, Latvia

E-mail: martins.briedis@vogelwarte.ch

Climate change is a major threat to biodiversity and ecosystem functioning worldwide. Although biological responses to climate change are widely documented, our understanding of large-scale trends in animal populations and their links to changes in environmental phenology remains limited. Single phenological measures like the average rate of climate warming may be insufficient to explain trends in animal populations and species' traits likely mediate their vulnerability to phenological changes.

In this study, I first characterise spring green-up phenology, its spatial variation and temporal changes across Europe during the last four decades. To this end, I use seasonal variation in vegetation greenness as inferred from remotely sensed NDVI (normalized difference vegetation index) data to examine three phenological elements: (1) onset of spring, (2) duration of spring, and (3) inter-annual variability in the timing of spring onset. Second, I integrate these elements of spring phenology and their recent changes at the breeding grounds of European landbirds with long-term species population trends.

NDVI data revealed that the timing of spring onset in Europe has on average advanced by nearly 10 days between 1983 and 2016 (a rate of 0.29 days per year). In the meantime, the duration of spring has extended by an average of 4.7 days, while the variability in the timing of spring onset showed an overall stabilizing trend. However, all three elements of spring green-up displayed distinct spatial patterns across Europe with some areas experiencing rapid phenological shifts while others remained relatively unaffected. Changes in landbird populations indicated disproportionately negative trends for species living under strong phenological advancement, but particularly so when combined with short and less variable springs. Furthermore, long-distance migrants and forest species were identified as particularly prone to suffer declines under such phenological conditions.

These findings clearly demonstrate that the consequences of climate change for animal populations depend not only on the rate of phenological advancement and life-history strategies of the affected species, but also on the broader eco-climatic context of where the phenological changes take place. This includes duration of spring, inter-annual variability in the timing of spring onset and their interplay with the rate at which spring green-up phenology is advancing.

PRESENTATIONS

MUTISKIE ZIŅOJUMI

USING BAROMETRIC PRESSURE FOR TRACING MIGRATION PATTERNS OF A SHORT-DISTANCE MIGRANT, THE COMMON STARLING *STURNUS VULGARIS*

Viesturs Vigants¹, Ivo Dinsbergs¹, Valts Jaunzemis¹, Ance Priedniece¹, Elza Zacmane¹, Oskars Keišs¹, Martins Briedis^{1,2}

¹ University of Latvia, Institute of Biology, Laboratory of Ornithology, Latvia

² Swiss Ornithological Institute, Department of Bird Migration, Switzerland

E- mail: viesturs.vigants@lu.lv

During the last decade classical light-level geolocation has revealed a plethora of new discoveries in bird migration, however when assessing geographic location, the margin of error is still relatively large. This opacity has limited the use of geolocators for tracking movements of short-distance migrants.

Here, we integrate light-level geolocation with activity and barometric pressure tracking to describe migration behaviour of Common Starlings *Sturnus vulgaris* tagged during the breeding season in North-East Europe, Latvia, at high spatiotemporal resolution. To estimate geographic locations, the recorded pressure data was compared with remotely sensed surface-level atmospheric pressure at 0.25x0.25-degree grid cells available at The Copernicus Climate Change Service.

Results indicated high correlation ($r=0.99\pm 0.01$, $p<0.001$) between the recorded and remote sensed atmospheric pressure values from the breeding site, yielding a location estimate with maximum error of 30km. Tracked birds wintered in the British Isles (~2000km from the breeding site) with stop-over sites near the southern coast of the Baltic Sea and the Wadden Sea. Starlings conformed to two distinct migration strategies: (1) with about half of the birds departing right after the breeding season in early June, and thus having three distinct migration phases during the annual cycle (summer-autumn-spring); (2) while the remaining individuals stayed close to the breeding sites until late autumn comprising to classical autumn-spring migration behaviour. Interestingly, in contrary to the literature most long-distance migratory flights (~70%) were carried out at night departing right after sunset with one individual completing most of the autumn migration in a single 22h-long flight. Even without the presence of mountainous barriers, maximum flight altitude reached up to 2500 masl.

This study shows that multi-sensor tracking has the potential to provide new details on migratory behaviour of individual birds along their entire annual cycle, and it also improves the precision of geographical locations derived from light-level geolocators.

CHANGES IN SPRING ARRIVAL PHENOLOGY OF COMMON STARLING *STURNUS VULGARIS* IN NORTHEASTERN EUROPE FROM 1922 TO 2017

Ivo Dinsbergs¹, Martins Briedis²

¹Laboratory of Ornithology, University of Latvia, Institute of Biology, Latvia

²Department of Bird Migration, Swiss Ornithological Institute, Switzerland

E-mail: ivo.dinsbergs@lu.lv

Climate change poses significant impacts on most migratory bird species altering their wintering distribution, migration distance and phenology. In this study we describe changes in spring arrival phenology of a short-distance migrant, the Common Starling *Sturnus vulgaris*, in Northeastern Europe and their relation to changes in the onset of meteorological spring during the last century.

Phenological data were obtained from an open access database *Chronicles of Nature Calendar* that holds over 4500 records of the 1st spring observation of Starlings from 196 observation sites between 1922 and 2017. Air temperature data was downloaded from *European Climate Assessment and Dataset database*.

We found that, spring arrival time of Starlings was positively correlated with the onset of spring on a local and broad scale. During the 96-year long period, Starlings on average advanced their spring arrival time by 12 days at a rate of 0.13 days/year. However, changes in the onset of spring occurred even more rapidly with an average rate of change of 0.29 days/year over the study period. These findings imply broad-scale adjustments in migratory patterns of a short-distance migrant that result from climate change induced shifts in spring phenology. However, adaptations in bird migration phenology are not occurring fast enough to track and compensate for the rapid increase in air temperature and consequently, the advancement in the onset of spring across Northeastern Europe.

GEESE IN LATVIA 2021: PILOT-PROJECT

Oskars Keiņš, Antra Stīpniece, Dmitrijs Boiko, Ivo Dinsbergs, Toms Endziņš, Artūrs Laubergs,
Jānis Bētiņš, Ainārs Auniņš
University of Latvia, Institute of Biology, Latvia

E-mail: oskars.keiss@lu.lv

Survey on geese during the spring season of 2021 were carried out in Latvia in order to get empirical knowledge on the numbers of geese, agricultural fields preferred by geese for feeding and time spent during the staging in Latvia. According to data of Rural Support Service of Latvia (LAD) there were total of 280446 fields with total area of 1813573 ha available for geese in Latvia in 2021. We grouped the cultures in following habitat categories: (1) grasslands, (2) winter crops, (3) winter raps, (4) maize, (5) spring crops, (6) legumes, (7) vegetables, (8) fallows, (9) bushes (including fruit tree plantations) un (10) unknown (not covered by Rural Support Service, including lands abandoned by agriculture). For modelling purposes 8495 visits on 6574 fields were used, including 1160 positive (with birds) and 7335 negative, when birds were not observed. According to our analyses, geese avoided winter raps and bushfields, but preferred grasslands, fallows and spring crops. Swans preferred winter raps and maize fields, but avoided vegetable fields and bushes. For both – geese and swans large fields were preferred and vertical elements – trees, poles and field margins were avoided. The maximum of swan migration in Latvia in spring of 2021 was in the middle of March, but for geese – at the beginning of April.

Additionally analyses of breeding population of Greylag Goose (*Anser anser*) in Latvia has increased considerably – observed in 55 squares (10×10 km) and confirmed breeding in 20 squares of the total. An increase from 30 total squares in the period 2013–2017 (five years) to 55 in the period 2020–2021 (two year period). 13 local Greylag Geese were color-ringed in the Lake Engure (compared to 8 total for the period 1925–2020) and it already yielded 3 foreign observations of them in the autumn of 2021 in Lithuania and Poland.

EXTRA-PAIR PATERNITY EXPLAINS COOPERATION IN THE PIED FLYCATCHER (*FICEDULA HYPOLEUCA*)

Indriķis Krams^{1,2,3}, Adèle Mennerat^{4,5}, Tatjana Krama^{3,6}, Ronalds Krams^{3,6}, Priit Jõers⁷, Didzis Elferts⁸, Severi Luoto^{9,10}, Markus J. Rantala¹¹, Sigrunn Eliassen⁴

¹Department of Zoology and Animal Ecology, University of Latvia, Latvia

²Institute of Ecology and Earth Sciences, University of Tartu, Estonia

³Department of Biotechnology, Daugavpils University, Latvia

⁴Department of Biological Sciences, University of Bergen, Norway

⁵EDYSAN, Université de Picardie Jules Verne, CNRS, France

⁶Chair of Plant Health, Estonian University of Life Sciences, Estonia

⁷Department of General and Microbial Biochemistry, University of Tartu, Estonia

⁸Department of Ecology and Botany, University of Latvia, Latvia

⁹School of Population Health, University of Auckland, New Zealand

¹⁰School of Psychology, University of Auckland, New Zealand

¹¹Department of Biology, Section of Ecology, University of Turku, Finland

E-mail: indrikis.krams@lu.lv

In many social animals, females mate with multiple males, but the adaptive value of female extra-pair mating is not fully understood. Here, we tested whether male pied flycatchers (*Ficedula hypoleuca*) engaging in extra-pair copulations with neighboring females were more likely to assist their neighbors in antipredator defense. We found that extra-pair sires joined predator mobbing more often, approached predators more closely, and attacked predators more aggressively than males without extra-pair offspring in the neighboring nest. Extra-pair mating may incentivize males to assist in nest defenses because of the benefits this cooperative behavior has on their total offspring production. For females, this mating strategy may help recruit more males to join in antipredator defense, offering better protection and ultimately improving reproductive success. Our results suggest a simple mechanism by which extra-pair mating can improve reproductive success in breeding birds.

SPECIES IDENTIFICATION OF THE REINTRODUCED *HYLA* TREEFROG: PRELIMINARY RESULTS

Elza Birbele¹, Alessandro Di Marzio², Gunita Deksnė^{1,3}

¹University of Latvia, Faculty of Biology, Latvia

²Riga National Zoological Garden, Latvia

³Institute of Food safety, Animal Health and Environment "BIOR", Latvia

E-mail: elza.birbele@gmail.com

The European tree frog *Hyla arborea* (Linnaeus, 1758) is a species complex which includes ten species, many of which are morphologically indistinguishable, distributed across Europe. Historical accounts have recorded the presence of European tree frog in Latvia during 18th and 19th century. In the 20th century, however the increase of agricultural pollution and disappearance of beavers drove tree frogs to extinction. In the late 1980s Riga Zoo's Laboratory of Ecology carried out the reintroduction of the species, collecting individuals from the Belarusian population for the captive breeding and release program of the European tree frog. The reintroduction process in Kurzeme was successful, establishing expanding populations. In recent years, phylogeographic studies of the populations of *Hyla* species throughout Europe (excluding Latvia) mapped distribution of the different species, showing that the Belarusian population was of the Eastern tree frog *Hyla orientalis* (Bedriaga, 1890). This calls for a re-examination of the reintroduced tree frog in Latvia. Additionally, *H. arborea* is protected by the EU Habitats Directive and included in IUCN Red List whereas *H. orientalis* is not.

Buccal and skin swab samples were collected from 35 tree frogs caught from eleven ponds across the distribution of *Hyla sp.* tree frog in Kurzeme. The genomic DNA was extracted and amplified using standard methods and *Hyla* genus specific primers *Chmf4* and *Chmr4* by following sequencing. Eleven sequences were compared with nucleotide sequences deposited in GenBank using BLASTn. Results showed all samples belonging to *Hyla orientalis* with on average $98,5 \pm 0,3\%$ certainty.

The taxonomy of *H. arborea* and its species complex has called in question many frog populations across Eurasia. Our results are among them proving, for the first time, that the *Hyla* species resident in Latvia is the Eastern tree frog. Since *H. arborea* is protected by Latvian legislation and EU directives, but *H. orientalis* is not, a course of action needs to be discussed.

THE DISTRIBUTION OF NORTHERN BEAR SPIDER *ARCTOSA CINEREA* IN LATVIA

Inese Cera

University of Latvia, Institute of Biology, Latvia

E-mail: inese.cera@lu.lv

The Northern Bear Spider *Arctosa cinerea*, the only protected spider species in Latvia, is distributed in Europe along the seacoast and in most cases of Central Europe and Great Britain – along sandy riverbanks. The species avoid areas with anthropogenic disturbance. It is large wolf spider, which hunts on insects along the coast and the only web structures are hidden in his shelter – an y-shape burrow in sand strengthened by a thread, and on the cocoon. The spider has a two-year life cycle. The mother usually carries the spiderlings on her abdomen for about two weeks after hatching.

The species is easily identified by large size (females up to 18 mm) and specific motion when running on the sand, sometimes also it can be found hiding under rocks in suitable habitats.

Most of the observations of *Arctosa cinerea* in Latvia are from the seacoast, just recently one observation comes from inland (~200km off the Baltic Sea) – Ziemeļgauja sandy riverbank where it has been observed for a few years. This confirms the assumption that species can be found more common inland as thought before. Also, the first spider species observer in Latvia Adolph Eduard Grube in 19th century found it at Gauja's sandy banks near Cēsis.

Previous spider researcher in Latvia – Māris Šternbergs in the Red Data book of Latvia (1998) mentioned five sites where species has been observed. Recent data of all available observations since 2004 results in 24 localities where this species is found in Latvia. In the Red Data books of Finland and Sweden this spider species is considered as having stable populations (after IUCN criteria – Least Concern). We do not see any strong negative factors affecting species in Latvia so – if the number of observed localities increase, the species may be classified as Least concern (stable population) by using IUCN criteria.

SUBSPECIES OF THE TERRESTRIAL SLUG *ARION ATER* (LINNAEUS, 1758) S.L. IN LATVIA

Iveta Jakubāne¹, Dainis Ruņģis², Kaiva Solvita Ruņģe², Digna Pilāte²

¹Institute of life sciences and technology, Daugavpils University, Latvia

²State Forest Research Institute “Silava”, Latvia

E-mail: iveta.jakubane@biology.lv

The group of large slugs of the genus *Arion* are one of the most mistakenly identified species in Europe. Even for the relatively well-studied area of Central and North-West Europe, different opinions still exist about the number and nomenclature of species or subspecies in the genus *Arion*. There are several reasons for the misidentification of species: variation in external morphology (mainly body colour), on which early original descriptions were based, the inter- and intrapopulation diversity in genital morphology and hybridization between the Spanish slug *Arion vulgaris*, *Arion rufus* and *Arion ater*. Due to the hybridization of species and the assimilation of local large *Arion* species, all species of *Arion* (except *Arion vulgaris*) have been combined into one complex *Arion ater* and three subspecies: *Arion ater ater*, *Arion ater rufus* and *Arion ater ruber*. This study is based on *Arion ater* (Linnaeus, 1758) s.l. species research in Latvia.

Genetic material was collected from the following localities: 4 local *Arion rufus* species populations – Embūte, near Otaņķi, on the bank of the Bārta river and Vībiņi, 4 invasive *Arion rufus* species populations - Rude, Priekule, Klampjuciems and Grobiņa, and 12 *Arion vulgaris* populations. The study was funded by the LVA project “Data collection on new populations of the Spanish slug (*Arion vulgaris*), species distribution routes, population viability and impact on the local red snail (*Arion rufus*) population” (No. 108/187/2020)

Initial results indicated that there are 3 species of the genus *Arion* found in Latvia: *A. vulgaris*, *A. ater* and *A. rufus*. Individuals of *A. rufus* were found in the populations of Grobiņa, Priekuli and Klampjuciems. Individuals of *A. ater* have been identified in Vībiņi, near Otaņķi and Rude; however, the Rudes population is genetically differentiated and differs from the Vībiņi and Otaņķi populations. Individuals of both *A. vulgaris* and *A. rufus* were identified in the Mārupe population.

OUTBREAKS OF THE GREAT WEB-SPINNING SAWFLY (*ACANTHOLYDA POSTICALIS* MATSUMURA, 1912) EFFECT ON THE REPRODUCTIVE SUCCESS OF GREAT TITS (*PARUS MAJOR* LINNAEUS, 1758)

Ronalds Krams^{1,2}, Tatjana Krama^{1,2}, Guntis Brūmelis³, Didzis Elferts³, Linda Strode³, Iluta Dauškane³, Agnis Šmits⁴, Indriķis Krams^{1,3,5}

¹Daugavpils University, Department of Biotechnology, Latvia

²Estonian University of Life Sciences, Institute of Agricultural and Environmental Sciences, Estonia

³University of Latvia, Faculty of Biology, Latvia

⁴Latvian State Forest Research Institute “Silava”, Latvia

⁵University of Tartu, Institute of Ecology and Earth Sciences, Estonia

E-mail: ronalds.krams@du.lv

The quality of habitat has a direct impact on the fitness of breeding organisms, that's why animals are generally considered to prefer the best possible habitats. Although, some animals may accidentally choose to breed in habitats that reduce their fitness, which results in “ecological traps”. In this research it was studied whether great tits (*Parus major* Linnaeus, 1758) attracted to areas affected by great web-spinning sawfly (*Acantholyda posticalis* Matsumura, 1912) outbreaks were characterized by fitness disorders associated with ecological traps. Sawfly larvae eat pine needles, which reduces the availability of resources for birds living together in the forest. By using artificial nesting sites, we found that great tits that inhabit the sites of the sawfly outbreaks had a similar clutch size as great tits that breed throughout the forest. Nevertheless, the number of new-borns was significantly lower and the condition of new-borns in the damaged forests was worse. Moth larvae are the most important food for bird nestlings and forest areas damaged by sawflies had the lowest larval biomass. Even though most ecological traps occur in human-altered environments, this research shows that pest insects can reduce the quality of habitats by creating ecological traps. The results of this research suggest that the attraction of birds nesting in cavities should be done with caution because it may adversely affect the nutritional status and reproductive fitness of these birds.

ARE LIVESTOCK DEPREDATION CASES IN LATVIA ASSOCIATED WITH THE AGE STRUCTURE OF WOLVES?

Jurgis Šuba, Agrita Žunna, Guna Bagraade, Dainis Edgars Ruņģis, Jānis Ozoliņš
Latvian State Forest Research Institute “Silava”

E-mail: jurgis.suba@silava.lv

Various estimates of wolf abundance in Latvia have indicated that the Latvian wolf subpopulation increased during the last two decades despite continuous culling. During this period, the number of livestock depredation cases reported to the State Forest Service has slightly increased as well, albeit without statistical significance.

Apart from controlling the abundance, intense wolf culling may lead to changes in the demographic and kinship structure of the population, as well as in animal behaviour. The mean age of wolves encountered in Latvia, considering only adult individuals, was 3.6 years, which corresponds to moderate hunting pressure on the population. Despite the fact that the majority of culled individuals were juveniles and estimated culling mortality for juveniles was 42%, exceeding yearling and adult mortality due to harvest (25.6% and 31.2%, respectively), removal of critical adults from the pack may drive the younger animals to livestock depredation. The majority of attacks on sheep, goats and cattle in Latvia have occurred between May and November, most frequently in August and September (50,2% of cases) after opening the hunting season in mid-July.

We analysed 427 records of livestock depredation cases caused by wolves in relation to estimated wolf age structure from carcass inspections in 10 major forestry units of Latvia. Generalized linear models were used, assuming a negative binomial distribution of the number of depredation cases and applying a logarithmic link function. The results indicated no significant impact of wolf age structure on the frequency of depredation cases (AIC = 522.01) compared to the model assuming stochastic variance around the mean with additional overdispersion parameter (AIC = 521.38). Livestock depredation is likely to result from complex factors, of which the ratio between subadults and adults in the wolf population may not be amongst the most significant. However, further analyses at a smaller spatial scale, combined with kinship investigation to determine breeder loss in packs, could provide better insight into the association between the age structure of wolves and depredation cases.

This study was conducted as part of the postdoctoral research project “Subpopulation 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 the European Regional Development Fund (agreement No. 1.1.1.2./16/I/001).

EVALUATION OF LIDAR DATA UTILITY IN SEARCH FOR LARGE NESTS

Pēteris Daknis, Didzis Elferts, Andris Avotiņš
University of Latvia, Latvia

E-mail: peteris.daknis@lu.lv

Emerging trends in the practical application of LiDAR data show the feasibility of classifying both smaller and more concealed objects in the data. The study looks at and quantifies the likelihood of finding large nests of birds of prey as objects in the LiDAR data. Finding such nests, due to their relatively rare occurrence, has always been a complicated and labor-intensive task in which remote sensing data are usually used as support tools. The scope of the study is the territory of Latvia, and Osprey (*Pandion haliaetus*) nests have been selected as the research subject.

The study found that in 60% of the cases, the intensity values of the LiDAR data points that lead to an indication of nesting materials have significantly higher intensity values than for the points that lead to an indication of surrounding vegetation. In 40% of the cases, the difference in the intensity values has not been clear enough, and reason for that is not yet entirely understood.

The study uses the functionality of R packages “lidR” and “sf” for data processing. The values of the LiDAR points are calculated both at the level of the circular sample area of 0.2 ha and by grouping the points within the sample using containers of different sizes. A “container” is a tree, viewed from above in outline form, with an imagined three-dimensional extruded shape extending all the way to the ground. The individual data point is one tree (or “container”). In simplified form, a spot of higher intensity appearing in the canopy could be a nest. “Intensity” in this case means reflectivity. The more reflective a part of a container is, the higher the intensity.

The resulting characteristics and their ratios have been used for the development of general linear models (GLM) and general mixed-effect linear decision tree models (GLMERTREE). Models were capable of correctly predicting 84-97% of the nests in the test data.

INFERRING WILD UNGULATE POPULATION METRICS FOR MONITORING PURPOSES USING A MACHINE LEARNING APPROACH

Alekss Vecvanags, Egils Avots, Gholamreza Anbarjafari, Jevgenijs Filipovs, Agris Brauns,
Dainis Jakovels
Institute for Environmental Solutions, Latvia

E-mail: alekss.vecvanags@vri.lv

Monitoring of wild ungulate populations is important for sustainability, wildlife conservation, and damage management for forestry and agriculture. Traditional methods for population abundance estimation and monitoring, such as grazing damage observation, pellet or snow track counts can take up large amounts of time, and require trained experts. Camera traps can be used due to their ease of use, non-intrusive nature and cost-effectiveness, as they have become a key tool in wildlife monitoring and conservation efforts. A negative aspect of camera traps is a large amount of acquired data that can take a long time to analyze, but this can be negated using modern machine learning algorithms.

This study aimed to derive population metrics of wild forest ungulates like relative abundance, temporal and spatial activity etc. for management purposes. 30 camera traps were deployed in a long term study in Rāmuļi, Latvia from January 18th 2021 till January 24th 2022. A convolutional neural network system YOLOv5 was used for automatically detecting animals from camera trap images and videos, and the results were used for data analysis.

RESULTS OF GPS MONITORING OF GREY SEALS RESCUED BY RIGA ZOO

Alessandro Di Marzio

Riga National Zoological Garden, Latvia

E-mail: research@rigazoo.lv

Driven to the brink of extinction in the recent past, the grey seal (*Halichoerus grypus grypus*) population in the Baltic Sea is slowly recovering. The increase of population has generated new challenges (e.g. conflict with fishermen). The study of the movements of grey seals within the Baltic Sea is important to identify potential areas for the conservation of the species.

In 2021 Riga Zoo started a pilot tracking project, equipping three grey seals (ID 183868-male, ID 183869-female, ID 183870-female) with GPS (SPOT-293, Wildlife computer). The objectives of this project were to evaluate the survival of the seals released from the rescue centre of the Riga Zoo and to study the migration of the animals. We received data from 183868 for 44 days (831 signals), from 183869 for 277 days (9735 signals) and from 183870 for 46 days (905 signals). During their migrations all three animals have chosen different routes, which seem to be related to the surface currents of the Baltic Sea. 183868 released into the Gulf of Riga, migrated towards the entrance of the Gulf of Bothnia, and then reached Denmark, moving close to the Swedish coast. 183869, released near Ventspils, migrated to southern Gotland, then remained near Bornholm. 183870, released into the Gulf of Riga, moved between the island of Rone, Saarema, finally remaining in the sea close to Ventspils.

The preliminary results indicate a good adaptation of the released animals (we assumed 183868 and 183870 stopped working due to technical problems). Our data could help future studies by providing more information on the migration of the species within the Baltic and the connectivity between breeding populations.

APPROBATION OF A CALIBRATED *GALLERIA MELLONELLA* BAIT TEST AS A QUANTITATIVE METHOD OF ASSESSING THE PRESENCE OF *STEINERNEMA FELTIAE* (FILIPIEV 1934) IN SAMPLES OF COCO COIR SUBSTRATES USED IN CUT ROSE PRODUCTION

Kārlis Rudenko¹, Uģis Kagainis^{1,2}

¹ University of Latvia, Faculty of Biology, Latvia

² University of Latvia, Institute of Biology, Latvia

E-mail: karlis.rudenko@gmail.com

With the broadening use of entomopathogenic nematodes in biological crop protection, and the multiple factors influencing their efficacy as biopesticides, there is a value in finding simple and reliable methods of determining their presence and numbers in various substrates.

A simple, quantitative method of assessing *Steinernema feltiae* (Filipiev, 1934) populations using *Galleria mellonella* (Linnaeus, 1758) larvae is calibrated and analysed for application in coco coir substrates of various ages used in cut rose production. Sterilised samples with known *S. feltiae* concentrations show a significant correlation between nematode concentrations and *G. mellonella* mortality within 48h both in fresh ($p < 0.01$, $r = 0.86$, $n = 25$) and three-year-old ($p < 0.01$, $r = 0.85$, $n = 25$) substrates. The calibrated test was used on coco coir samples collected over five weeks from rose greenhouses, where heterogeneity in the dispersion of *S. feltiae* after the application was demonstrated, and a negative influence of high collembolan numbers of *S. feltiae* in greenhouse substrates ($p < 0.01$, $r = -0.4$, $n = 45$).

The similarity of results obtained in the two different kinds of coco coir substrates shows the promise of this method likely being of use in various other materials such as sphagnum peat or various types of soil.

POSTERS

STENDA REFERĀTI

CONTROL OF INVASIVE PREDATOR SPECIES AT ENGURE LAKE NATURE PARK IN 2021

Jānis Bētiņš¹, Antra Stīpniece¹, Roberts Šiliņš²

¹ University of Latvia, Institute of Biology, Latvia

² Engure Lake Nature Park Fund, Latvia

E-mail: janis.betins@lu.lv

Predators are an essential part of nature, agents of natural selection. Yet invasive predator species, like American mink (*Neovison vison*) in Europe, can cause detrimental impact to the native species, both prey and the native predators. Latvian Hunting Regulation allows killing the species all the year.

American mink as a regular duck nest predator on Engure Lake has been registered since 1978. Our work area comprised 28.3 ha of islands (Lielrova, Kazrova, Lopsalrova) and 10.0 ha of emergent vegetation stands (Titaniks, Lopsalcers) in the central part of the lake. The previous management in the work area has included building dry, high islets (Lielrova 1982 and 2016, Lopsalrova 1983 and 2008, Akmeņrova autumn 2021), irregular vegetation management and moderate predator control (in 2000-2016 2-12 traps have been exposed during duck nesting season and 0-12 American minks trapped annually). In Lielrova predator control had ceased in 2010. Since beginning of the century mammals have become predominant duck nest predators in the area.

In 2021 30 unbaited cage traps were used. Most exposition took place end of March – end of October. Traps were checked twice-trice a week.

Duck nest searches were performed May 24-June 9. Nests found alive were payed a repeated visit close to the calculated hatching date and apparent nesting success was calculated. For predated nests the predator was guessed relying on the visual appearance of the nest remnants.

In total 42 American minks *Neovison vison* (15 males, 8 females, 19 unidentified), 1 Brown rat *Rattus norvegicus* and 1 juvenile Raccoon dog *Nyctereutes procionoides* were trapped. At least 3 mink male territories were present in Lielrova in the beginning of the season (3 animals trapped the same day in March). Peaks in number of animals trapped were observed in the beginning of the season and in August when families fall apart.

Ice situation prevented access to most work areas before end of March. Therefore, predator control took place simultaneously with the nesting season. Still, duck apparent nesting success slightly increased. In total 34 duck nests were counted in the work area in 2021, 12 of them successful.

Creating dry islets provide breeding habitat not only for ducks but also for American mink. Such management without accompanying predator control can be considered creating an ecological trap.

COMMUNAL REPRODUCTION OF RELATED AND UNRELATED FEMALES OF TWO SUBSPECIES OF THE HARTING'S VOLE *MICROTUS HARTINGI* (RODENTIA: ARVICOLINAE) UNDER EXPERIMENTAL CONDITIONS

Tatjana Zorenko, **Larisa Kurenkova**
Faculty of Biology, University of Latvia, Latvia

E-mail: tatjana.zorenko@lu.lv; larisakurr@gmail.com

Inbreeding is mainly viewed as a force driving species to extinction (Charlesworth 2009), however in few cases it can cause speciation and theoretically might be a driver of evolution of sociality in animals (Tabadkani 2012). Series of experiments aimed to model an experimental polygyny have shown a different attitude towards communal grouping (CG) in two subspecies of Harting's vole (Zorenko, in press). In *M. h. hartingi*, the successful reproduction in polygynous groups appeared to be in favour of mating with sisters: even with both related and unrelated females propagating, the reproductive success was asymmetrical. In monogamous *M. h. lydius* only one female in the group has been reproducing successfully, which marks the subspecies as dissimilar in terms of inbreeding tolerance and makes them a suitable model object for studying links between sociality and inbreeding (Zorenko, Kurenkova 2021). Therefore, the goal of the research is to evaluate reproductive success of related and unrelated females when modelling CG with one male and two females of opposite blood status.

The results of the study showed that males copulated with both sisters and unrelated females, which indicates the absence of incest taboo mechanism in them, while mating order was dependent on female receptivity time. A high degree of inbreeding tolerance is also characteristic of females: 58% of sisters in *M. h. lydius* and 67% in *M. h. hartingi* bred in CG.

However, a pronounced competition in females was noted, often resulting in one's death. Aggression level in CG was directly connected with blood status. In outbred *M. h. lydius* groups the aggression was registered only in 10% cases (Zorenko, in press), but in CG (sister and non-kin females) mortality has reached 67%, In *M. h. hartingi* the proportion was 30% and 50% respectively. Death score being divided evenly between both females. After the death of one female, the other one would successfully rear offspring: in *M. h. lydius* the survival rate of pups was 63 (sisters) and 78% (non-kin), and in *M. h. hartingi* – 100 and 57% respectively. Litters in all the CG were evaluated as significantly smaller than in monogamous pairs, which is indicative of social stress. Communal reproduction was registered in 25% cases for *M. h. lydius* and 58% for *M. h. hartingi*. Survival rate in experimental groups was lower, than in monogamous pairs. In *M. h. lydius* non-kin females (control group) reared 4, and sisters (brother and sister) - 3 pups on average. In our study non-kin females reared 1.7, but sisters 1 pup on average. In *M. h. hartingi* these results were 5, 4.8, 0.6 and 1.4 accordingly. Offspring mortality was increased by social stress, which indicates the low possibility of existence of such groups in natural habitats for *M. h. lydius*. However, related individuals seem to be able to form temporal or constant pairs, though natal dispersal in this subspecies decreases the possibility of inbreeding. On the contrary, for *M. h. hartingi* communal living under habitat fragmentation leaves less possibility for migration as vacant places are rare, which increases the possibility of inbreeding. Inbreeding in Asian subspecies appears to be an external event, but in European subspecies is widely spread.

ZOONOTIC PARASITES IN RED FOXES (*VULPES VULPES*) AND RACCOON DOGS (*NYCTEREUTES PROCYONOIDES*)

Maira Mateusa^{1,2}, Maija Selezņova¹, Gunita Deksnē^{1,3}

¹ Institute of Food Safety, Animal Health and Environment “BIOR”, Latvia

² Faculty of Veterinary Medicine, Latvia University of Life Sciences and Technologies, Latvia

³ Faculty of Biology, University of Latvia, Latvia

E-mail: maira.mateusa@bior.lv

Red foxes (*Vulpes vulpes*) and racoon dogs (*Nyctereutes procyonoides*) may carry zoonotic parasites like, *Cryptosporidium* spp., *Giardia duodenalis*, *Echinococcus* spp., and *Trichinella* spp. Therefore, these animals may pose a threat by either excreting eggs, oocysts and cysts into the environment or being a potential reservoir for humans and other animals. The aim of this study was to determine the presence of zoonotic parasites in red fox and raccoon dog in Latvia.

Between October-November, 2020, 54 racoon dog and 100 red fox carcasses were gathered from Eastern Latvia during official survey for anti-rabies vaccination efficiency. Viscera and forelimb muscles samples were collected from each animal and kept frozen for at least 10 days at -80 °C before further analyses. The appropriate methods were used for parasite detection in muscle, viscera and faeces. Statistical analysis was carried out by IBM SPSS Statistics 27.0.1.0 and OpenEpi Version 3.01.

Overall, the prevalence of parasites in red foxes was 96.0% (95%CI 89.8-98.8) out of which 40.6% (95%CI 31.3-50.6) were parasites with a zoonotic potential and in racoon dogs 94.4% (95%CI 84.3-98.7) and 29.4% (95%CI 18.6-43.1), respectively. In red fox the highest prevalence was observed for *Trichinella* spp. (43.0%, 95%CI 32.7-53.6) followed by both *Cryptosporidium* spp. and *G. duodenalis* (33.3%, 95%CI 23.7-44.0), and *Echinococcus* spp. (28.1%, 95%CI 19.4-38.2). Meanwhile in racoon dog the highest prevalence was observed for *G. duodenalis* (36.5%, 95%CI 22.1-53.0) followed by *Cryptosporidium* spp. (29.2%, 95%CI 16.1-45.5), *Trichinella* spp. (22.2%, 95%CI 12.0-35.6) and *Echinococcus* spp. (10.2%, 95%CI 3.4-22.2). There was a significant difference of *Trichinella* spp. (p=0.01) and *Echinococcus* spp. (p=0.01) prevalence in red foxes and racoon dogs, with foxes being more infected.

The present study indicates that red foxes and racoon dogs carry zoonotic parasites and therefore could potentially contaminate the environment and pose a risk for human and other animal health.

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