PROGRAMME & ABSTRACTS

22nd European Congress of HERPETOLOGY

XXII European Congress of Herpetology, University of Wolverhampton, United Kingdom

4th–8th September, 2023

Local Organising Committee

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Dear Colleagues,

Welcome to Wolverhampton in the heart of the Black Country!

We are very pleased to be able to host the XXII European Congress of Herpetology and welcome you to the University of Wolverhampton.

This is the first SEH conference organised in a consecutive year, following the successful XXI Congress in Belgrade in 2022, with congresses usually occurring biennially on odd-numbered years. This is also the first time the SEH Congress has been hosted in the United Kingdom since the 5th European Congress was held in conjunction with the 1st World Congress of Herpetology, at the University of Canterbury, Kent, in September 1989, 34 years ago!

Delegates from 24 countries around the world have registered to attend this event, and we hope you all have a fantastic time sharing knowledge, meeting old friends, and making some new ones. We have 99 talks and 52 posters lined up, covering a wide range of topics including conservation, systematics, evolution, physiology, disease ecology, museology, and climate change. We are also planning to run a range of social events and discussions to which you are cordially invited.

We would like to thank the Societas Europaea Herpetologica for inviting us to host this event, all the delegates, our sponsors, and the scientific committee for helping to make the 22nd European Congress of Herpetology happen.

XXII SEH Local Organizing Committee

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Conference Programme

Monday 4th September 2023

ATRIUM	
14:00 – 18:00	Registration / Refreshments
18:00 – 20:00	Opening of Conference / Ice Breaker

POOL FROG ROOM	
16:00 – 17:00	Induction for session chairs

GREAT CRESTED NEWT ROOM	
17:00 – 18:00	Student activity: Drop-in session

Tuesday 5th September 2023

ATRIUM	
09:00 – 10:00	Registration / Refreshments

GREAT CRESTED NEWT ROOM	
09:00 – 16:00	Student safe space: presentation practice

ADDER ROOM	
10:00 – 16:20	Safe space: Streaming of presentations from Pool frog room

POOL FROG ROOM Chair: John Wilkinson	
10:00 – 11:00	**Griffiths, R.A.** Reintroductions and rewilding in a changing world [PLENARY]

ATRIUM	
11:00 – 11:40	Refreshments

	POOL FROG ROOM	SAND LIZARD ROOM	NATTERJACK TOAD ROOM
	Symposium: Rewilding and reintroductions Chair: Rob Ward	**Ecology** Chair: Natasha Kruger	**Conservation** Chair: Mark O'Shea
11:40 – 12:00	**Mizsei, E.** Restoration by diversification of plants on formerly ploughed low-diversity secondary grasslands enhances occupancy of the threatened Hungarian meadow viper (*Vipera ursinii rakosiensis*)	**Clément, V.** Spatial ecology and terrestrial habitat selection of the green toad (*Bufotes viridis*): the example of slagheaps in Eastern France	**Morris, R.M.** Do good things come to those who wait? The value of regenerating rainforest on herpetofaunal communities
12:00 – 12:20	**Foster, J.** International assisted colonisation as a response to climate change: exploring UK practitioner views on a significant conservation dilemma	**Budai, M.** Microhabitat selection of meadow and steppe vipers enlightened by digital photography and image processing to describe grassland vegetation structure	**Lo Parrino, E.** Estimating population trends from abundance and occupancy data: a comparison Student
12:20 – 12:40	**Owens, J.B.** A population genomic approach to assess isolated sand lizard (*Lacerta agilis*) populations and the implications for ex-situ conservation Student	**Valenti Martinez, A.** Environmental and anthropogenic factors determining the distribution of amphibian species in the upper Val d'Agri (Basilicata, Italy) Student	**Sos, T.** Abundance and conservation status of *Vipera ursinii rakosiensis* in Romania
12:40 – 13:00	**Kaczmarek, J.M.** An attempt to translocate the population of the green toad *Bufotes viridis* from the centre of Poznań	**Dalgo, D.** Diversity of foraging niches of the Galápagos marine iguanas (*Amblyrhynchus cristatus*) Student	**Thomas, A.** Influence of stream habitat variables on distribution and abundance of tadpoles of the endangered purple frog, *Nasikabatrachus sahyadrensis* (Anura: Nasikabatrachidae) and implications on its conservation
13:00 – 13:20	**Kloskowski, J.** Urban green space planning makes a difference: amphibian species richness and diversity in a city with a green wedge design		**Ashpole, S.L.** 20-years of collaborative regional amphibian conservation efforts, South Okanagan Valley, Canada (2003 to 2023)

	ATRIUM
13:20 – 14:40	Lunch
14:40 – 15:00	Conference photo

	POOL FROG ROOM	SAND LIZARD ROOM	NATTERJACK TOAD ROOM
	Symposium: Rewilding and reintroductions Chair: Jim Foster	**Herpetology** Chair: Judit Vörös	**Development** Chair: Natasha Kruger
15:00 – 15:20	**Bickerton, K.T**. Return to Round Island: reintroducing a prey species into a system of native predator Student	**Maddock, S.T.** Rectal parasites, venomous amphibians, or holy creatures? Using social surveys to understand the myths and the ecology of caecilian amphibians in Indonesia	**Ćirković, G.** Preliminary results of geometric and traditional morphometric analysis of *Rana dalmatina* and *Rana temporaria* tadpoles exposed to polyethylene microplastics
15:20 – 15:40	**Ward, R.J.** Thirty years in recovery: efficacy of conservation interventions for the agile frog (*Rana dalmatina*) in Jersey	**Armfield, R.E.** Is bigger always better: Will we ever find a "gape-limited snake" in the fossil record? Student	**van Elsen, M.** Experimental predation of native and non-native fish species on different life stages of common spadefoot toad *Pelobates fuscus* and common frog *Rana temporaria* Student
15:40 – 16:00	**Smart, A.C.** Hissing Heathlands	**O'Donnell, M.J.** Filtering for frogs: Trials and tribulations for eDNA monitoring in the tropics Student	**Dimitrova, B.** Negative effects of high concentrations of ammonium nitrate on survival, growth and activity in *Rana dalmatina* tadpoles are not reflected in high avoidance Student
16:00 – 16:20	**Petrovan, S.O.** Evidence-based guidelines for mitigating the impact of roads on herpetofauna- a novel and transparent tool for practitioners	**Lobón-Rovira, J.** Unveiling cranial diversity and its evolutionary history on a non-adaptive radiation of dwarf geckos	**Eterovick, P.C.** Interactive effect of thermic and pollution stress on tadpole gut microbiome

	GREAT CRESTED NEWT ROOM
16:40 – 18:00	Speed Networking activity

	SMOOTH SNAKE ROOM
16:40 – 19:00	European Board of Herpetological Societies meeting

	ATRIUM
19:00 – 21:00	Alcohol-free social

Wednesday 6th September 2023

ATRIUM	
09:00 – 11:40	Refreshments

GREAT CRESTED NEWT ROOM	
09:00 – 14:40	Student safe space: presentation practice

ADDER ROOM	
09:20 – 16:00	Safe space: Streaming of presentations from Pool frog room

POOL FROG ROOM Chair: Rémi Martin	
09:20 –10:00	**Mark O'Shea** Amphibian and reptile art in mixture: adventures in herpeto-philately
10:00 – 11:00	**NGO Spotlight**

SMOOTH SNAKE ROOM	
09:20 – 11:40	SEH Council Meeting

	POOL FROG ROOM	SAND LIZARD ROOM	NATTERJACK TOAD ROOM
	Population Genetics Chair: Simon Maddock	**Disease** Chair: Aaron Bauer	**Ecology** Chair: Dušan Jelić
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12:00 – 12:20	**Martin, R.** Broad scale population genetics of the common toad (*Bufo bufo*) in Britain Student	**Reinhardt. T.** Phoenix from the ashes – hope for the fire salamander?	**Martínez-Freiría, F.** Reproductive ecology of Western Mediterranean vipers (*Vipera aspis* and *V. latastei*) in two contact zones in northern Spain
12:20 – 12:40	**Uesseler, F.S.** Population genomics of Galápagos marine iguanas: Seeking footprints of local adaptation and gene flow Student	**Coutinho, C.D.** Dynamics of Ranavirus in ecosystem invaded by *Xenopus laevis* Student	**Speybroeck, J.** How much is enough? The role of sampling effort in capture-mark-recapture studies of great crested newt *Triturus cristatus* in Flanders (Belgium)
12:40 – 13:00	**Hester, R.** Utilising genomics to unravel the invasion history of the non-native alpine newt *Ichthyosaura alpestris* in the UK Student	**Klynova, O.** The first report about the spread of snake fungal disease (SFD) in Ukraine Student	**Glover, N.G.** Wildlife detection dogs, a viable method to locate great crested newts *Triturus cristatus* at distance and through substrate? Student

13:00 – 13:20	**Duchatel, C.** Genetics and demography of fragmented adder (*Vipera berus*) populations in the Netherlands Student		**Jeffrey, L.** Aesculapian snakes (*Zamenis longissimus*) show a preference for anthropogenic features in their introduced range in North Wales Student

	ATRIUM
13:20 – 14:40	Lunch

	POOL FROG ROOM	**SAND LIZARD ROOM**	**NATTERJACK TOAD ROOM**
	Evolution – adaptation Chair: María Torres-Sánchez	**Herpetology** Chair: Hinrich Kaiser	**Workshop** STEM Response Team
14:40 – 15:00	**Gower, D.J.** Retinas and the early evolutionary history of snakes	**Mancuso, M.** Resistance is not futile: Widespread convergent evolution of resistance to alpha-neurotoxic snake venoms in caecilians (Amphibia: Gymnophiona) [Virtual]	**Research Communication for Outreach**
15:00 – 15:20	**Simões, B.F.** Molecular evolution of vision in lizards and snakes	**Parmar, D.** Egg incubation of some Indian squamate reptiles from The Western Ghats, India.	
15:20 – 15:40	**Zaman, S.** Recurrent evolution of adhesive skin-secreted defence systems in amphibians Student	**Julian, A.M.** 'Dragons in the Hills': engaging citizen science and community action to conserve Northern Ireland's amphibians and reptiles	
15:40 – 16:00	**Vicent-Castelló, P.** Walking or hanging: how body shape evolution is moulded by habitat use in lacertid lizards Student	**de Celis, A.** A geometric morphometric approach to palatal ontogeny in Crocodylia	

	ATRIUM
16:00 – 18:00	**Poster Session 1**

	SMOOTH SNAKE ROOM
18:00 – 20:00	Reptile & Amphibian Conservation Europe meeting

Thursday 7th September 2023

ATRIUM	
09:40 – 10:00	Refreshments

GREAT CRESTED NEWT ROOM	
09:00 – 13:00	Student safe space: presentation practice

ADDER ROOM	
10:00 – 16:00	Safe space: Streaming of presentations from Pool frog room

POOL FROG ROOM Chair: Deepak Veerappan	
10:00 – 11:00	**Campbell, P.D. & Streicher, J.W.** The role of museum collections in 21st century herpetology [PLENARY]

ATRIUM	
11:00 – 11:40	Refreshments

	POOL FROG ROOM	SAND LIZARD ROOM	NATTERJACK TOAD ROOM
	Symposium: The role of museums in the age of extinction Chairs: Jeffrey Streicher & Patrick Campbell	**Herpetology** Chair: Andreas Maletzky	**Physiology** Chair: Frances Orton
11:40 – 12:00	**Fritz, U.** Time travel through 20 years of using herpetological collections for DNA sequencing	**Patro, S.** How do lizards talk? Integration of signalling traits in a complex signalling system [VIRTUAL]	**Di Canio, V.** Anthropogenic and genetic impacts on stress-related traits in the Italian wall lizard (*Podarcis siculus*) Student
12:00 – 12:20	**Jensen, E.** Museomics enabled conservation of the Galapagos giant tortoises	**Smolinský, R.** Tough life of sand lizard females during the reproduction season	**Üveges, B.** Does the glucocorticoid stress response make toads more toxic? An experimental study on the regulation of bufadienolide toxin synthesis
12:20 – 12:40	**Petzold, A.** Solving taxonomic cold-cases with museomics: calling in genetic data from name-bearing types for a revision of cophyline frogs (Microhylidae: Cophylinae)	**Barzaghi, B.** Study on the differences of Body Mass Index between olms found in cave and the ones sampled in spring	**Bettencourt-Amarante, S.** The impact of anthropogenic changes on amphibians Student
12:40 – 13:00	**Deepak, V.** Mitochondrial and nuclear DNA from historic museum samples of Asian softshell turtles	**Martínez-Freiría, F.** Microclimate variables deepen our understanding of distributional patterns of five viper species at a contact zone in South-Western Morocco	**Martin, C.M.** Chemical pollution and oxidative stress in amphibians across life stages

13:00 – 13:20	**Wilkinson, M.** On *Herpele* (Amphibia: Gymnophiona: Herpelidae)		**Merleau, L-A.** Where and When? Determinants of pesticide concentrations in a threatened freshwater turtle (*Emys orbicularis*) in the Camargue Wetland, France Student

ATRIUM	
13:20 – 14:40	Lunch

	SMOOTH SNAKE ROOM
14:00 – 16:00	SEH Conservation Committee meeting

	POOL FROG ROOM	SAND LIZARD ROOM	NATTERJACK TOAD ROOM
	Symposium: The role of museums in the age of extinction Chairs: Jeffrey Streicher & Patrick Campbell	**Disease – UK** Chair: Alice Pawlik	**Conservation** Chair: Natasha Kruger
14:40 – 15:00	**Bauer, A.M.** Bones of a giant: The osteology of the extinct Cape Verdean skink *Chioninia coctei*	**Allain, S.J.R.** The impacts of ophidiomycosis on the survival and detection of the barred grass snake (*Natrix helvetica*), at a site in Eastern England	**Zinenko, O.** Impact of Russia's war of aggression against Ukraine on nature and herpetology [VIRTUAL]

15:00 – 15:20	**Hallermann, J.** A review of the house snakes of East and Northeast Africa - a further step to unscramble the *Boaedon fuliginosus* species complex	**Hesten, A.** Understanding disease risk in the UK pet trade of reptiles and amphibians Student	**Ursenbacher, S.** Swiss reptile Red List - monitoring of 303 square kilometres to evaluate the decrease of species distribution
15:20 – 15:40	**Sørensen, P.** Ventral scales numbers, anomalies and body mass index in three sympatric snake species within Norway	**St Roas, M.** Agent-based models to explore Ranavirus infection outcomes in UK common frog populations Student	**Petrovan, S.O.** Four decade decline of a widespread amphibian in Britain and Switzerland
15:40 – 16:00	**Neokleous, D.N.** Uncovering the cryptic diversity of "ugly brown frogs" on Borneo		**Miccolis, E.** Shedding light on diel patterns: extinction risk and daily temporal activity of European amphibians

ATRIUM	
16:00 – 18:00	**Poster Session 2**

MOLINEUX STADIUM	
19:00 – late	**Gala Dinner**

Friday 8th September 2023

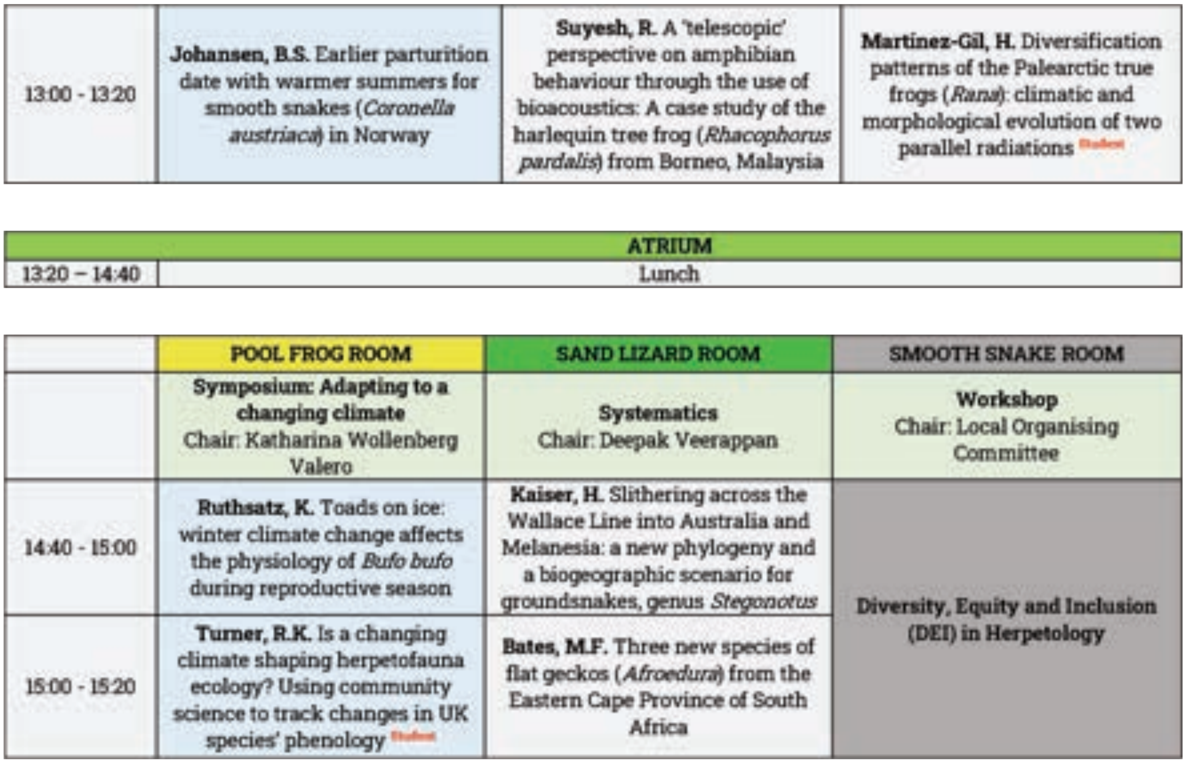
ATRIUM	
09:40 – 10:00	Refreshments

POOL FROG ROOM Chair: Natasha Kruger	
10:00 – 11:00	**Katharina Wollenberg Valero** Functional genomics of abiotic environmental adaptation in lacertid lizards (and other vertebrates) [PLENARY]

ADDER ROOM	
10:00 – 16:00	Safe space: Streaming of presentations from Pool frog room

ATRIUM	
11:00 – 11:40	Refreshments

	POOL FROG ROOM	SAND LIZARD ROOM	NATTERJACK TOAD ROOM
	Symposium: Adapting to a changing climate Chair: Katharina Ruthsatz	**Herpetology** Chair: Angela Julian	**Biogeography** Chair: Simon Maddock
11:40 - 12:00	**Muraro, M.** Reproductive responses of *Rana dalmatina* and *Rana latastei* to drought conditions	**Spawls, S.** The unique forest and montane herpetofauna of Ethiopia	**Ghosh, A.** Independent origin or single dispersal? Phylogenetic study supports early Cenozoic origin of three endemic Indo-Sri Lankan lygosomine (Reptilia, Scincidae) skink genera [VIRTUAL]
12:00 - 12:20	**Raselimanana, M.** The heat is on! Mild winter temperatures increase behavioural response in hibernating wall lizards Student	**Dittrich, C.** Spot(s) on: Are larger spots more effective against predation in an aposematic amphibian?	**Hurtado-Gómez, J.P.** Diversity and biogeography of South American mud turtles elucidated by multilocus DNA sequencing (Testudines: Kinosternidae) Student
12:20 - 12:40	**Freitas, I.** Physiological adaptations of Western Mediterranean vipers and their hybrids at contact zones suggest distinct vulnerability to climate change Student	**Sørensen, P.** Different body size, sexual size dimorphism, and reproductive strategy in two populations of the smooth snake *Coronella austriaca* Laurenti 1768	**Dinis, M.** Recurrent introgression and multiple waves of colonization: the puzzling biogeographic history of a North Palearctic disjunction in *Salamandra salamandra*
12:40 - 13:00	**Araspin, L.** Locomotion and physiology depending on temperature in *Xenopus laevis* native and invasive populations Student	**Halpern, B.** Individual behavioural variation of juvenile Hungarian meadow vipers (*Vipera ursinii rakosiensis*)	**Brennan, I.G.** Populating a continent: Phylogenomics reveal the timing of Australian frog diversification



13:00 - 13:20	**Johansen, B.S.** Earlier parturition date with warmer summers for smooth snakes (*Coronella austriaca*) in Norway	**Suyesh, R.** A 'telescopic' perspective on amphibian behaviour through the use of bioacoustics: A case study of the harlequin tree frog (*Rhacophorus pardalis*) from Borneo, Malaysia	**Martinez-Gil, H.** Diversification patterns of the Palearctic true frogs (*Rana*): climatic and morphological evolution of two parallel radiations Student

	ATRIUM
13:20 – 14:40	Lunch

	POOL FROG ROOM	SAND LIZARD ROOM	SMOOTH SNAKE ROOM
	Symposium: Adapting to a changing climate Chair: Katharina Wollenberg Valero	**Systematics** Chair: Deepak Veerappan	**Workshop** Chair: Local Organising Committee
14:40 - 15:00	**Ruthsatz, K.** Toads on ice: winter climate change affects the physiology of *Bufo bufo* during reproductive season	**Kaiser, H.** Slithering across the Wallace Line into Australia and Melanesia: a new phylogeny and a biogeographic scenario for groundsnakes, genus *Stegonotus*	**Diversity, Equity and Inclusion (DEI) in Herpetology**
15:00 - 15:20	**Turner, R.K.** Is a changing climate shaping herpetofauna ecology? Using community science to track changes in UK species' phenology Student	**Bates, M.F.** Three new species of flat geckos (*Afroedura*) from the Eastern Cape Province of South Africa	

15:20 - 15:40	**Gilbert, E.** Unravelling stress and the environment: what contributes to baseline stress markers in the Tenerife lizard (*Gallotia galloti*) Student	**O'Shea, M.** Untangling the Bootlaces: New eyes and ideas for solving an old problem in the Papuan elapid genus *Toxicocalamus* (Elapidae, Hydrophiinae)	
15:40 - 16:00	**Delgadillo, A.** Desiccation risk responses in tadpoles of a tropical extreme environment: the inselbergs in Colombian Orinoquía		

	ATRIUM
16:00 – 17:00	Awards / Conference closing

Poster session 1 (Wednesday 6th September)

Mészáros, B. Snakes living in urban habitats: effects of urban environment on the developmental stability, condition and size of dice snakes (*Natrix tessellata*) living in a human-modified shoreline	**Berlijn, B.D.** The importance of education in herpetofaunal conservation
Gemeinhardt, L. How to standardise fire salamander research, get the help of citizen scientists but minimise the risk of spreading the "Salamander Plague" Student	**Kovács, T.** Frogs, Beavers and Wastewater
Lukanov, S. Effect of continuous winter activity on body condition in *Triturus ivanbureschi*	**Drăgan, O.** Fish introduction in mountain lakes and its effect on amphibian communities
Nekrasova, O.D. Modelling the distribution of the natterjack toad, *Epidalea calamita* (Laurenti, 1768), in Europe: Accounting for connectivity suitability and dispersal	**Julian, A.** 'Stowaway' data for amphibians, reptiles, and invertebrates entering the United Kingdom from 2018-23; highlighting introductions of potentially invasive species, risks to public safety, and other ecological and conservation impacts
Torres-Sánchez, M. Using museum specimens to understand ecological and evolutionary consequences of local extinction in salamander communities	**Czurda, J.** Anuran phylogeographic patterns in Congo Basin rainforests Student
Bjelica, V. Preliminary results indicate localized adaptation in the duration of unkenreflex in fire-bellied toads (*Bombina bombina*, Bombinatoridae) Student	**V. Deepak.** Unveiling hidden diversity: Herpetological explorations in Northeast India

Jordan, E.A. Using expert elicitation to estimate habitat suitability for the translocation of a newly described skink species Student	**Florina, S.** Age estimation in non-avian reptiles using growth marks in skeletal and non-skeletal hard tissues
Coutinho, C.D. Buccal swabbing as a refined method for Ranavirus screening in fish Student	**Cogalniceanu, D.** Age and growth-size variation in the common frog across a latitudinal gradient
de Celis, A. Optimising the molecular phylogeny of Crocodylia	**Donnan, R.** The freeloaders of toads: Parasite diversity in UK populations of *Bufo bufo* Student
Head, O. Visual evolution in subterranean lizards Student	**Simpson, S.** Turtle Tally UK Citizen Science: 5 years monitoring introduced pet terrapins in the UK
Fernández, S.P. Unveiling the spatial ecology and conservation implications of *Bufotes balearicus* (Boettger, 1880) in the Balearic Islands: Insights from capture, mark, and recapture studies	**Attewell-Hughes, C.R.I.** Effects of water temperature on growth and development in tadpoles of red eyed tree frogs Student
Kásler, A. The joint effects of mild winter conditions and two pyrethroid insecticides on the development and survival of juvenile common toads (*Bufo bufo*) Student	**Freitas, I.** Comparing genetic and morphological patterns between the Western Mediterranean vipers, *Vipera aspis* and *V. latastei* across a hybrid zone in northern Spain Student
Ujszegi, J. Sex ratio in the presence of the chytrid fungus (*Batrachochytrium dendrobatidis*) in a common European amphibian	**Sherlock, M.** Genomic phylogeography of the Iberian frog *Rana iberica* Student

Poster session 2 (Thursday 7th September)

Ashpole, S.L. Global amphibian decline: Applying a research focused mixed-method pedagogical approach to undergraduate learning	**Mahlow, K.** Ontogenetic development of skull shape in *Bothrops jararaca*, with special emphasis on the pit organ and the venom gland
Budai, M. Reconstruction and comparison of the flora of the former and existing habitats of the Hungarian meadow viper (*Vipera ursinii rakosiensis*) Student	**Joudrier, N.** Unravelling the disease ecology of *Ophidiomyces ophidiicola*: high genetic variability and ecological basis of the agent of snake fungal disease
Göktaş, M.C. Classification of the Marmaris lycian salamander, *Lyciasalamandra flavimembris* and Göcek lycian salamander, *Lyciasalamandra fazilae* by an electronic nose	**Mizsei, E.** Weather conditions and detection probability in the occupancy monitoring of the Hungarian meadow viper (*Vipera ursinii rakosiensis*) and other reptile species
Darkin, J. Mitochondrial phylogeography of the common toad (*Bufo bufo*) in Britain Student	**Nečas, T.** The first molecular analysis of the Lanza's frog (*Lanzarana largeni*) from the Horn of Africa supports its unique position in the family Ptychadenidae Student
Fănaru, G. How long is a snake? Comparison of different measurement methods	**North, A.** Key informant surveys demonstrate biases and benefits for invasives species rapid status assessments Student
Fernández, S.P. Photo-identification of *Bufotes balearicus* (Boettger, 1880) using individual colour patterns for population studies	**Nygaard, M.** Natural history museum collections as an untapped reservoir for pathogen studies: a case study of snake fungal disease in Norway
Gherghel, I. Exploring climate change impact on phenotypic diversity and geographic distribution in the sand lizard (*Lacerta agilis*)	**O'Brien, A.R.** Diversity of *Anolis* lizards in Cusuco National Park, Honduras

Gray, R. Speciation, hybridization and introgression as evolutionary processes in Galapagos giant tortoise Student	**Rees, J.P.G.** The evolutionary and morphological constraints of arboreality in geckos Student
Kaczmarski, M. Increasingly cautious sampling, not the black colouration of unpalatable prey, is used by fish in avoidance learning	**Russo, G.** Anatomical and molecular characterisation of *Strophurus ciliaris* tail regrowth
O'Shea, M. Hidden diversity and natural history of the secretive New Guinean worm-eating snakes, genus Toxicocalamus (Elapidae: Hydrophiinae), revisited	**Sos, T.** Within-individual variance and population-level repeatability of the voluntary thermal maximum of grassland vipers (*Vipera* sp.)
Kovács, G. Community-level response of reptiles to grassland reconstruction to connect isolated Hungarian meadow viper habitats Student	**Wenner, B.** Predation pressure on the endangered Hungarian meadow viper (*Vipera ursinii rakosiensis*) in grazed and mowed grassland habitats: insights from plasticine models Student
Kovács, T. Range reduction of *Rana temporaria* in Pilis Hills, Hungary, after 22 years of monitoring	**Parmar, D.** Human-snake conflict mitigation data sheds light on snake occurrence patterns in a peri-urban setting in western India.
Lukanov, S. Initial toxicological characterization of the skin secretion of Buresch's crested newt (*Triturus ivanbureschi*)	**Oungbe, K.V.** Specific diversity of Helminth parasites of the edible frog *Hoplobatrachus occipitalis* (Günther, 1858) in an agricultural environment in the south-east of Ivory Coast, Africa

Symposium: Rewilding and Reintroductions

Plenary Speaker: RICHARD GRIFFITHS

Session chair: ROB WARD

PLENARY

Reintroductions and rewilding in a changing world

RICHARD A. GRIFFITHS

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The rewilding agenda has provided a new dimension to reintroducing species into the wild. However, although there are many examples of successful reintroductions of amphibians and reptiles, herpetofauna are rarely considered within rewilding projects. Although they play important roles in ecosystems, the evidence supporting amphibians and reptiles as providers of ecosystem services is less compelling than that for mammals and birds. Nevertheless, the biodiversity and climate crises are driving calls for urgent reintroductions that do not always embrace over three decades of research on how to improve success and reduce risks. To improve the profile of amphibians and reptiles within rewilding projects, there needs to be a shift in focus towards their historical, cultural and societal value rather than their scientific and commodity value. Likewise, arguments for their role within the provision of ecosystem services are likely to resonate more strongly if the emphasis is on amphibian and reptile habitats and landscapes rather than the species themselves.

Key words: landscapes, habitats, amphibians, reptiles, herpetofauna

Restoration by diversification of plants on formerly ploughed low-diversity secondary grasslands enhances occupancy of the threatened Hungarian meadow viper (*Vipera ursinii rakosiensis*)

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Grasslands, as one of the most species-rich and endangered ecosystems globally, face a significant decline in their coverage, leading to the endangerment of species adapted to these habitats, such as the Hungarian meadow viper (*Vipera ursinii rakosiensis*). The species richness of grasslands plays a crucial role in their stability, resistance, and resilience against disturbances and environmental changes. In recent decades, abandoned arable fields, particularly those unsuitable for crop production due to inadequate edaphic and climatic conditions, have been converted into grasslands, which become low-quality secondary grasslands after abandonment or restoration. We employed floral diversification by sowing native plant seeds from over 50 species characteristic of primary viper habitats, covering an area of more than 100 hectares. To assess the impact of grassland restoration on the habitat occupancy of the Hungarian meadow viper, we employed a Before-After/Control-Intervention (BACI) experimental design. A stratified random sampling design was utilised, consisting of 10 control plots (abandoned cropland without restoration) and 12 intervention plots (abandoned cropland with restoration), each measuring 50×50 metres. Viper observations were recorded during ten surveys conducted in the spring and autumn seasons of 2020–2023. The occupancy model, fitted to the Hungarian meadow viper observation data, revealed an increase in occupancy rates at diversified sites. Moreover, the colonisation probability showed a significant increase, while the extinction probability significantly decreased compared to the control sites. Furthermore, at a larger spatial scale, we discovered individual vipers in two of the restored grasslands where no previous data supported their presence. This study demonstrates the positive impact of diversifying secondary grasslands on the population of *V. u. rakosiensis* and the floral diversity of regenerating Pannonic sand grasslands. These findings highlight the importance of restoration efforts and the role of diversification in enhancing habitat occupancy and conservation of threatened species in grassland ecosystems.

Key words: occupancy modelling, restoration, grasslands, biodiversity, plants

International assisted colonisation as a response to climate change: exploring UK practitioner views on a significant conservation dilemma

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Climate change is altering species distributions globally, and this generates intriguing dilemmas for conservation policy. “Climate-tracking” species may expand or contract their ranges via local dispersal, but the limited dispersal powers of many amphibians and reptiles mean that they often cannot take advantage of altered climate envelopes. Being an island nation, the United Kingdom will not naturally accumulate new herpetofauna resident in continental Europe as their climate envelopes inevitably shift northwards. In this situation, is it right to translocate such species into the UK and consider them to form a new, climate-adapted UK herpetofauna? In doing so, how would the gains of assisting so-called “climate refugees” be reconciled with the risks of introducing non-native species? The views of 131 UK herpetofauna conservation practitioners were examined in an online workshop in February 2021. There was broad yet heavily caveated support for further exploration of international assisted colonisation. There was increased support for this intervention after the climate change effects and general background had been explained, and following online discussion within the workshop (46% in favour before discussion, rising to 70% after). There was only equivocal support for a change in the approach to existing populations of non-native species on the basis of climate change (6% suggesting they are actively conserved). Participants broadly agreed on the need for more research, international agreement, and on maintaining conservation efforts for native species threatened by climate change in the UK. Given the predictions of substantial range losses to European herpetofauna, the potential benefits and risks of international assisted colonisation should be given serious consideration. However, such an intervention would challenge conventions, and is an interesting example of current debates around conservation values and outcomes in the age of a biodiversity crisis. Given this background, any policy discussion would benefit from international, cross-taxonomic collaboration.

Key words: climate change, translocation, assisted colonisation, reintroduction

A population genomic approach to assess isolated sand lizard (*Lacerta agilis*) populations and the implications for ex-situ conservation.

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Globally, reptile populations are under ongoing pressure from habitat encroachment and fragmentation leading to genetically isolated populations. These populations may benefit from human intervention via re-introductions, however, the genetic consequences and pre-introduction requirements are unknown. Within the UK, sand lizard (*Lacerta agilis*) populations have been subject to re-introductions and ex-situ conservation efforts, both official and clandestine. In both scenarios, the genetic health and ancestry of captive stock has not been assessed at the genome scale. Here, we use low-medium coverage genomic techniques to investigate UK sand lizard populations. We first determine the source of UK populations by uncovering their genetic ancestry. Next, we assess the diversity of these populations across the genome to determine their genetic health and inform future conservation efforts. Our current findings demonstrate high average genetic diversity on the genome-wide scale but the presence of homozygotic runs which may be a result of inbreeding. We also determined that populations stemming from unofficial releases in Wales originate from Welsh and/or Sefton Coast populations. Ongoing investigations will allow us to determine if admixture between isolated populations will aid in producing genetically diverse individuals, regardless of diversity loss at the population level. This will allow better informed captive breeding and re-introduction decisions not only for sand lizards but other isolated populations across the globe.

Key words: *Lacerta agilis*, Re-introductions, Genomics, Genetic Health, Isolated Population

An attempt to translocate the population of the green toad (*Bufotes viridis*) from the centre of Poznań

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The population of the green toad *Bufotes viridis* in a stormwater reservoir located just by the railway station in Poznań (W Poland) developed approximately 15 years ago, soon after its construction. It was the only relatively large population of the species surviving in the densely built-up city centre. However, each year, mass mortality of juveniles during dispersion was observed, and the reservoir was scheduled for demolition. Therefore, we attempted to translocate the population in agreement with the local nature protection authority. In spring 2022, using a system of drift fences and pitfall traps, we collected 70 adult (33♂:37♀) and 22 subadult toads. Adults were marked with PIT-tags and all toads were moved to a newly constructed breeding pond located within a large patch of suitable terrestrial habitat. The new habitat was temporarily fenced; additionally, the animals were initially released into small pens to enable safe acclimatisation. The released animals spawned successfully; both tadpoles and metamorphs reached high densities. We planned habitat monitoring for the next few years as well as an acoustic monitoring system to survey the calling activity of males. In 2023, only three individuals were caught at the original site. We also found two dead toads. At the translocation site, a fraction of individuals (6) were detected; however, all of them were male. Additionally, 12 out of 22 subadult toads that were not tagged in 2022 were recaptured and tagged in 2023. Despite male calling activity, there was no breeding success (while two strings of spawns were detected, there were no tadpoles nor metamorphs). Although *B. viridis* is a pioneer species, long-term success in translocating its populations may be difficult to achieve. The differences in post-breeding dispersal as well as winter survival between males and females may contribute to the success or failure of translocation attempts.

Key words: urban, conservation, pioneer species, acoustic monitoring, PIT-tags

Urban green space planning makes a difference: amphibian species richness and diversity in a city with a green wedge design

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Urbanisation has been documented to negatively impact biodiversity; typically, amphibian abundance and breeding occurrence tend to decline towards the urban core. On the other hand, urban networks of green space and blue infrastructure provide valuable habitats for wildlife. In Poznań (western Poland), presently a city of over half a million inhabitants, urban planning in the early 20th century was based on the inclusion of green wedges, i.e. ducts of green space from the surrounding rural areas into the city centre. We surveyed ponds within the administrative boundaries of the city for the presence and abundance of breeding populations of amphibians, and also collected data on pond features and the characteristics of the surrounding landscape. The green wedges maintained pond connectivity better than the areas outside the radial green infrastructure. Amphibian species richness and diversity were positively related to pond size, while fish presence adversely affected amphibian richness, but not diversity. Neither of the diversity measures was related to the urban gradient developed by combining the indices of distance to the city centre, density of public roads, level of artificial light at night, and proportion of built-up areas. The abundances of insects preying on amphibian larvae showed a similar pattern and were not correlated with larval amphibian densities, indicating that habitat urbanisation was not consistent with release from insect predators. As most of the Poznań ponds were situated within or close to the radial green space, we argue that green wedges fulfil their function as ecological corridors for amphibians and may offset the effects of urbanisation. Municipal forest and park system planning at the scale of whole cities is crucial to prevent habitat loss and fragmentation.

Key words: green infrastructure, amphibian diversity, habitat selection, urban ecology, urbanisation

Return to Round Island: reintroducing a prey species into a system of native predator

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Round Island, Mauritius, was the last remaining refuge for several endemic reptiles driven to extinction elsewhere by invasive species. In the last 30 years, it has provided source populations for reintroductions of predatory reptiles across the outer islands of Mauritius, improving the resilience of key members of the ecosystem. Although Round Island was never invaded by mammalian predators, goats and rabbits were introduced, destroying much of the native vegetation which in turn led to the loss of soil. This limited the natural recolonization of native flora after the eradication of goats and rabbits in the 1980s, lowering the abundance of food available for native reptiles and the amount of refugia for prey species. This is thought to be the main reason for the absence of several key prey species that persisted on other islands despite invasive mammalian predators, such as the lesser night gecko (*Nactus coindemirensis*), the smallest of the three species of *Nactus* endemic to Mauritius. In November 2022, we translocated 120 lesser night geckos into four soft-release enclosures on Round Island, designed to limit dispersal and prevent predation by native reptiles. Here, we detail the planning process, logistics and post-release monitoring for the translocation. We present our preliminary analysis of survival using capture-recapture models and post-release dispersal for the first six months following release. The preliminary results suggest a monthly survival probability of between 0.7-0.95 dependent on sex and release site, and reduced dispersal over time within the soft-release enclosures. We will explain how this information will be used to inform management of the species and future translocations of prey species to Round Island.

Key words: Reintroduction, Conservation Translocation, Soft Release, Capture-Recapture, Endemic

Thirty years in recovery: efficacy of conservation interventions for the Agile Frog (*Rana dalmatina*) in Jersey

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Evaluating conservation interventions is a vital step in developing evidence to help target conservation action and appropriate allocation of limited resources. Of the various tools available, head-starting and other captive management approaches are often considered during efforts to recover declining amphibian populations. However, these approaches can incur considerable cost, and are not suitable for all species. Across the British Isles, *Rana dalmatina* is found only on the island of Jersey. Anthropogenic pressures led to localised population declines throughout the 1900s, resulting in seven localities remaining by the 1970s, and a single breeding site by 1987e. Recovery efforts have been underway since, utilising multiple management strategies to increase the size and distribution of the population through reintroduction and translocation. We assess the influences of head-starting, spawn clump protection, and climate on annual spawn clump counts as a proxy for population size of breeding females. We discuss the contribution of these management strategies to recovery success, and calculate the return on investment for head-starting. Since 1987, efforts driven by a partnership of the Government of Jersey – Natural Environment, Durrell Wildlife Conservation Trust, and Jersey Amphibian and Reptile Group have, in all likelihood, averted the local extinction of this species. Annual spawn counts have displayed high variability, but have increased from 12 in 1987 to a peak of 159 in 2015. Over the 37 years of recovery efforts, 262 spawn clumps have been head-started, supplying 80,749 young for release at four localities. We conclude that reproductive success has been influenced by environmental variation, and that both head-starting and spawn protection have contributed to increases in annual spawn counts. However, we acknowledge the complexity in attributing population changes to specific management actions where climatic influences also play a role, and highlight the need to consider the benefits and costs of head-starting as an intervention.

Key words: *Rana dalmatina*, ex-situ, in-situ, Jersey, species recovery

Hissing Heathlands

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The loss of heathlands over the recent past has had significant implications for reptiles and amphibians, particularly reptiles. Heathland removal has led to the loss of populations, reduction in population size because of edge effects and inbreeding, fragmentation of metapopulations and has increased distance from potential recolonisers. One of the challenges for rewilding and the recreation of natural habitats is identifying priority areas for management to enhance existing wildlife populations and reduce the distance between habitat patches. This presentation outlines the development of a new Artificial Intelligence (AI) process that identifies heathland areas lost in the last century and indicates where relic patches of heathland may still exist, or where management could recreate a heathland environment. The model was developed through funding from the Natural England Species Recovery Programme and involves the creation of a Deep Learning (AI/Machine learning) GIS system. The Deep Learning process was provided with images of mapped heathland symbols from Ordnance Survey 1:2500 maps between 1906 and 1939 creating an AI system that recognises individual symbols for heathland. The heathland recognition process created an historic map of Surrey heathland, identifying 37% more hectares than manual mapping. Analysis of Natural England's Priority Habitat Mapping within Surrey highlighted 534ha of heathland that was not identified as such on the historic map series. Repeating the process for Hampshire generated a similar set of maps, providing a valuable function for future land management and rewilding. Undeveloped historic heathland locations between existing heathland blocks could be targets for rewilding, enabling re-establishment of reptile habitat as part of the current focus on biodiversity recovery and habitat restoration. Further development could create an extension to the AI process that identifies areas free from permanent development that would minimise gaps between existing heathland habitat, to generate priority targets for restoration.

Key words: AI, heathland, mapping, reptiles, restoration

Evidence-based guidelines for mitigating the impact of roads on herpetofauna- a novel and transparent tool for practitioners

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Road mitigation is urgently needed in Europe due to the high and increasing threat posed by roads for taxa including herpetofauna, but it is vital that this is based on evidence, and cost data where available, to ensure cost-effective decisions. Amphibian road mitigation has progressed substantially and there are now many implemented examples in Europe of designs that can effectively prevent road mortality and ensure safe passage of a generally high proportion of individuals. Important issues remain however on insufficient implementation standardisation, some flawed or untested mitigation designs and poor maintenance, all of which can lead to ineffective solutions. In addition, unclear measures of conservation success and low-quality monitoring continue to hamper learning and quantifying what has worked or not. We used systematic literature searches and expert opinion to produce a guidance document for mitigation to reduce the impacts of roads for amphibians and reptiles based on the best available evidence. This guidance aims to encourage a better approach in relation to the mitigation hierarchy (i.e. avoidance first) as well as for providing pragmatic advice for diverse stakeholders to achieve better mitigation outcomes for herpetofauna. We identify and discuss several areas where the existing evidence is very weak, in particular for reptiles, and discuss research gaps and long-term issues that have not been resolved despite numerous examples of practical implementation. The transparent use of evidence helps ensure that resources are optimised and not wasted on ineffective or even harmful actions, which can demotivate practitioners, funders and policymakers from further supporting the implementation of such actions.

Key words: amphibian mitigation, environmental mitigation, reptile mitigation, road ecology, conservation guidance

Symposium: The Roles of Museums In The Age Of Extinction

Plenary Speaker (s): PATRICK CAMPBELL & JEFF STREICHER

Session chair(s): PATRICK CAMPBELL & JEFF STREICHER

PLENARY

The role of museum collections in 21st century herpetology

PATRICK D. CAMPBELL & JEFFREY W. STREICHER

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Over hundreds of years, the Natural History Museum, London, UK (NHM) grew from a small private collection to a vast storehouse of some 80 million specimens of animals, plants, fossils, and minerals. We present a brief history of the NHM's Herpetology Section and its privileged custodians past and present who have been tasked with caring for and enhancing the collection. Dating from the late 18th century, it is one of the oldest herpetology collections in the world, including important historical collections made by Charles Darwin, Alfred Russel Wallace, David Livingstone, Lionel Walter Rothschild, John D. Godman, Malcolm A. Smith, Frank Wall, Fernand Lataste, Jacques von Bedriaga and many others. The geographical range of the collection is worldwide with historical strengths in Africa, Europe, Arabia, and India, largely in areas that were old British colonies. Along with the world's largest collection of type specimens, it also holds important historical and modern specimens from the Americas and Australia. Hence, the NHM collection is very diverse and ideally placed for serving the scientific community at large in the 21st century. We will cover some of the modern ways in which these collections are being used to study taxonomy, evolution, conservation, global change, materials science, and ecology. Despite these examples demonstrating the relevance of herpetological collections to modern research, we will also highlight several areas of untapped potential. The current role of museums in herpetology will likely increase further as collection accessibility is improved through digitisation and global collaboration.

Key words: Specimens, Preservation, Curation, Natural History, Museomics

Time travel through 20 years of using herpetological collections for DNA sequencing

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This talk summarises our experiences in using herpetological museum specimens for DNA sequencing, and covers the development from Sanger sequencing to the Illumina approaches used today. Even though contamination and the generation of chimerical DNA sequences remain a risk, the advent of NGS short-read technology was a tremendous leap forward and unlocked the majority of historical museum specimens for DNA research, and to a lesser extent, archaeological and subfossil museum material. Our initial studies were based on Sanger sequencing and used painfully reconstructed short historical DNA (hDNA) molecules of crucial museum specimens – i.e., short mitochondrial DNA sequences from types, extinct taxa, or material from inaccessible regions. Today, we are routinely including whole mitochondrial genomes and nuclear DNA sequences from museum material, and recently we released the first genome of a 20-year-old type specimen. Methods developed for sequencing ancient DNA (aDNA) using in-solution hybridization capture and Illumina platforms are excellent tools to process collection material. Now, aDNA and hDNA enable us to study rate or extinct species on a broad scale and to “anchor” nomenclature with name-bearing types. This further allows comparison of the genetic diversity of the same taxon or local population at different temporal horizons to test for recent loss of genetic diversity, an often voiced but rarely proven concern in conservation. In times with increasing legal challenges for collecting and processing genetic samples, museum specimens are also becoming more important in studies of widely distributed taxa.

Key words: Herpetological collections, aDNA, hDNA, Illumina, Sanger

Museomics enabled conservation of the Galapagos giant tortoises

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The Galapagos giant tortoises (*Chelonoidis* spp.) are charismatic emblems of evolutionary biology, and conservation icons. Despite decades of study, new discoveries about them are being made both in the field and laboratory, with the latter thanks to genomic analysis of historical specimens. From confirming the rediscovery of a species thought extinct, to informing captive breeding, museum collections and whole genome sequencing are enabling conservation programs to preserve species and restore the unique ecosystem of the Galapagos.

Key words: Conservation genetics, Taxonomy, Ancient DNA

Solving taxonomic cold-cases with museomics: calling in genetic data from name-bearing types for a revision of cophyline frogs (Microhylidae: Cophylinae)

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Natural history collections represent treasure troves of past biodiversity, housing a wealth of genetic data stored in museum specimens. Thanks to recent advances in the field of museomics, we are now able to access the so-called ‘archival DNA’ from name-bearing types using recent methods adapted to the work with degraded samples, e.g. barcode-fishing and target-enriched DNA sequencing. By assigning sequence data from type specimens to known genetic lineages, we can overcome some typical obstacles hampering taxonomic progress, such as morphologically cryptic species and uncertainties in the allocation of historical species names. We are using state-of-the-art museomic methods to resolve the taxonomy of cophyline frogs, a microhylid subfamily endemic to Madagascar with currently 115 described species classified in nine genera. Half of these species were described only in the last 30 years, and approximately 50 identified candidate species are still awaiting taxonomic description, but are partly locked in species complexes, like the *Anodonthyla boulengerii* complex. In a first approach, we sequenced mitochondrial data for 44 name-bearing types, including the holotype of *A. boulengerii*. Together with newly generated sequences for mitochondrial (12S, 16S3, 16S5, COI) and nuclear (BDNF, CMYC, Rag1) markers from contemporary individuals, we were able to infer a new multi-gene phylogeny for the genus *Anodonthyla* and unravel the *A. boulengerii* species complex. In a second approach, we used a hybrid-enrichment approach to gather 15,000 markers for 141 modern samples, using a universal bait set for anuran species called FrogCap, as well as an additional 4,000 markers for 44 name-bearing types, using a newly established bait set called MuseoFrogCap. All data will be integrated in a broad phylogenomic analysis to tackle the species complexes in question and pave the way for the formal description of the remaining candidate species for cophyline frogs.

Key words: amphibians, museum, barcode-fishing, hybrid-enrichment

Mitochondrial and nuclear DNA from historic museum samples of Asian softshell turtles

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Advances in Next Generation Sequencing (NGS) techniques help us generate better quality genetic data for historic museum samples. Asian softshells are poorly studied and many of the large-bodied species are protected, making the sampling of living specimens nearly impossible. We included five genera of softshell turtles in this study namely: *Amyda*, *Dogania*, *Nilssonia*, *Pelochelys* and *Trionyx*. Historically collected and preserved skeletons, skulls or whole specimens were loaned from five European and two American natural history museums. Additionally, we also included fresh tissue samples stored at the Senckenberg Natural History Collections in Dresden. Fifty-one turtle samples (30 historic and 21 fresh samples) were processed, the historic material in a dedicated aDNA facility. All fresh samples were ethanol-preserved tissues. Eight of the historic samples were stored in industrial methylated spirit (IMS) or ethanol, the rest were dry specimens. Seven of the dry specimens were bones, and 16 were dry tissue and/or nails. The oldest samples included were 75–136 years old. Applying an in-solution hybridisation capture approach with self-made DNA baits from fresh samples of the five genera, we targeted the entire mtDNA and seven nuclear markers (AHR, BDNF, HMGB2, PAX1P1, PSMC, R35, RAG1). We successfully generated mitogenomes with an average coverage above 50-fold for 57% and at least 20-fold for 19% of the historic samples. We obtained all targeted nuclear fragments from 63%, and between five and six fragments from 17% of the historic samples. All except two fresh samples had high quality reads for mitochondrial and all the seven nuclear fragments. In-solution hybridisation capture method has been successfully applied for various organisms in the past and is useful in generating DNA sequence data from both fluid and dry preserved historic samples. Natural history museum collections are an invaluable resource to understand systematic relationships of critically endangered species.

Key words: Asia, historicDNA, Museum, NGS, softshell turtles

On Herpele (Amphibia: Gymnophiona: Herpelidae)

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Of the two named species of *Herpele* Peters 1880, the type, *H. squalostoma* (Stutchbury, 1836) was the first caecilian described from Africa and is well-known by caecilian standards. It has a broad distribution, may be locally abundant, is represented by many specimens in scientific collections, is frequently available in the pet trade, and there are reports of its life history, ecology and of cardiovascular features that are unique among tetrapods. In contrast, the second species, *H. multiplicata* Nieden, 1912, was known only from the brief original description of the unique holotype specimen that, for more than 50 years, was thought to be lost. I recently rediscovered the missing holotype in the zoological collections of the Museum für Naturkunde Berlin, and add to our knowledge of this hitherto poorly known and enigmatic caecilian species. Re-examination confirms the accuracy of the type description of *H. multiplicata*. Micro CT scanning has been used to investigate the osteology of the two species of *Herpele*, revealing that, despite some noteworthy differences, the species are mostly very similar and are almost certainly each other's sister taxa and *Herpele* is monophyletic. Although the holotype of *H. multiplicata* is too old and fragile for extensive dissection, the CT scanning reveals an osteological correlate of the cardiovascular features reported as unique in *H. squalostoma*, providing a clear-cut synapomorphy of *Herpele*. Despite considerable efforts in the field, no further specimens of *H. multiplicata* have been found and that it is extinct is a possibility that merits serious consideration.

Key words: Amphibia Caecilian Systematics Extinction Rediscovery

Bones of a Giant: the osteology of the extinct Cape Verdean skink *Chioninia coctei*

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Chioninia coctei (formerly *Macroscincus coctei*) was one of the largest skinks to have ever lived. In the course of a little more than 100 years it was discovered, ignored, described, forgotten, rediscovered, became a popular zoo and terrarium animal, and became extinct in the wild, with the last living captives straggling into the early 20th century. Despite numerous anatomical studies, no previous researchers have characterised the skeleton of this giant skink in detail. We prepared high-resolution x-ray CT-scans of an adult female specimen in the collection of the Royal Belgian Institute of Natural Sciences in Brussels and conducted a bone-by-bone analysis of the skull and postcranial skeleton. Although similar to congeners and other mabuyine skinks, the skull is particularly robust and the circumorbital elements, especially the jugal, are massive, as is the mandible, which has a very prominent coronoid bone. In the basicranium, the basipterygoid processes are robust and the paroccipital processes are broad. The dentition, as has long been known, is distinctively multicuspid. The axial and appendicular skeleton is consistent with this lizard's presumed rupicolous habits. The specimen we examined was likely part of the large collection of living *C. coctei* assembled in Torino by Mario Peracca in the late 19th century. Like several other modern studies of this species, our osteological investigation was dependent on museum collections, which allow us to extract data from now extinct taxa.

Key words: Scincidae, morphology, skeleton, skull, CT-scan

A review of the house snakes of East and Northeast Africa - a further step to unscramble the *Boaedon fuliginosus* species complex

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In the last ten years, several new species of the genus *Boaedon* were described from Central and West Africa, but the diversity in eastern Africa is also high and remains unresolved. Within the genus *Boaedon* we conducted a molecular study based on 112 mitochondrial 16S rRNA sequences, which revealed 20 monophyletic species-level groups in Africa, five of these in East and Northeast Africa. Using an integrative Taxonomic approach of molecular genetics and morphological methods we described two new species from Ethiopia and Somalia and we confirmed the specific status of *B. arabicus* by molecular-genetic methods. The morphological variation of the recently described *B. montanus* from Central Africa is shown and discussed over its whole distribution area. Moreover, we provide a new country record for Sudan and South Sudan, namely of *B. paralineatus*. Finally, we provide an updated distribution map for all *Boaedon* species occurring in Northeast and East Africa.

Key words: Evolution, Genetics, Morphology, Taxonomy, Reptiles

Ventral scales numbers, anomalies and body mass index in three sympatric snake species within Norway

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Island studies indicate that reductions in genetic diversity may cause altered number of ventral and subcaudal scales in snakes. Today, Norway represents the northwestern distribution border of *Natrix natrix*, *Coronella austriaca* and *Vipera berus* on continental Europe. The post-glacial dispersal of these three snake species into Fennoscandia may have resulted from a few founder individuals able to survive in the northern climate. Extant snakes are larger in size in Norway compared to central and southern Europe. This increase in body size may be caused by a larger number of vertebrae/ventral scales. Our aim is to evaluate whether regional differences in number of ventral and subcaudal scales exist within Norway for the three snake species and make comparisons with other European studies. We additionally test for other regional morphological differences, as the occurrence and number of anomalies in supralabial, ventral and subcaudal scales. We measured, weighed, and photographed snake specimens from museum collections and live snakes. All the scales and anomalies were counted by the first author, and an anomaly-code system was developed based on earlier systems.

Key words: *Coronella austriaca*, *Natrix natrix*, *Vipera berus*

Uncovering the cryptic diversity of "ugly brown frogs" on Borneo

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With around 200 species, the island of Borneo is a hotspot of amphibian diversity. Over the past 16 years, our museum has compiled an extensive collection of anurans from Borneo, including adults, tissue samples and larval stages from numerous localities, which can serve as a broad and solid basis for studies on the evolution of this diversity and its distribution patterns. Species with little morphological differentiation have now been identified in many genera of Southeast Asian frogs, most of which are considered as "cryptic" diversity. A particularly striking example of this phenomenon is the *Limnonectes* "*kuhlii*" species complex, which comprises about two dozen undescribed, genetically highly divergent evolutionary lineages that together form a monophyletic group whose distribution is restricted to Borneo. Using the extensive museum collection, we have found that in many areas two to six of these cryptic lineages occur sympatrically. While some lineages are only local endemics of a mountain range, others are widespread. Even though this is an outstanding example in terms of the number of genetically differentiated lineages, comparable complexes of cryptic species have meanwhile also become known from other genera. The complex interaction of tectonic and climatic changes of the Sunda Shelf and adjacent biogeographical regions over millions of years has shaped the amphibian diversity on this island. Only on the basis of extensive scientific collections can the evolution and distribution patterns of this cryptic diversity be revealed using morphological and genetic data. These results are particularly important for the long-term conservation of this diversity, as the ranges of individual lineages are consequently much more limited, making their potential threat from habitat loss, climate change or random events more likely.

Key words: frogs, phylogenetics, cryptic diversity, museum collection

Symposium: Adapting to A Changing Climate

Plenary Speaker:

KATHARINA WOLLENBERG VALERO

Session chair: KATHARINA WOLLENBERG VALERO

PLENARY

Functional genomics of abiotic environmental adaptation in lacertid lizards (and other vertebrates)

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Understanding the genomic basis of adaptation to different abiotic environments is important in the context of climate change and resulting short-term environmental fluctuations. Using functional and comparative genomics, we here investigated whether signatures of genomic adaptation to a set of environmental parameters are concentrated in specific subsets of genes and functions in lacertid lizards and other vertebrates. We first identify 200 genes with signatures of positive diversifying selection from transcriptomes of 24 species of lacertid lizards and demonstrate their involvement in physiological and morphological adaptations to climate. To understand how functionally similar these genes are to previously predicted candidate functions for climate adaptation and to compare them with other vertebrate species, we then performed a meta-analysis of 1100 genes under selection obtained from -omics studies in vertebrate species adapted to different abiotic environments. We found that the vertebrate gene set formed a tightly connected interactome, which was 23% enriched in previously predicted functions of adaptation to climate, and to a large part (18%) involved in organismal stress response. We found a much higher degree of identical genes being repeatedly selected among different animal groups (43.6%), a higher degree of functional similarity, and posttranslational modifications than expected by chance, and no clear functional division between genes used for ectotherm and endotherm physiological strategies. 171 out of 200 genes of Lacertidae were part of this network. I will also give some further characterisations of these genes' network properties and some examples on how this knowledge could be applied. These results highlight an important role of a comparatively small set of genes and their functions in environmental adaptation and narrows the set of candidate pathways and markers to be used in future research on adaptation and stress response related to climate change.

Key words: Climate adaptation, genetics, genomics, Lacertidae

Reproductive responses of *Rana dalmatina* and *Rana latastei* to drought conditions

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Climate change plays a crucial role in the loss of biodiversity. Severe and widespread droughts are expected in the next few years as a result of decreased precipitation events and/or increased evaporation. Within vertebrates, amphibians are the group showing the largest proportion of threatened species. Water bodies are crucial for their reproduction and prolonged droughts could have a strong impact on amphibian populations. In this study, we investigated the impact of droughts on the reproductive strategies of two brown frogs, *Rana dalmatina* and *Rana latastei*, to unravel whether and how these species responded to a changing environment. We collected data on the number of clutches and number of dry sites in clusters of reproductive sites of these species in Lombardy during a period of 7 years, from 2017 to 2023. We implemented two piecewiseSEM, one for each species, that included several linear mixed models to assess the reproductive strategies of the two-target species against droughts, accounting for the presence of amphibian predators in reproductive sites. Our findings reveal a difference in the response of *R. dalmatina* and *R. latastei* to drought-induced reproductive site scarcity. *Rana dalmatina* skips reproduction when its breeding sites experience drought. *Rana latastei* responds to drought by both skipping the reproduction and selecting other non-dry sites of the cluster. This difference between species is likely attributed to *R. dalmatina*'s avoidance of sites where fishes are present, that restrict its ability to select alternative sites for reproduction during droughts. On the other hand, *R. latastei* does not seem to avoid water bodies with predators. As a result, both species are highly susceptible to the adverse effects of droughts, and we can predict a significant population decline in the upcoming years of expected droughts.

Key words: brown frogs, climate change, philopatry, reproductive strategies, structural equation modelling

The heat is on! Mild winter temperatures increase behavioural response in hibernating wall lizards

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Winter is an important season for reptiles, which can spend over half of their time budget in a dormant or half-dormant state to save energy in a period of low resources. Due to global climate change, winter conditions are becoming more variable and rising at an alarming rate compared to summer temperatures. This raises concerns about the resulting biological disruption. However, the impacts of warming winter temperatures on animal physiology and behaviour remain poorly documented, particularly in the reptiles. We conducted a hibernation experiment using the Common wall lizard (*Podarcis muralis*) to examine the influence of increased overwinter temperatures on body condition and brumation behaviour of temperate reptiles. We collected 39 lizards from Bournemouth (southern England) and brumated them under three different overwintering temperature regimes: a cold winter (4±1°C), a relatively mild winter (8±1°C), and a winter with fluctuating temperatures (5 days at 4°C, 2 days at 8°C). Here we show that body mass loss and reactivity to light and tactile stimuli differ significantly between the three treatment groups. We found that lizards brumating under cold winter temperatures experience greater mass loss compared to other groups. Additionally, lizards are more responsive to stimuli in the mild treatment group. Our findings indicate that a moderate rise in overwintering temperatures could potentially be favourable for certain temperate reptiles. They create conditions that allow wall lizards to be more active and readily emerge from their light-sleeping state to forage and drink. Nonetheless, this higher activity level could lead to faster energy depletion that could affect fitness. Further examination of the effects of warming winters on reproductive output is necessary to draw conclusive findings, which represents the next step of our study.

Key words: reptiles, winter warming, climate change, animal behaviour

Physiological adaptations of Western Mediterranean vipers and their hybrids at contact zones suggest distinct vulnerability to climate change

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Understanding physiological adaptations is required to address species responses to climate change. The Western Mediterranean vipers, *Vipera aspis* and *Vipera latastei*, display parapatric distributions that reflect contrasting climatic niches. Coexistence and hybridization occur in two contact zones in northern Spain. However, knowledge on the physiological tolerances of these species and their hybrids is still lacking. In this study, we aim to compare the eco-physiological traits of both species and hybrids, particularly in a climate change context. We expect *V. aspis* to be cold and wet adapted when compared to *V. latastei* and thus, more vulnerable to the ongoing climate change. First, we compared the eco-physiology of pregnant females of *V. aspis* and *V. latastei* and the hybrids. We used openflow respirometry to measure standard metabolic rate (SMR) and total evaporative water loss (TEWL) and at 15, 25 and 33°C on 38 pregnant females (15 *V. aspis*, 14 *V. latastei* and 9 hybrids). We found that pregnant *V. aspis* have faster metabolic rates at preferred temperature (33°C) than pregnant *V. latastei*, suggesting metabolic cold adaptations. Females *V. aspis* also showed higher TEWL reflecting their elevated metabolic rate. Second, we examined the effects of water deprivation on 161 neonates (54 *V. aspis*, 75 *V. latastei* and 32 hybrids), born from these females. We simulated a short heatwave (14 days) associated with water-deprivation or not. Body size and mass were measured before and after treatment. Water restriction resulted in higher mass loss and slower growth rates but these effects were more pronounced in neonates *V. aspis*. Hybrids showed intermediate responses in both experiments. Overall, our study shows that these species have different physiological adaptations and vulnerabilities to climatic change. Because *V. latastei* is adapted to drier and warmer conditions it should be less susceptible to water and energy constraints imposed by climate change.

Key words: vipers, hybrids, eco-physiology, climate change

Locomotion and physiology depending on temperature in *Xenopus laevis* native and invasive populations

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Ectothermic species are dependent on temperature, which drives many aspects of their physiology. The distribution of native and invasive populations of the frog *Xenopus laevis* is characterised by an exceptional latitudinal and altitudinal range. Along these gradients, the thermal environment changes and populations experience different temperatures. We assessed phenotypes depending on the temperature of individuals coming from six native and one invasive populations. We measured the thermal dependence of locomotor performance in adults given its relevance to dispersal, predator escape, and prey capture. Results show that the thermal performance optimum differs among populations, and the minimum critical temperature varies among populations coming from different altitudes. Then, we compared the standard metabolic rate (energetic cost of organismal maintenance; SMR) depending on temperature, as locomotor performance strongly relies on metabolic activity. We tested SMR in populations from the native range, inhabiting low (South Africa) and high altitudes (Lesotho), and from the invasive range (France). Regarding the contrasting climatic environments of the studied populations, differences in the SMR depending on temperature are expected. We found that populations exhibit different energetic costs in metabolic activity and that populations show reduced metabolic activity in the temperature range the most encountered in their environment (i.e., in cold temperatures for populations from colder environments and in hot temperatures for populations from warmer environments). The ability of this species to change its optimal temperature for locomotor performance and its metabolic activity across extremely different climatic environments may help explain its invasive potential. These findings highlight the extraordinary thermal adaptation ability of the species. This ability to cope with a wide range of variation in environmental temperatures suggests that the species may be particularly good at invading novel climatic areas.

Key words: Locomotion, physiology, temperature, *Xenopus laevis*, phenotypes

Earlier parturition date with warmer summers for smooth snakes (*Coronella austriaca*) in Norway

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The reproductive ecology of smooth snake, *Coronella austriaca*, is poorly understood as mating and parturition rarely have been documented. In Norway, the smooth snake lives on the northern border of its distribution. At these latitudes, it is unknown whether the summers are long enough for the females to mate, fulfil the pregnancy and give birth before hibernation. There are also concerns about how global climate change may influence the reproduction in this rare species. It is red listed but as Least Concern on Europe/Global level, and Near Threatened on National level. This study shows that the Norwegian smooth snakes have an extended mating period, both during spring and autumn. We also report how the parturition date varies with summer temperature. Our results display that deviation from average temperature during July significantly influences the parturition date. In Kristiansand, southern Norway, the birth date was also influenced by average temperature deviations in June and August. The warm and dry summer climate along the southern coast of Norway does forward the gestation period of gravid females and parturitions to mainly August, the same time as in continental Europe. The climate change prognoses along the southern coast of Norway are warmer summers and wetter winters with more heavy rain or snowfall. This study demonstrates that warmer summers may have a positive impact on the female smooth snake gestation period. Further research is needed to evaluate the effect of wet winters on hibernating reptiles.

Key words: Smooth snake, *Coronella austriaca*, parturition date, climate change, mating period

Toads on ice: winter climate change affects the physiology of *Bufo bufo* during reproductive season

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Climate change is causing significant changes to winter conditions, which has important effects on ecosystems. Various organisms, including early spring breeding amphibians, are experiencing shifts in their seasonal activities due to changing winter climates. Consequently, amphibians may face increased metabolic costs due to longer periods of activity and are at risk of being exposed to late spring freezes. In this study, we examined how the common toad (*Bufo bufo*) responds physiologically to warmer winters and spring freezes. To simulate these conditions, the toads were exposed to temperatures of either 4°C or 8°C for 48 hours to mimic warmer winters, and temperatures of either 4°C or -2°C for 6 hours to simulate spring freezes. We measured their standard metabolic rate to understand their daily energy requirements and assessed their body condition under different winter temperatures. Additionally, we analysed the gene expression in their liver and muscle tissues and measured their blood glucose levels to investigate their molecular responses to freezing. Toads acclimated to higher temperatures showed an increased daily energy demand, indicating a faster decrease of their energy reserves during warmer winters. Nevertheless, toads also showed signs of acclimation to warmer temperatures. Frozen toads had higher blood sugar levels, suggesting the activation of cryoprotective glucose with the onset of freezing. Analysis of gene expression patterns revealed changes in genes associated with cellular metabolism. Overall, our findings demonstrate that amphibians have some strategies to cope with the challenges posed by changing winter climates. However, they also highlight that warmer winters and repeated freeze-thaw cycles have physiological costs, leading to reduced energy reserves and potentially posing a significant threat to breeding adults.

Key words: winter climate change, *Bufo bufo*, freeze tolerance, false springs, metabolic rate

Is a changing climate shaping herpetofauna ecology? Using community science to track changes in UK species' phenology

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Temporal advancements in herpetofauna breeding and hibernation cycles in response to climate change have been reported across Europe. A key question is whether phenological shifts are incurring a cost to species fitness in regions undergoing rapid change. To answer this question, long-term studies which track changes in biological cycles and environmental conditions are required. But these are not always available for all species and regions. The UK benefits from a vibrant and sizable herpetofauna recording community, resulting in a plethora of community-contributed data on the occurrence of species across space and time. Meanwhile, advancements in climate modelling have led to the development of sophisticated tools which accurately compute changes in environmental conditions. We made use of these developments to predict phenological changes in populations of UK herpetofauna and the risk of exposure to adverse environmental conditions. Here, we present published data on microclimate-driven trends in *Vipera berus* spring-emergence phenology in Cornwall. Using a mechanistic microclimate model, we predicted adder emergence in response to a suite of environmental cues, with implications for the interpretation of predicted trends. We found evidence for a potential 'climate trap' – a climatically-driven desynchronisation of the cues that determine life-cycle events and fitness later in the season. We found that adders had advanced their phenology towards earlier emergence, but with some populations experiencing a consequential increased exposure to ground frost. Additionally, we disclose preliminary findings from the national natterjack toad monitoring programme which indicate complex variation in the breeding phenology of *Epidalea calamita* over the last decade. These preliminary findings underscore the need for researchers to select biologically meaningful "phenometrics" when assessing herpetofauna phenological responses to climate change.

Key words: spring-emergence, breeding phenology, climate change, microclimate

Unravelling stress and the environment: what contributes to baseline stress markers in the Tenerife lizard (*Gallotia galloti*)

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Understanding how organisms respond to their abiotic environment is critical in predicting population trajectories under climate change. Physiological adaptation is well studied across taxa; however, less is known about the biochemical mechanisms underpinning adaptation. Here, we measured levels of constitutive stress biomarkers, including the molecular chaperones GRP94 and HSP70, and of protein post-translational modifications associated with oxidative stress, such as carbonylation and 3-nitrotyrosine, in tail tips of the lizard *Gallotia galloti* sampled across the heterogenous environments on the island of Tenerife. We found variable expression of GRP94 and levels of protein carbonylation, but not of HSP70 and 3-Nitrotyrosine, across localities. Through iterative model selection, we showed that GRP94 and protein carbonylation levels depend on solar radiation variables and topology. We report, for the first time in a wild animal population, a strong negative correlation between the baseline levels of GRP94 expression and protein carbonylation, which is influenced by lizard operative temperature. This suggests a trade-off between cellular homeostasis and oxidative damage towards environmental adaptation.

Key words: Environmental adaptation, Heat shock proteins, Lizard, Oxidative stress, post-translational modification

Desiccation risk responses in tadpoles of an tropical extreme environment: the inselbergs in colombian Orinoquía

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An environment is extreme when there is a drastic variation in physical factors or when resources have low availability or predictability. The rocky outcrops in South America, known as inselbergs, have exceptionally high and fluctuating temperatures and a marked seasonality in precipitation patterns. On these outcrops, eroded depressions form precipitation-dependent pools. During the rainy seasons, these ponds fill with water and harbour numerous anurans who depend on water to reproduce and survive. These pools are short lasting with very high temperatures, representing extreme environments for amphibian development. One of the expected effects of climate change on these rocky ponds is a reduction in pond duration, but the consequences of this phenomenon on inselberg tadpoles have not yet been studied. *Leptodactylus lithonaetes* is a frog specialised on the rocky outcrops and must cope with the challenging conditions of rocky ponds. We aim to evaluate responses to the risk of pond drying in *Leptodactylus lithonaetes* tadpoles, experimentally manipulating different pond drying regimes. For this purpose, we characterised the biotope of pools in a rocky outcrop in Colombian Orinoquía and evaluated morphological and locomotor responses of *Leptodactylus lithonaetes* tadpoles exposed to different levels of desiccation risk. Our preliminary results show that the water volume of some ponds decreased in just a few days, and water temperatures can exceed critical thermal values of tadpoles, compromising tadpole survival. Simulated pond-drying induced larger size in *L lithonaetes* larvae. In addition, tadpoles at risk of pond drying showed greater maximum swimming acceleration than tadpoles from constant high-water levels. These results are opposed to findings reported for other species, where tadpoles usually respond to desiccation risk by developing faster but attaining smaller sizes at metamorphosis. Our findings highlight the importance of continuing exploring responses to desiccation risk in amphibians, including those already adapted to extreme environments.

Key words: Desiccation risk, phenotypic plasticity, tadpoles, extreme environment, tropics

Oral presentations

Spatial ecology and terrestrial habitat selection of the Green toad (*Bufotes viridis*): the example of slagheaps in Eastern France

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Although most amphibians spend most of their life in terrestrial habitats, batrachological research and conservation has mainly focused on breeding habitat. In France, the Green toad (*Bufotes viridis*) benefits from a National Action Plan. European legislation prohibits habitat destruction, at least without a suitable compensation measure; until now the law was primarily enforced for breeding sites, ignoring an important part of the species life cycle. We conducted a radio-telemetry study which took place between the months of April and October, in two former mining sites in the Grand Est region, where solar farms should soon be constructed. We monitored 26 individuals in La Houve slagheap in 2021 (Creutzwald, Moselle), and 31 individuals in Eugène slagheap in 2022 (Wittenheim, Haut-Rhin). Each toad was equipped with a VHF tag and was located at least twice a week by homing-in with an antenna. Average summer home range was 0.60 ha with a maximum at 4.03 ha. The results showed a non-random selection of refuges characterised by sandy, silty or artificial substrate, sometimes with sparse herbaceous layer. A variety of shelters were used by the toads, most notably micromammal burrows, pre-existing crevices in natural ground or concrete, and self-made burrows in loose substrate when available. An Ecological Niche Factor Analysis was also carried out to characterise the habitat used at a wider scale, which showed a strong preference for artificial and pioneer environments, as the species is renowned for. This study should allow for the integration of the terrestrial compartment of the Green toad into the mitigation hierarchy, especially in the era of the EU Green New Deal, when many renewable energy projects could threaten the remainder of the habitats in eastern France.

Key words: radio telemetry, amphibian monitoring, conservation, habitat use, *Bufotes viridis*

Microhabitat selection of meadow and steppe vipers enlightened by digital photography and image processing to describe grassland vegetation structure

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Understanding animals' selection of microhabitats is important in both ecology and biodiversity conservation. However, there is no generally accepted methodology for characterising microhabitats, especially for vegetation structure. We studied the microhabitat selection of *Vipera* snakes by comparing grassland vegetation structure between viper occurrence points and random points in three grassland ecosystems: *V. graeca* in mountain meadows of Albania, *V. renardi* in loess steppes of Ukraine, and *V. ursinii* in sand grasslands in Hungary. We quantified vegetation structure in an objective manner by automated processing of images taken of the vegetation against a vegetation profile board under standardised conditions. We developed an R script for the automatic calculation of four vegetation structure variables derived from raster data obtained in the images: leaf area (LA), the height of closed vegetation (HCV), the maximum height of vegetation (MHC), and foliage height diversity (FHD). Generalized linear mixed models revealed that snake occurrence was positively related to HCV in *V. graeca*, to LA in *V. renardi* and to LA and MHC in *V. ursinii*, and negatively to HCV in *V. ursinii*. Our results demonstrate that vegetation structure variables derived from automated image processing significantly influence viper microhabitat selection. Our method minimises the risk of subjectivity in measuring vegetation structure, allows upscaling if neighbouring pixels are combined, and is suitable for comparing or extrapolating across different grasslands, vegetation types or ecosystems.

Key words: biodiversity monitoring, habitat selection, Viperidae, visual obstruction reading, habitat diversity

Environmental and anthropogenic factors determining the distribution of amphibian species in the upper Val d’Agri (Basilicata, Italy)

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Amphibians are important components of ecosystems, indicators of environmental health, and important factors in ecological processes. Understanding the factors influencing their distribution is crucial for effective conservation and management. Land use, such as deforestation, agriculture, and urbanisation, can fragment habitats, disrupt connectivity, and reduce suitable breeding sites. The aim of this study is to analyse the environmental and anthropogenic factors that determine the distribution patterns of amphibian species in the Val d'Agri in Basilicata region, Italy. The Val d’Agri area is significantly impacted by human presence, including extensive agricultural fields and oil extraction activities. Moreover, the Basilicata region is the least investigated of Southern Italy in terms of its biodiversity, although it is considered a major Italian hotspot of endemicity of the entire country. To address this knowledge gap and gain insights into amphibian distribution in this area, we recorded breeding activity of 9 amphibian species during repeated surveys in 45 sites, for a total of 330 records. We tested the detection/non-detection probabilities of the species in our sites through the implementation of occupancy models. We then analysed the impact of oil well presence and land use on amphibian distribution accounting for environmental characteristics of the sampling sites. The present work adds relevant information for a better understanding of the ecology and distribution of amphibians in Val d’Agri, a particularly understudied and anthropized area.

Key words: Amphibia, Conservation, Southern Europe, Land use, Occupancy model

Diversity of foraging niches of the Galápagos marine iguanas (*Amblyrhynchus cristatus*)

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Marine iguanas are endemic species of the Galápagos Archipelago where they inhabit all major islands and smaller islets. For most islands, each marine iguana population is characterized by one genetic cluster, except for San Cristóbal Island, where two subspecies (*Amblyrhynchus cristatus mertensi* and *A.c. godzilla*) are present. Marine iguanas are the only lizards worldwide that forage on marine macroalgae, showing special nutritional adaptations. The consumed algae species have been identified previously only by direct observations during feeding activities and microscopic identification in faeces samples. In our study we use a newly established and non-invasive DNA metabarcoding approach to identify consumed algal species from marine iguanas faeces. We developed primers for the ribulose-bisphosphate carboxylase gene and for the nuclear ribosomal 18S gene and applied metabarcoding to faeces samples collected in representative sites from eleven islands of the archipelago. These primers also allowed us to identify collected macroalgae specimens to construct the first DNA reference library of macroalgae from the Galápagos. The first results of our study suggested that the trophic niches between the two subspecies found in the San Cristóbal Island differ with respect to consumed macroalgal taxa and also indicates a clear preference towards red algae as a food item. Despite the fact that the number of consumed algal species did not differ between the two subspecies (OTU richness; $P = 0.383$), diet overlap level between *A. c. mertensi* and *A. c. godzilla* was low (Schoener index = 0.345), suggesting that the subspecies consumed different algal species in their natural environment. Further analyses of our collected data in other Islands from the Archipelago will reveal if other subspecies also differ in their foraging niche and whether such difference of consumed algae reflects disparities in the abundance of algal species between habitats, or whether iguanas of genetically differentiated subspecies prefer distinct algal species.

Key words: Metabarcoding, Galápagos, foraging ecology, marine iguanas.

Do good things come to those who wait? The value of regenerating rainforest on herpetofaunal communities

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Regenerating forest is likely to become the dominant forest type of the future, making it a priority habitat to study. Herpetofauna are an ideal indicator group for regeneration studies, exhibiting sensitive responses to environmental change, yet they are largely understudied. Herpetofaunal communities were continuously sampled from 2012 to 2019 within a regenerating lowland rainforest in the cultural buffer zone of the Manu Biosphere Reserve, Peru. The site has three distinct disturbance histories: completely cleared (CC), partially cleared (PC), and selectively logged (SL); disturbance activities ceased between 1970–80, and now has a contiguous closed canopy. Herpetofauna were sampled at 96 locations using visual encounter surveys (VES) and pitfall traps. We investigated community and trait differences between disturbance histories and assessed the influence of survey methodology and season on observed community trends. A total of 6058 individuals were sampled representing 72 amphibian and 60 reptile species. Mean species richness and diversity was highest in SL, although there was no significant difference between disturbance histories. Community dissimilarity (NMDS) was significant between all disturbance histories, with a clear trend following disturbance severity. Eleven species were found to be indicators of CC, two for PC, and eleven for SL, with SL forest supporting the greatest diversity of reproductive strategies and the only endangered species *Ameerega shihuemoy*. Species richness and diversity was significantly higher in communities sampled during the dry season, and diversity was significantly higher in communities sampled by VES. Community dissimilarity was also significantly different between seasons and sampling methods, however trends between disturbance histories were not influenced by either. These results highlight that forest degradation has serious impacts on herpetofauna, but given the right conditions for recovery, communities follow a trajectory toward similarity with old growth forest and regenerating forests should therefore be protected for their conservation value and potential.

Key words: Regenerating rainforest, disturbance history, community composition, long-term monitoring, indicator species

Estimating population trends from abundance and occupancy data: a comparison

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Temporal trend assessment is the essential prerequisite to identify the causes of change and comprehend how to address and reverse declines of animal populations. To do so, two different categories of data can be used: presence/absence or abundance. Assessing abundance provides a direct indication of how the population size of a species changes over time, making it the most straightforward method for evaluating population trends. Moreover, when species experience declines, it is likely that a decrease in abundance precedes a reduction in their presence over a given area. As a result, trend estimation from presence/absence data may underestimate population declines due to the delay between reductions in population size and local extinctions. However, obtaining accurate abundance measures can be challenging due to difficulties in detecting individuals or the need for labour-intensive techniques, such as capture-mark-recapture. Species presence data, on the other hand, is relatively easier to obtain, because detection probability of the species is higher than detection probabilities of individuals. In this study, we examined the temporal trends of four amphibian species (two frog and two newt species) in Northern Italy using two different approaches: occupancy models, which utilise detection/non-detection data, and abundance models based on counts of egg masses (for frogs) or adult individuals (for newts). Concerning the occupancy models, we found a decline in the occupancy of three out of four species. In the abundance models, however, the 95% credible intervals for the abundance trend overlapped zero for all species. Contrary to our initial hypothesis, the abundance models underestimated population declines, likely due to the requirement for additional data to obtain accurate measures of abundance.

Key words: abundance, amphibians, occupancy, temporal trends

Abundance and conservation status of *Vipera ursinii rakosiensis* in Romania

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Vipera ursinii rakosiensis is listed as endangered under the IUCN Red List and is considered one of the most endangered vertebrate taxa in the Council of Europe area. Previous assessments and action plans for its conservation are outdated, and recent discoveries of populations in Romania indicate the need for updated information. The subspecies face various threats in Romania, including agricultural conversion, overgrazing, burning, and mechanised hay cutting. The magnitude and spatial extent of these threats remain largely unknown. In this study, we surveyed a total of 780 ha across five habitats in Romania and included data from two Hungarian populations and the Danube Delta (*Vipera ursinii moldavica*) for comparison. At each habitat, we conducted surveys in at least four sampling units (100×100 m) on 15 occasions during spring. To estimate abundance, we employed Bayesian n-mixture models. The average density of *V. u. rakosiensis* in Romania ranged from 1.29 to 2.63 individuals per hectare. In Hungary, the average density of *V. u. rakosiensis* ranged from 1.45 to 1.91 individuals per hectare. Comparatively, the average density of *V. u. moldavica* was 4.68 individuals per hectare, indicating a higher abundance in this subspecies. These density estimates suggest higher abundances of *V. u. rakosiensis* at certain sites in Romania compared to Hungarian populations, with the Danube Delta population of *V. u. moldavica* exhibiting the highest density. These findings highlight the importance of continued monitoring and conservation efforts in both Romania and Hungary to ensure the persistence of *V. u. rakosiensis* populations. The reported Favorable (FV) conservation status for *V. u. rakosiensis* in the last Romanian Natura2000 Species assessments raises questions, as the data and decision-making process behind this status remains unknown. This highlights the need for transparent and up-to-date assessments for effective conservation measures.

Key words: abundance, conservation status, Bayesian n-mixture model, Romania

Influence of stream habitat variables on distribution and abundance of tadpoles of the endangered Purple frog, *Nasikabatrachus sahyadrensis* (Anura: Nasikabatrachidae) and implications on its conservation

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Nasikabatrachus sahyadrensis Biju and Bossuyt, 2003, is one of the two extant members in family Nasikabatrachidae, a Western Ghats endemic amphibian family that has evolved independently for around 100 million years. The species has many peculiar morphological features making it well adapted for a subterranean lifestyle. Although an explosive breeder, the species exhibits a lek type mating wherein the males gather and vocalise around seasonal streams, while females approach males at their calling site, form amplexus and then carry males to suitable oviposition sites in the streams. The rheophilous tadpoles of the species have suctorial mouthparts that enable them to occupy an unique microhabitat within torrential streams. Various abiotic factors and biotic interactions help determine the specific microhabitat, which ultimately influences abundance and distribution of a species' larvae in a given habitat. We examined the influence of four stream habitat variables, i.e. water flow velocity, slope of substrate, depth of water column and water temperature, on the distribution and abundance of *N. sahyadrensis* tadpoles. A total of 204 measurements were recorded for all the four variables in 68 marked grids along a 100 m section of two selected streams. Statistical analysis showed that water flow velocity was the best predictor for abundance of tadpoles in both streams. When the number of tadpoles was modelled as a function of each environmental variable, the relationship ranged from linear (w.r.t water flow velocity and water temperature) to unimodal humped curves (w.r.t slope of substrate and depth of water column). The results provide a better understanding of adaptive behavioural strategies of these tadpoles to survive and thrive in this specialised microhabitat. It also highlights the threats posed by dams and reservoirs on tadpole microhabitat as well as puts in perspective the traditional knowledge of indigenous communities related to tadpole consumption practices.

Key words: Amphibia, larva, microhabitat, stream

20-years of collaborative regional amphibian conservation efforts, South Okanagan Valley, Canada (2003 to 2023)

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Canadian Species at Risk policy utilises a collaborative bottom-up governance with habitat stewardship, restoration, education, and outreach at the centre of its priority actions. Amphibian conservation efforts in the South Okanagan Valley fall within the federal multi-species and priority places framework. This biodiversity hotspot is an intensively modified landscape, where wetland and riparian habitat loss exceed 85%. Increasing regional land development, agricultural contaminants, invasive predatory species, and roadway expansion provide a multi-stressor landscape for amphibian species. Research driven conservation efforts since 2003 have had various levels of social and ecological success. Within the valley bottom 74% of discrete wetland sites have less than two of six native amphibian species detected annually. Moreover, absence of reproductive success or low relative amphibian abundance (<10 individuals) is observed among 67% sites. Consequently, a collaborative multi-stakeholder approach to habitat restoration and species recovery was adopted in 2006 through private landowner stewardship. The goal is to increase the quantity, quality, and connectivity of lowland wetland breeding habitat. Twenty-two wetlands have been restored within the study area, effectively doubling the number of available fishless ponds and metamorphic success has been observed in thirteen of 22 restored ponds. Additionally, restoration outcomes include invasive predatory species mitigation for the American Bullfrog (*Lithobates catesbeianus*). The outcome of an adaptive management plan initiated in 2003, has resulted in a single e-DNA hit and no other bullfrog detection since 2011. Habitat stewardship and restoration actions have increased the number of available breeding ponds, engaged landowners, and possibly aided species recovery. Yet, local threats to upland terrestrial and breeding habitat continue to escalate which impedes amphibian movement corridors. The implementation of mitigation fencing along the main highway expansion has reduced mortality, but raises many conservation concerns. Management challenges remain, namely enforcement of wetland protection measures and moving beyond like-minded collaborations and towards targeted stewardship of less motivated persons.

Key words: anthropogenic stressors, monitoring, wetland restoration, invasive species management, road ecology

Rectal parasites, venomous amphibians, or holy creatures? Using social surveys to understand the myths and the ecology of caecilian amphibians in Indonesia

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Caecilians are a secretive, poorly understood group of amphibians, despite their ecological importance. A large part of the reason for caecilians lacking research effort is because most species are fossorial and thus difficult to study. However, local communities are likely to encounter caecilians opportunistically whilst going about their daily business. Unlike many caecilian species throughout the world, the caecilians of Indonesia (genus *Ichthyophis*) are semi-fossorial and semi-aquatic meaning that they are often encountered by people above ground and in water. We exploit this fact to better understand Indonesian caecilian ecology, conservation and local beliefs, by performing a questionnaire-based survey, something which has rarely been done. We surveyed 246 people throughout several regions of Indonesia (Central, East and West Java; Central, South and West Kalimantan; and West Sumatra), with varying backgrounds, living in very different environments. Out of all surveyed regions, people in South and West Kalimantan were better able to identify caecilians; and throughout the survey areas, people in rural regions were best able to identify caecilians. Four people in West Sumatra and two people in Central Java indicated that they think populations of caecilians had declined within the last 15 years, although all of those from West Sumatra were from the same university and so some underlying biases may be present. One of the most common misconceptions of participants was that caecilians were highly venomous. Our study demonstrates the importance of local knowledge and beliefs to understanding species that are generally difficult to study and why questionnaire-based surveys incorporating local knowledge should be more widely used to inform conservation activities.

Key words: Gymnophiona, Amphibian, Questionnaire, Conservation, Local ecological knowledge

Is bigger always better: Will we ever find a "Gape-Limited Snake" in the fossil record?

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Establishing the feeding ecology of fossil alethinophidians is a task hindered by multiple factors: a fossil record lacking diagnostic cranial material, difficulty in calculating ancestral state reconstructions due to a lack of phylogenetic consensus between morphological and molecular data, and a limited understanding of functional morphology within extant taxa. The cranial morphology of the gape-limited non-caenophidian alethinophidians *Anilius scytale* and *Cylindrophis* have been alternately considered as representative of the ancestral alethinophidian condition, or as secondarily adapted for small-gaped feeding from a wide-gaped ancestor. In colubroidean alethinophidians there are multiple independent examples of gape-limited taxa arising from a wide-gaped ancestor. Using these colubroid taxa we test whether modifying the skull from that of a wide-gaped ancestor to a small-gaped feeder leaves a distinct morphological signal across cranial skeletal anatomy and cranial muscle architecture in a morphodynamic context. Using microCT and DiceCT techniques to examine the musculoskeletal system of the alethinophidian snake skull, combined with geometric morphometric analysis and the use of ternary plots, our results produce an inconsistent signal across colubroid taxa, both between and within major clades. Our results suggest there are multiple morphological avenues that facilitate the production of a gaped-limited snake, and that the size and location of soft-tissue systems can greatly alter the functional resultant movement of skeletal elements. We recommend caution to those aiming to describe the functional morphology and thus extrapolate the feeding ecology of fossil taxa, due to the high level of morphological disparity seen within our sample of colubroids.

Key words: Snakes, Colubroidea, Palaeontology, Musculoskeletal anatomy, DiceCT

Filtering for frogs: trials and tribulations for eDNA monitoring in the tropics

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The last few decades have seen alarming declines in global amphibian populations, with some regions such as Central America, being more severely affected. The amphibians of Costa Rica have been especially impacted with 58 of the 221 native species threatened by extinction, 4 declared extinct and a further 18 classified as data deficient. Conservation interventions are reliant on the availability of accurate data concerning the habitat, distribution, and populations of target species. In species-rich regions, with complex topography; traditional surveying techniques can be resource intensive and consequently neglected. The focus of this research is to explore the application of environmental DNA (eDNA) metabarcoding to detect extinct or endangered amphibians in the remote central highlands of Costa Rica. Extensive testing of lab methodologies (i.e. primers) and equipment (i.e. preservatives) was conducted through pilot studies in Manchester Museum, UK, which informed field sampling conducted in Braulio Carrillo National Park in 2022. This is the start of an ambitious project to survey across five national parks in the Área de Conservación Central, Costa Rica in 2023. Through these water samples we will test the field application of filtering techniques and equipment, sample storage and transportation, optimisation of lab methodology, including an exploration of primer efficacy. This development will predicate future large scale monitoring efforts, with the aim to develop a robust methodology that is fit for the realities of field sampling and eDNA-based monitoring of amphibians in the tropics. Results generated from these will be delivered directly to government departments (MINAE; SINAC), researchers, and NGOs responsible for conservation interventions in Costa Rica, to ultimately assist in the protection of some of the rarest amphibians in the world.

Key words: eDNA, conservation, ecology, molecular, metabarcoding

Unveiling cranial diversity and its evolutionary history in a non-adaptive radiation of dwarf geckos

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The evolutionary processes underlying phenotypic differentiation remain incompletely known because of the complexity of possible underlying scenarios. This is even more notable in non-adaptive radiations, in which multispecies clades present high levels of morphological similarity. Accordingly, homoplasy is widespread, and understanding such evolutionary trends becomes a daunting task. We explored the morphological diversity and evolutionary patterns of the skull and inner ear of the gekkonid *Lygodactylus*, using geometric morphometrics on 3D CT-reconstructions for 79 species. Importantly, we found a strong influence of a common allometric trend shaping cranial evolution across the studied species that was fully independent of phylogenetic signal. Additionally, we did not detect the influence of ecological traits on skull shape diversity. This supports the strong developmental constraints on the skull, with cranial structures being unlinked to ecological pressures due to the high evolutionary integration between cranial elements. This is perhaps explained by the multifactorial character of the cranial structures. Consequently, we corroborate that cranial diversity in *Lygodactylus* follows a common pattern in which the speciation processes are the result of vicariant processes (primarily allopatric), in which little or no adaptive processes are involved (i.e., non-adaptive radiation).

Key words: CT-scan, geometric morphometrics, Craniofacial evolutionary allometry, CREA, evolutionary constrain.

Preliminary results of geometric and traditional morphometric analysis of *Rana dalmatina* and *Rana temporaria* tadpoles exposed to polyethylene microplastics

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Microplastic pollution has become one of the most common forms of environmental pollution. However, the impact of microplastics (MPs) on anurans, one of the most threatened animals globally, has been poorly studied. With the aim of assessing the effects of microplastic exposure on the body size and shape of *Rana dalmatina* and *R. temporaria* tadpoles, we exposed tadpoles to a specific concentration of HDPE-MP during their development. Traditional and geometric morphometric methods were used to investigate whether the body size and shape of the tadpoles changed as a result of exposure to MPs. The results showed that there was no significant difference in body size and shape between the tadpoles exposed to MPs and the control group, but the geometric morphometric analyses indicated that there was little change in body shape of the tadpoles exposed to MPs. The greatest difference was observed in the shape of the top of the head and robustness of the body. The explanation could be that the MP concentration or the duration of exposure was low, or that microplastic particles were ingested and egested quickly and therefore had no significant effect on the changes in body size and shape. *Rana* tadpoles are opportunistic feeders and can tolerate MPs in small amounts and in some cases expel them very rapidly. To date, the effects of MPs on changes in body size and shape of tadpoles have not been studied using geometric and traditional morphometric methods, so knowledge is lacking, results are inconsistent, and there is a huge need for further research. Part of this research is immunohistochemical analysis of the digestive system of tadpoles and is in progress.

Key words: Amphibia, larva, development, pollution

Experimental predation of native and non-native fish species on different life stages of common spadefoot toad *Pelobates fuscus* and common frog *Rana temporaria*

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Worldwide amphibian decline has been ascribed to multiple factors, including the presence of invasive predatory fish. Although predatory and non-predatory fish frequently coexist with amphibians, ponds containing fish are less frequently inhabited by amphibians. The rapid proliferation of non-native fish species, coupled with the simultaneous decline of amphibian populations, gives rise to the hypothesis that non-native fish species have an additional impact on amphibian species. Limited knowledge exists regarding the species-specific relationships between fish and amphibians. To investigate species-specific trophic relationships, we conducted ex-situ experiments involving eight fish species, comprising five native (sunbleak, European bitterling, tench, crucian carp, and ten-spined stickleback) and three non-native (stone moroko, pumpkinseed, and eastern mudminnow) fish species, along with two native amphibian species (common frog and common spadefoot toad)., All native fish and amphibian species were obtained from captive-bred sources, except for ten-spined stickleback. Non-native fish were obtained from invasive populations. The experiments were conducted using mesocosms in the Research Center for Aquatic Fauna, part of the Research Institution for Nature and Forest in Belgium. We assessed several effects of different fish species on eggs of common frog and tadpoles of both common frog and common spadefoot toad. None of the fish species had a significant impact on the survival of common frog eggs. However, the impact on tadpoles of both amphibian species varied significantly between the fish and amphibian species. The eastern mudminnow exhibited the fastest and most significant effects on both amphibian species, whereas the European bitterling had no significant effect on either amphibian species. The other fish species had intermediate effects on larval survival. Our findings offer novel insights into the impact of fish on larval amphibians, which has implications for the management of natural habitats where coexistence between fish and amphibians is inevitable or may benefit the wider ecosystem.

Key words: Amphibians, fish - amphibian relations

Negative effects of high concentrations of ammonium nitrate on survival, growth and activity in *Rana dalmatina* tadpoles are not reflected in high avoidance

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Amphibians are often found in agricultural areas, and with their permeable skin, they are particularly vulnerable to chemical pollution, as various pesticides and fertilisers have been found to have negative effects on their survival and development. In this study, we tested how the survival, growth and movement activity in Agile frog tadpoles were affected by increasing concentrations of ammonium nitrate (50, 100 and 200 mg/l). Frog eggs were collected from a wild, non-contaminated site, reared in laboratory conditions, and testing began after tadpoles reached active swimming stages. Tadpoles were measured from photographs at the beginning and the end of the experiments, which lasted 22 days and were conducted in duplicate series using four 25-litre aquariums (c0, c50, c100 and c200), with 30 tadpoles in each aquarium (for a total of 240 tested tadpoles). Aquariums were divided in three sections, and movements across sections were recorded every fourth day. Mann-Whitney U tests revealed no statistically significant differences in study parameters between the two series, so results from both were combined. For mortality, these were as follows: 0 (c0), 11 (c50), 20 (c100), 47 (c200). A Kruskal-Wallis test confirmed the significantly higher mortality in c200 compared to the other treatments and the same tendency was true for size and activity, with tadpoles in c200 significantly smaller and less mobile than the rest. Parallel to these experiments, avoidance tests (in duplicate series) were conducted using a four-compartment linear system with the same increasing concentration gradient and 20 tadpoles in each compartment (a total of 160 tested tadpoles). Tadpole distribution was recorded for a five-hour period and compared between control and test series. Results indicated that tadpole numbers decreased in c50 and increased in c0, but remained stable in both c100 and c200 despite movement between compartments, suggesting difficulty in avoiding the higher concentrations.

Key words: Agile frog, agriculture, experiments, development, fertiliser

Interactive effect of thermic and pollution stress on tadpole gut microbiome

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Endosymbiont diversity positively influences thermal tolerance of their hosts, as well as their ability to deal with other sources of stress. Stressful conditions such as extreme temperatures and pollution, on their turn, are likely to decrease microbiome diversity. We raised 675 *Rana temporaria* tadpoles hatched in water from their natural habitat and posteriorly allocated to combinations of six temperature regimes (18, 22, 26, 28°C, and a fluctuating 18-28°C treatment) and three levels of nitrate exposure (0 – control, 10, 50 and 100 mg per litre of rested tad water). We euthanized tadpoles on developmental stage 38-39 for gut microbiome analyses. Mass and CORT levels were measured as surrogates for health and thermic stress, respectively. A bacterial V4 16S rRNA library was prepared with duplicate PCRs per sample and sequenced with Illumina MiSeq500. Tadpoles kept at 18°C had the lowest microbiome diversity, followed by tadpoles subjected to fluctuating temperatures (FT). Tadpoles kept at 22°C had higher microbiome diversity than tadpoles at 18, 26, or 28°C and grew the most, followed by those at 18°C. The latter, despite a low microbiome diversity, probably had a good growth performance because they were exposed to temperatures like those in their natural habitat, avoiding thermic stress, what is corroborated by their low CORT levels. The interaction between temperature and nitrate concentration on microbiome composition led to more variation within the 18°C treatment, tadpoles in the highest nitrate concentration showing high occurrence of Cyanobacteria and Bacteroidetes. CORT levels increased with temperature, the FT treatment resulting in CORT levels similar to the 18°C treatment. Above 22°C, tadpole growth was inversely related to temperature and CORT levels increased (except for the FT treatment). Our results show that multiple stressors can interact and affect both microbiome composition and diversity in developing anurans, with important implications for their health and growth.

Key words: microbiome, *Rana temporaria*, temperature effects, nitrate pollution, environmental stress

Habitat connectivity inferred from landscape genetic models at multiple spatial and temporal scales in two newt species (*Lissotriton montandoni* and *L. vulgaris*)

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The movement of organisms across landscapes is influenced by multiple environmental variables that are experienced at spatial and temporal scales determined by species ecology. Landscape genetic studies are therefore advised to directly incorporate such processes by analysing the contribution of multiple variables at different scales. Here, we investigate how the analyses of multiple variables at multiple scales improves our understanding of population and habitat connectivity in the closely related but ecologically distinct Carpathian newt (*Lissotriton montandoni*) and smooth newt (*L. vulgaris*). Our results show the importance of forested habitats for maintaining population connectivity in both species, and further support the requirement of open forest for *L. vulgaris* found in previous studies. The negative effect of cropland and urban areas was clear for *L. montandoni*, but almost undetectable for *L. vulgaris*. For both species, models built using land-cover available within distances of ~1 to 2 km predicted population genetic differentiation better than models based on other land-cover scales. This suggests that the amount of suitable habitat available at distances close to the species' maximum per-generation dispersal range is a key determinant of connectivity. Analyses of historical forest data showed that recent (post-1970) forest cover following a major reforestation event was a better predictor of current genetic differentiation. This suggests that deep time lags greater than 40 years (approximately 10 newt generations), are unlikely. Overall, we find that considering multiple spatial and temporal scales has improved our understanding of population and habitat connectivity.

Key words: amphibians, connectivity, landscape genetics, scale of effect, time lag

Broad scale population genetics of the common toad (*Bufo bufo*) in Britain

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Common toad (*Bufo bufo*) population declines in Britain have been reported for decades, especially in southern and central England. The severity of this trend led to a classification of *B. bufo* as Near Threatened in the national IUCN Red List assessment compiled by the Amphibian and Reptile Conservation (ARC) Trust in 2021. Despite recognition of its declines, little is known about the extent and causes, partly due to a lack of extensive demographic surveying of common species when compared to rarer ones. Toad counts performed by volunteer toad patrollers over the years and across the country represent valuable sources of information about population size and trends. However, other important information regarding the demographic, genetic and conservation status of populations are still lacking, as gathering this type of information represents years of data collection and the need for many surveyors at different sites at the same time of the year. Due to the patchy nature of in-depth demographic studies, genetic assessment of populations across the country represents a viable approach to assess population status over a large area in a shorter amount of time. Using a citizen-science based approach, we were able to gather more than 850 genetic samples corresponding to 55 localities across Britain and measured indices of genetic diversity and structuring of populations based on eight microsatellite markers. We will present results of this study which compares genetic diversity with changes to site specific toad population size estimates, which can be used as a proxy for wider scale population health estimates. This approach will provide insights into present and potential future population trends of toad populations in Britain.

Key words: amphibians, population genetics, microsatellites, decline

Population genomics of Galápagos marine iguanas: Seeking footprints of local adaptation and gene flow

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The Galápagos marine iguana (*Amblyrhynchus cristatus*) represents a promising study system for investigating evolutionary divergence. Since its split from its sister lineage, the Galápagos land iguanas (genus *Conolophus*), approximately 4.5 million years ago, the marine iguana has established an archipelago-wide distribution and differentiated into eleven genetically distinct island populations, recognized taxonomically as distinct subspecies. Despite clearly detectable population-level genetic differentiation, the divergence times among the evolutionary lineages of the marine iguana are surprisingly recent. It has been hypothesised that this pattern might be the result of two simultaneously acting but contrasting evolutionary forces: inter-island gene flow and local adaptation within populations. To investigate this hypothesis, we apply low coverage whole genome resequencing to an archipelago-wide population genetic dataset of the marine iguana. First results of this study, reexamining marine iguana population structure, indicate the presence of previously unrecognised genetically distinct lineages within this species, but otherwise support results from previous studies. In addition to characterising the genetic diversity within and among differentiated populations, we aim to identify genomic regions under differential selection, indicative of local adaptation within populations. By investigating the extent of gene flow between populations and identifying introgressed genomic regions, our objective is to elucidate how the interplay of gene flow and local adaptation might have affected the evolutionary history of the Galápagos marine iguana.

Key words: population genomics, local adaptation, gene flow

Utilising genomics to unravel the invasion history of the non-native alpine newt *Ichthyosaura alpestris* in the UK

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The status of invasive species as one of the greatest threats to global biodiversity is well established. Underpinning every successful biological invasion is the invasion process, a complex series of steps which facilitates the transition from introduced, non-native organisms to widespread invasive populations. Population genomics tools are increasingly being employed to investigate the genetic processes and phenomena associated with the process of invasion in these unique populations. Analyses of molecular markers, such as Single Nucleotide Polymorphisms (SNPs), can provide insight into various stages of the invasion process, such as routes of invasion and number of introductions. Invasion genomics also offers an opportunity to study demographic events, such as genetic bottlenecks, as well as evolutionary processes such as inbreeding and adaptation. Furthermore, SNP analyses enables the study of the current genetic structure of invasive populations, which can provide insight into invasion history. More than half of wild amphibians in the UK are invasive or non-native. The alpine newt *Ichthyosaurus alpestris* is native to mainland Europe, and has become well-established at various locations in the UK. Findings from this research provide evidence of clear population structure among UK alpine newts, and also suggest both primary introductions from its native range, and secondary translocations from established sites of invasion. Further SNP-based research is also utilised to investigate other phenomena associated with biological invasions, such as founder size, potential routes of invasion and effective population size. Utilising genomics allows us to describe and determine the various mechanisms that underpin successful biological invasions, and inform management decisions.

Key words: Population genomics, invasive species, invasion history, Single Nucleotide Polymorphisms, RAD-seq.

Genetics and demography of fragmented adder (*Vipera berus*) populations in the Netherlands

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An increased promiscuity and disrupted dispersal patterns are typically found in fragmented, small populations, enhancing the risks of mating with relatives. Low-vagility species like reptiles are especially subjected to stay confined within habitat fragments, suggesting an increase in inbreeding. However, only a few case studies of severe inbreeding depression are currently described in this class, and heterozygosity loss has not been consistently found in small reptile populations. Here, we compare demographic factors to heterozygosity rates and genetic diversity in 3 monitored Dutch populations of the European adder (*Vipera berus*), a philopatric species often restricted to fragmented habitats in Western Europe. A small (n ~ 43), severely isolated population showing a high rate of intercanthal scale anomalies was compared to a small, isolated population showing no signs of inbreeding depression and a non-isolated population part of a larger metapopulation. For each population, Cormack-Jolly-Seber and POPAN Jolly-Seber models were built to estimate sex-specific survival rates and population sizes, from which estimates of yearly heterozygosity loss were deducted according to the minimum viable population theory. These results were juxtaposed to genetic data from 50 buccal swabs collected across the 3 study sites (n = 16–17 per site) and genotyped at 12 microsatellite loci. A disbalanced sex ratio in favour of females and an enhanced mortality in males were highlighted in the small population showing signs of inbreeding depression. These population factors are not expected to be found in the other two populations and are hypothesised to correlate with a loss of heterozygosity. It is therefore expected that males are an overly vulnerable group in some small, fragmented habitats due to their greater dispersal, further exposing such populations to inbreeding. The results of this study are currently being analysed to be presented at the SEH congress.

Key words: inbreeding, heterozygosity loss, genetic diversity, habitat isolation, *Vipera berus*

Divergent population responses following salamander mass mortalities and declines driven by the emerging pathogen *Batrachochytrium salamandrivorans*

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The emerging pathogen *Batrachochytrium salamandrivorans* (*Bsal*) causes dramatic declines in European salamander populations, and is considered a key threat to global salamander diversity. While epidemiological models predict extirpations of host populations, real-life outcomes remain largely uncharacterized. We present a multidisciplinary assessment of the longer-term effects of *Bsal* on wild fire salamander (*Salamandra salamandra*) populations, a highly susceptible European species, by comparing four of the earliest known outbreak sites to uninfected reference sites. Based on large-scale monitoring efforts, we found population persistence at a strongly reduced abundance up to more than a decade after *Bsal* invasion, while a single presumed extirpation was recorded of an initially small-sized population. Post-outbreak pathogen detection meanwhile remained sparse, suggesting limited opportunities for identifying *Bsal*-related declines. Persisting populations furthermore displayed an ongoing scarcity of large reproductive adult individuals, with varying recruitment success. Spatial comparisons indicated variable distribution patterns following recent outbreaks, including persistence of a population remnant in aberrant habitat. Finally, we thus far detected no severe loss of genetic diversity in the reduced post-outbreak populations, and provisionally detected no increased host resistance. Hence, our results reveal diverse population-level responses, offering insights into the ongoing impacts of *Bsal* in the face of a novel amphibian pandemic.

Key words: Amphibian, chytridiomycosis, impact, population persistence, survival

Phoenix from the ashes – hope for the Fire Salamander?

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Since its description in 2014, the chytrid fungus and amphibian pathogen *Batrachochytrium salamandrivorans* (*Bsal*) has spread throughout Europe. The so called “Salamander Plaque” — which is the visible result of an infection with *Bsal* — was detected in salamander and newt populations in the Netherlands, Belgium, Germany, and Spain. It has caused mass mortalities in many infected populations. Typically, populations decline drastically after contact with *Bsal*, to a point at which their survival is jeopardised. This was also the case in several fire salamander populations in the Ruhr-district in Germany (State of North-Rhine-Westphalia - NRW). Here, we report on an unusual case of apparent survival of a salamander population, despite infection with *Bsal*. The “Kruppwald” forest in the city of Essen (NRW) currently harbours a stable population of fire salamanders despite proven cases of *Bsal* infection and some related mortalities. At the same time, neighbouring populations were decimated by salamander plaque-related mass mortality events. We are now investigating the ecology, genetics and population trajectories of fires salamander in the Kruppwald population and in neighbouring populations — alongside data on the presence of *Bsal* —in order to better understand how this population, withstand the impact of this disease. We will consider whether the Kruppwald population might provide a suitable basis for reintroducing fire-salamander populations in the area where mass-mortalities have caused population declines. Under this premise, we aim to investigate whether reintroductions and translocations of fire-salamanders can be successful despite *Bsal*. Herein, we provide preliminary data on this recently started project.

Key words: *Salamandra salamandra*, *Bsal*, reintroduction, conservation

Dynamics of Ranavirus in ecosystem invaded by *Xenopus laevis*

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The African clawed frog, *Xenopus laevis*, is amongst the four most invasive anuran species in the world, having been introduced into several countries, including Portugal where it is the subject of an eradication program. The species is responsible for changing ecosystems, competing and preying on native species, and acting as vectors for emerging pathogens. The species has been indicated as a potential vector for Ranavirus (Rv), a deadly genus of viruses capable of infecting both herpetofauna and fish, and often linked to mass mortality events worldwide. The initial detection of Rv in Oeiras (Portugal), in 2012, indicated a possible link to the current *Xenopus laevis* invasion in these freshwater systems. Resistant species such as *Xenopus* can carry the virus without developing the disease, making it a perfect reservoir. Nevertheless, alternative scenarios of the pathogen's native status have not been tested in systems invaded by *Xenopus*. We assessed the role of *Xenopus* in Rv maintenance in the freshwater systems of Oeiras, while removing the invasive host from the streams. By testing native amphibians and fish in streams with and without this invader, we analysed whether the pathogen was introduced or native to the system. Ranavirus was detected even in streams not invaded by *Xenopus*, and sequencing data revealed a single strain (FV3-like Rv) circulating in the streams, raising the possibility of Rv having native status in this system. Ranavirus prevalence was the lowest in *Xenopus* and did not change with the decrease in host density. These results support the role of *Xenopus* as a reservoir and possible vector for Rv, helping to maintain the pathogen in the system and possibly having an active epidemiological interaction with native species.

Key words: Emerging infectious pathogens, Frog Virus 3, Amphibians, Fish, Eradication

The first report about the spread of snake fungal disease (SFD) in Ukraine

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Ophidiomyces ophidiicola is an emerging fungal pathogen of wild snakes in the USA, which causes lesions of varying severity and in some cases population declines. Given the potential threat posed by *O. ophidiicola* to snakes, there is a necessity to study this pathogen in Europe, including Ukraine. The objectives of the study were to determine the distribution and prevalence of *O. ophidiicola* in Ukraine, as well as to identify the link between the presence of *O. ophidiicola* and infection severity. Methods. Snakes of various species were examined from the territory of Ukraine. Immediately after catching, a standardised swab was collected by swiping several times over the ventral and dorsal side (in duplicate from each snake). DNA was extracted from swabs using Prepman Ultra Sample Preparation Reagent. Following previously established protocols, qPCR was performed by amplifying the internal transcribed spacer specific for *O. ophidiicola*. In the period from March 2020 to November 2021, 132 samples were collected from 66 wild snakes representing 8 species (mostly of the genus *Vipera* and *Natrix* – 45 and 10 individuals, respectively). Skin lesions were present in 25 individuals. Of the nine *Natrix natrix* individuals in the study, seven had visible skin lesions and the presence of the *O. ophidiicola* was confirmed by qPCR. The only doubtful positive sample was obtained from *V. b. nikolskii* without skin lesions. In one case fungus from skin lesion of *V. b. nikolskii* was isolated in culture and identified using ITS barcoding region as *Beauveria* sp. The presence of the pathogenic fungus *O. ophidiicola* in free-living snake populations was detected for the first time in Ukraine, all from the same species – the grass snake. All individuals with confirmed *O. ophidiicola* had skin lesions. Other species of fungi, in our case *Beauveria* sp. can infect snakes too.

Key words: fungal pathogen, snake fungal disease, *Natrix*, *Ophidiomyces ophidiicola*, Ukraine

Feeding habits of the smooth snake (*Coronella austriaca*) and the effect of prey availability on its habitat choice in the Felső-Kiskunság Turjánvidék

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Hungarian Meadow Vipers (*Vipera ursinii rakosiensis*) were common in the Carpathian basin, but most of its populations disappeared; now the main threat is predation pressure. Smooth Snakes (*Coronella austriaca*) are known reptile and viper predators. Since the Smooth Snake is considered common in one of the most important habitats of the meadow viper, I conducted a study to answer the following questions: 1) What taxa make up the food spectrum of the Smooth Snake in the study area? 2) Does the Smooth Snake consume vipers in the study area? 3) Is the control of the Smooth Snake population needed to protect the vipers? We also conducted a study on the habitat choice of the Smooth Snake, with the following question: How does prey availability in the study area affect the density of the Smooth Snake? During the diet study, we captured the Smooth Snakes, then kept them isolated until they defecated, and then released them at their capture sites. Of the 82 captured snakes 58.73% defecated, and the most common prey found in the faeces were lizards (66.67%) followed by mammals (16.67%) and Orthopterans (11.11%). In each case, I found beetles (2.78%) and Smooth Snake remains (2.78%). No viper remains were found. The density of the Smooth Snake in the sampling quadrats depending on the combined and individual density of each prey species, as well as the reptile diversity was calculated with reptile densities estimated from the reptile monitoring data, using a linear mixed model. Based on our results, the occurrence of the Smooth Snake was positively affected by the reptile diversity, while the Eastern Green Lizard's (*Lacerta viridis*) density had a negative effect.

Key words: diet, habitat choice, reptiles, ecology, predator-prey interactions

Reproductive ecology of Western Mediterranean vipers (*V. aspis* and *V. latastei*) in two contact zones in Northern Spain

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Studying the reproductive ecology of species at secondary contact zones is essential to understand life-history strategies and predict population dynamics under anthropogenic change. *Vipera aspis* and *Vipera latastei* are two phylogenetically closely-related Western Mediterranean vipers with parapatric ranges, viviparous reproduction and contrasting climatic affinities. In northern Spain, they are in contact at their distribution limit in two environmentally distinct areas, High Ebro (a natural landscape) and Oja-Tirón (an intensive agriculture landscape), likely experiencing contrasting ecological pressures. Previous knowledge on the ecology of these species was gathered from a few reproductive females in High Ebro and suggested that reproductive effort was different between species. However, how anthropogenic landscape change and inter-annual climatic variation affect the reproductive ecology of females remain unaddressed. Here, we analysed the reproductive traits (pre- and post-parturition) of 91 pregnant females (49 *V. aspis*, 42 *V. latastei*), collected in High Ebro (n = 27) and Oja-Tirón (n = 64). We performed analyses of variance (ANOVA) considering as factors the species, the contact zone, the year and their interaction. Our results confirm that both species differ in the reproductive effort, with females of *V. aspis* showing lower number of newborns than females of *V. latastei*. No evidence of possible negative effects of the agriculture landscape on reproduction was found.

Indeed, the number of stillborn was higher in the females from the High Ebro than in the females from Oja-Tirón. Marked inter-annual variation in female body condition (pre- and post-parturition) and parturition date of females were observed. These patterns reflect annual variation in climatic conditions, with remarkable differences in rainfall and temperature, which presumably affected the annual activity and the resources acquisition of the vipers and, therefore, shaped the reproductive output of both species.

Key words: Anthropogenic landscape change, Iberian Peninsula, reproductive strategies, population dynamics, Viperidae

How much is enough? The role of sampling effort in capture-mark-recapture studies of great crested newt *Triturus cristatus* in Flanders (Belgium)

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High quality monitoring data is crucial to inform conservation decisions. If sampling effort is limited, false results are likely to be drawn. To assess the regional trend of the great crested newt *Triturus cristatus* in Flanders, two fyke traps are placed in each pond twice overnight. To investigate how close, or rather far, this is from a thorough assessment of newt numbers in each pond, we placed four or five fyke traps for sixteen to twenty consecutive days in a total of seventeen ponds across three study sites. Population modelling estimated the investigated water bodies to be inhabited by 4 up to 1794 crested newts, and densities of the species ranging from 0.05 to 2.98 adults per m². Pond size was negatively correlated with the captured proportion of the estimated abundance. For seven of the investigated ponds, stable estimates with stable confidence intervals were only obtained after fourteen or even more consecutive days of capture. While the accuracy required will depend on the research question, we argue that low-effort sampling may be misleading.

Key words: capture-mark-recapture, monitoring, great crested newt, *Triturus cristatus*

Wildlife detection dogs, a viable method to locate great crested newts *Triturus cristatus* at distance and through substrate?

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Detection dogs are increasingly used to locate cryptic wildlife species, but their use for amphibians is still rather underexplored. In this study we focus on the great crested newt (*Triturus cristatus*), a European species which is experiencing high conservation concerns across its range, and assess the ability of a trained detection dog to locate individuals during their terrestrial phase. More specifically, we used a series of experiments to document whether a range of distances between target newts and the detection dog (odour channelled through pipes 68 mm in diameter) affects the localisation, and to assess the ability and efficiency of target newt detection in simulated subterranean refugia through 200 mm of two common soil types (clay and sandy soil, both with and without air vents to mimic mammal burrows, a common refuge used by *T. cristatus*). The detection dog accurately located all individual *T. cristatus* across the entire range of tested distances (0.25 m–2.0 m). The substrate trials revealed that the detection dog could locate individuals also through soil. Contrary to existing studies with detection dogs in human forensic contexts, however, detection was generally slower for *T. cristatus* under sandy soil compared to clay soil, particularly when a vent was absent. Our study provides a general baseline for the use of detection dogs in locating *T. cristatus* and similar amphibian species during their terrestrial phase, particularly subterraneously.

Key words: amphibians, conservation dogs, great crested newts, urodeles, subterranean refuges

Aesculapian snakes (*Zamenis longissimus*) show a preference for anthropogenic features in their introduced range in North Wales

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Understanding the potential success of an animal in novel environments is increasingly important as more species are being introduced by humans outside their native ranges. Introduced species often utilise anthropogenic features present in their environment and demonstrate a higher tolerance towards human disturbance. Aesculapian snakes (*Zamenis longissimus*) are native to mainland Europe. However, they have been introduced in the UK twice, with the population in Colwyn Bay, North Wales, being the northernmost extant population of the species. We studied the spatial ecology of this population by radiotracking twenty-one snakes daily over two years to estimate their home range size and space use requirements. We used Integrated Resource Selection Functions to identify preferences for habitat features for thirteen snakes and Integrated Step Selection Functions to further explore how habitat features influence movement for twenty-one snakes. Additionally, we explored the timing of reproductive activity and identified where snakes spent long periods stationary to identify shelter locations. Estimates for home range and space use varied significantly between individuals and males on average had larger home ranges than females. We found activity peaks during the egg-laying period in females and the mating season in males, with increased mean daily displacement when compared with the rest of the year. Male snakes exhibited habitat generalism, but with a preference towards buildings, gardens, and hedgerows. We were unable to determine habitat preferences for females. Buildings were selected by five of the eight males included in the resource selection analysis as their most frequent shelter sites. Our results show high variability between individuals toward habitat selection and snakes showed a strong preference for buildings, this reliance may be due to this population being close to their thermoregulatory tolerance limit. Snakes likely benefit from the abundance of anthropogenic structures in the suburban Colwyn Bay area.

Key words: Aesculapian snake, spatial ecology, habitat selection, seasonality, home range

Retinas and the early evolutionary history of snakes

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The ecological nature of the origin and early evolutionary history of snakes is much debated. The unusual nature of aspects of the eyes of snakes has been cited as evidence to support competing hypotheses about snake origins, from ancestors that were aquatic, terrestrial burrowing and/or nocturnal. Increasingly strong DNA sequence evidence for scolecophidian paraphyly has recently prompted the hypothesis that the ancestral snake was scolecophidian-like, having small, reduced eyes adapted for fossoriality. The few morphological and molecular genetic studies carried out on scolecophidians thus far do not support this hypothesis, instead suggesting that their visual systems are too derived in their reduction to serve as accurate models for the eye of the most-recent common ancestor of all living snakes. However, few techniques have been applied and taxon sampling has been sparse thus far. We present new data for the eyes of scolecophidians and other non-caenophidian snakes for anatomy, gene-expression and molecular genetics. These data provide evidence of notable visual-system diversity among these mostly burrowing snakes, including surprising patterns of visual-opsin gene co-expression. Our new evidence indicates that the results of previous studies offered a false impression of the degree of visual-system reduction in some lineages. The results remain preliminary, these studies face technical challenges, and sampling remains very sparse, but one interpretation of some of the data is that dedicated fossoriality in the ancestral snake is not so implausible.

Key words: Vision, eyes, Scolecophidia, evolution, visual opsins

Molecular evolution of vision in lizards and snakes

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Squamata, the clade that comprises lizards and snakes, is one of the biggest major lineages among land vertebrates, with huge ecological and taxonomic diversity. Multiple squamate lineages have undergone independent ecological transitions including switching between diel patterns, epigeal to subterranean habits, and land-to-sea lifestyles. However, despite the vast diversity of ecological niches, multiple ecological transitions and over 250 MY of evolutionary history, the study of the visual system of squamates is still poorly understood. Vision is a key sense for many animals, and the evolution of vision plays an important role in understanding ancient ecologies and is part of long debated theories such as the ancestral diel pattern of geckos or the origin of snakes. With the aim of improving understanding of the evolution and function of the squamate visual system, we generated eye transcriptomes and searched published genomes of more than 150 squamate species spanning many major lineages and ecotypes. Our results show multiple vision gene-losses across several squamate lineages, and positive selection in the phototransduction pathway as result of ecological transitions in some squamate lineages. This talk will discuss the evolution of vision among lizards and snakes as it relates to their phylogeny, ecology and exceptional retinal photoreceptor diversity.

Key words: Evolution, Vision, Squamates, Ecological Transition

Recurrent evolution of adhesive skin-secreted defence systems in amphibians

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Animals often develop convergent solutions in response to diverse environmental pressures. One such example involves adhesive secretions that have evolved recurrently throughout the animal tree of life, serving functions ranging from long-term substrate attachment (e.g., mussel byssus) to locomotion (e.g., echinoderm tube feet), to prey capture (e.g., spider silk threads). Among amphibians, a fraction of species has evolved viscous fluid secretions from their skin that quickly solidify into a sticky mass - or glue - which acts as a rapid onset defense mechanism against predators. Although glue secretion for antipredator defense has evolved independently in several distantly related frog families, little is known about the genetic basis of this adhesive system. Here we show that amphibian glues evolved through the recruitment and remodeling of universally available molecular templates. By conducting transcriptomic and proteomic analysis of the skin and secretions of the Madagascan tomato frog, *Dyscophus guineti*, we identified two protein families that are central to its stickiness. Subsequent comparisons with homologous proteins of other amphibians uncovered the genetic changes that led to the parallel evolution of glue in at least two different frog lineages. The selection and repurposing of existing structures for a new functional role demonstrates how animals frequently arrive at similar solutions to an adaptive problem, and highlights the pragmatism and predictability of evolution.

Key words: convergent evolution, bioadhesives, antipredator defence

Walking or hanging: how body shape evolution is moulded by habitat use in lacertid lizards

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Body shape, which refers to the relative proportions of the head, tail, and limbs, plays an essential role in the way organisms interact and survive in their environment. Additionally, the performance of organisms in their habitats can induce selection that leads to different body shapes, as has been well documented in the Anolis lizard radiation. In the Caribbean Anolis radiation, several ecomorphs with different body shapes have evolved due to selection on different habitats. In this study, we use lizards from the family Lacertidae as a model system. First, we divided our species set into two main groups based on their habitat use. The first group is referred to as "terrestrial" for species that spend most of their time on the ground and move horizontally. The second group is called "climbers" for species that exploit the vertical axis, including both vegetation and rocky structures. We test whether locomotor mode results in body shape adaptations at the macroscale across 188 lacertid species. We compare rates and patterns of evolution for seven linear biometric traits. As expected, our results showed discrepant evolutionary patterns for some morphological traits depending on locomotor mode. In the shape of the head a clear pattern of diversifying evolution was observed depending on the way species use the habitat. By contrast, we found support for different evolutionary models for limb length. Consistent with previous observations at the microscale, head height and width are influenced by habitat use; hence climbers exhibit flatter, narrower heads than ground dwelling species. However, despite previous studies demonstrating the benefit of longer hind limbs for terrestrial species, our findings do not support similar patterns for limbs and trunk proportions in lacertids. Additional research will be conducted to determine the relationship between the evolutionary differences discovered among climbers and ground dwelling species and the species' performance capabilities.

Key words: Ornstein – Uhlenbeck, macroevolution, morphometrics, phylogenetic comparative methods, Lacertidae

Resistance is not futile: widespread convergent evolution of resistance to alpha-neurotoxic snake venoms in caecilians (Amphibia: Gymnophiona)

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Predatory innovations impose reciprocal selection pressures upon prey. The evolution of snake venom alpha-neurotoxins has triggered the corresponding evolution of resistance in the post-synaptic nicotinic acetylcholine receptors of prey in a complex chemical arms race. All other things being equal, animals like caecilians (a legless Order of amphibians) are quite vulnerable to predation by fossorial elapid snakes and their powerful alpha-neurotoxic venoms; thus, they are under strong selective pressure. Here, we sequenced the nicotinic acetylcholine receptor alpha-1 subunit of 37 caecilian species, representing all currently known families of caecilians from across the Americas, Africa, and Asia, including species endemic to the Seychelles. Three types of resistance were identified: (1) steric hindrance from N-glycosylated asparagines; (2) secondary structural changes due to the replacement of proline by another amino acid; and (3) electrostatic charge repulsion of the positively charged neurotoxins, through the introduction of a positively charged amino acid into the toxin-binding site. We demonstrated that resistance to alpha-neurotoxins convergently evolved at least fifteen times across the caecilian tree (three times in Africa, seven times in the Americas, and five times in Asia). Additionally, as several species were shown to possess multiple resistance modifications acting synergistically, caecilians must have undergone at least 20 separate events involving the origin of toxin resistance. On the other hand, resistance in non-caecilian amphibians was found to be limited to five origins. Together, the mutations underlying resistance in caecilians constitute a robust signature of positive selection which strongly correlates with elapid presence through both space (sympatry with caecilian-eating elapids) and time (Cenozoic radiation of elapids). Our study demonstrates the extent of convergent evolution that can be expected when a single widespread predatory adaptation triggers parallel evolutionary arms races at a global scale.

Key words: nicotinic acetylcholine receptor, neurotoxin-binding, toxin resistance, Darwinian selection

Egg incubation of some squamate reptiles from the Western Ghats, India

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Most of the contemporary Indian herpetological literature is largely dominated by publications on diversity, evolutionary history, and historical biogeography of the taxa of focus. However, natural history information is poorly documented for many species. Details such as reproduction and parturition are once-in-a-season occurrences that demand long-term or continual monitoring of animals, often in semi-captive conditions that enable close and recurrent observations of those same individuals studied. This necessarily challenging aspect of study translates into either opportunistic and sporadic observations on wild individuals or a well-structured and pre-designed study on captive reptiles. Here, we present our documentation on egg incubation based on observations on nine species of reptiles found in the Northern Western Ghats of India belonging to seven genera and four families i.e., *Ptyas mucosa* (Linnaeus, 1758), *Amphiesma stolatum* (Linnaeus, 1758) and *Coelognathus helena* (Daudin, 1803) from Colubridae, *Python molurus* (Linnaeus, 1758) from Pythonidae, *Hemidactylus murrayi* Gleadow, 1887*, Hemidactylus leschenaultii* Duméril & Bibron, 1836, *Hemidactylus prashadi* Smith, 1935 and *Cnemaspisis goaensis* Sharma, 1976*,* from Gekkonidae, and *Calotes vultuosus* (Harlan, 1825) from Agamidae. Our present study provides information on the oviposition period along with the clutch size ranging from 5–19 in snakes and 2–12 in lizards, selection of oviposition site, incubation period at 25–35 °C ranged from 49–65 days in snakes and 39–55 days in lizards, osmosis in eggs, use of various dripping methods, use of different substrates for incubation, rupturing of eggs, morphology, morphometrics, and behaviour of hatchlings at birth and ecdysis period of hatchlings.

Key words: Breeding, India, Natural history, Oviparous, Reproduction, Reptilia

‘Dragons in the Hills’: engaging citizen science and community action to conserve Northern Ireland’s amphibians and reptiles

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The Common Lizard (*Zootoca vivipara*) is Northern Ireland’s only terrestrial reptile and a priority species under the Wildlife (Northern Ireland) Order 1985. However, it is generally under-recorded and information on its distribution in Northern Ireland is patchy. Northern Ireland’s two native amphibians, the common frog (*Rana temporaria*) and smooth newt (*Lissotriton vulgaris*), are similarly under-recorded across the country. ‘Dragons in the Hills’ is a partnership project with Newry, Mourne and Down District Council (NMDDC), Amphibian and Reptile Groups of the UK (ARG UK), The Herpetological Society of Ireland (HSI), The Mourne Heritage Trust (MHT) and the University of Central Lancashire supported by The National Lottery Heritage Fund. The project aimed to increase understanding and conserve these three native species through community action. The project focused on educational outreach and knowledge-sharing with local schools, communities, volunteers with an existing interest in wildlife, and land managers. The 3 year programme included over 780 local families and 12 schools, reaching over 1,000 children; as well as training over 200 rangers and volunteers in ecological survey and monitoring techniques and amphibian and reptile ecology. Evaluation by the team at UCLan indicates that participants in the study greatly valued the positive impact of project activities on their mental well-being, particularly following the restrictions imposed by the COVID-19 lock down, and enjoyed learning more about their native wildlife. Community scientists recruited to the project were encouraged to combine their local knowledge with the predictions from a habitat suitability model to identify suitable places to search for common lizards. This ‘informed’ process enabled the project team to identify important common lizard sites right across the region, including some that were previously un-recognised. These records will support habitat management work at these new sites, with the support of local volunteers and land managers.

Key words: common lizard, *Zootoca vivipara*, common frog, *Rana temporaria*, smooth newt, *Lissotriton vulgaris*, community science, recording, outreach, education

A geometric morphometric approach to palatal ontogeny in Crocodylia

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During the development and growth process of an animal, it is often observed that different anatomical structures undergo changes in their morphology and relative proportions in a phenomenon known as ontogenetic allometry. In extant crocodylians, their ontogenetic cranial series show an increase in the relative size of the rostral versus postrostral region of the cranium, and changes in the relative size of the orbits, and the shape of the cranial table, among many others. These morphological changes in the dorsal aspect of the cranium are widespread and well documented in the ontogenetic series of most crocodylians. However, the ontogenetic changes that occur in the palate have not been thoroughly characterised and analysed in most crocodylian species. Therefore, the ontogeny of the crocodylian palate was analysed using 2D geometric morphometrics on a sample of 334 craniums from 23 species, ranging from hatchling to adult individual specimens. The morphological changes that occur in the palate throughout ontogeny were analysed and characterised including molecular and morphological phylogenetic frameworks, and the shifts in morphospace occupation and disparity across ontogenetic stages were also analysed. The results show that, contrary to what might be expected from previous ontogenetic analyses in the dorsal view of the cranium, the shape and relative size of the suborbital fenestrae, and the shape of the palatines and their relative position to the suborbital fenestrae are more important than changes in the rostral length of the palate. Furthermore, crocodylian clades occupy distinct areas of the palatal morphospace from early ontogenetic stages onwards, and disparity analyses show an increase in disparity during ontogeny that is heterogeneously distributed between ontogenetic stage shifts. Finally, the analyses between ontogenetic trajectories show that some species have distinct trajectories, and that these differences are more pronounced in some brevirostrine and longirostrine taxa.

Key words: Ontogenetic allometry, ontogenetic trajectories, disparity, Crocodylidae, Alligatoridae

How do lizards talk? Integration of signalling traits in a complex signalling system

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Animal communication is complex. During social interactions, animals display various static and dynamic signalling traits that are mediated by the neuroendocrine system. Across diverse vertebrate species, colour and behavioural displays signal internal quality, dominance, fighting ability and resource holding potential. However, stress that animals experience due to challenging external as well as internal environmental conditions can disrupt homeostasis and shift baseline hormone levels. Change in hormone levels due to stress can directly affect bodily systems producing a range of effects on colour expression and social behaviour. Thus, for an animal to signal effectively during social interactions, the traits involved in generating an optimal communication strategy should be suitably coordinated. In this study, we tested how animals use multiple colour and behaviour traits for communication and whether steroid hormones such as testosterone and corticosterone play a role in expression of these signals. Males of the agamid lizard, *Psammophilus dorsalis*, have elaborate social behaviours involving dynamic changes in body colour and behaviour, along with increase in steroid hormone levels. Using wild-caught lizards, we staged male-male interactions and recorded their responses to quantify behaviour and colour. Blood samples were taken to measure baseline and social interaction-induced hormone levels. We find that some aspects of body colour, i.e. maximum chromatic contrast of dorsal yellow and the size of the UV patch in males, are positively correlated with aggressive behaviour. Despite the range of potential signals, only the dorsal colour of opponents influenced the colour and behaviour of males. Additionally, animals with higher baseline corticosterone levels had less intense dorsal colours, indicating a role of stress in expression of these colours. Overall, we show how multiple signalling traits as well as stress-induced hormone levels can interact in complex communication systems, with consequences for the outcome of an interaction.

Key words: Animal Communication, Social Behaviour, Steroid hormones, Dynamic colour change

Tough life of sand lizard females during the reproduction season

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In prey-predator interactions, the predator primarily targets the population's most common or highly noticeable prey phenotype. Therefore, in organisms with sexual dichromatism, conspicuously coloured males should be subject to higher predation pressure than cryptically coloured females. From the perspective of predation, the conspicuous colouration of males is a handicap, but in the reproductive period, it increases attractiveness to females and discourages rivals. We predicted that the sex ratio would change across age cohorts to the disadvantage of males (the sex at higher risk of predation). Our study investigated whether predation risk and predator escape success in common lizards (*Lacerta agilis*) in their natural environment differed between the sexes. We determined the frequency of tail regeneration and the probability of survival for different sexes and age cohorts. A regenerated tail indicated that an individual had avoided a predator attack. We found a stable sex ratio within age cohorts, a balanced frequency of tail autotomy between sexes, and a similar survival success rate in the study population. However, our results also showed a lower survival probability for females, especially during the egg-laying period. This suggests that gravid females of poikilothermic organisms, in particular, may be subject to even higher selection pressure from eurythermic predators than males with distinctive colouration due to compensatory thermal needs.

Key words: caudal autotomy, CJS model, escape rate, predation risk, reptile

Study on the differences of Body Mass Index between olms found in cave and the ones sampled in spring

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Adaptations to cave life such as blindness, depigmentation and extremely reduced metabolism are key features of stygobiont species (which live in underground aquifers) that should also prevent their survival in surface habitats. Nevertheless, the olm *Proteus anguinus*, a completely stygobious amphibian, has been reported in spring environments. Moreover, our previous results showed that its presence is linked to very specific factors such as hydroperiod and the absence of potential predators. In light of these results, we conducted a study with the aim of verifying whether the *Proteus* benefits from exploiting the trophic resources of spring habitats. Since June 2020 we have sampled 64 springs and 12 caves in the Monfalcone province (Italy), finding a total of 73 specimens (36 in springs, 37 in caves). We photographed, measured, and weighed each individual and then calculated their Body Mass Index (BMI). At the same time, we sampled the macrobenthos community by counting in a 30x30 cm plot each 2x2 m^2 to quantify the trophic resources. Finally, we tested the relationship between BMI, place of sampling and macrobenthos using GLMMs. Our results show that olms found in springs had a significantly higher BMI than those found in caves. Furthermore, the BMI of springs' olms was significantly related to the amount of trophic resources available. These findings strongly suggest that *P. anguinus* does benefit from being in surface environments and that its presence in spring habitats is most probably due to the larger amount of trophic resources available.

Key words: *Proteus*, Cave, Spring, Trophic resources, Ecotones

Microclimate variables deepen our understanding of distributional patterns of five viper species at a contact zone in South-Western Morocco

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Studying the distribution patterns of ecologically similar species at contact zones is key to understanding driving-forces of spatial coexistence and segregation. Ecological niche-based models (ENM) are frequently used for this purpose. However, ENMs are limited by the ability of commonly available environmental variables to capture species-specific biologically meaningful processes. Here, we show the application of ENMs using microclimate variables – developed with biophysical microclimatic models to describe the temperature and humidity experienced by the organisms at their location – to predict the distributions of five North-Western African vipers (*Bitis arietans*, *Cerastes cerastes*, *Cerastes vipera*, *Daboia mauritanica*, and *Echis leucogaster*) in a contact zone at South-Western Morocco. Using Maxent, we analysed 454 occurrences gathered for the five species at 2x2 km and six microclimatic variables, with the major aims of (1) identifying the most important variables affecting species distributions, (2) comparing species responses to these variables, and (3) inferring potential areas of sympatry between species pairs. ENMs allowed the identification of four variables that play a major role in the distribution of the five vipers. Despite their distinct bioclimatic affinities, similar occurrence profiles were found for *C. cerastes* and *E. leucogaster* in the relative humidity of the soil, for *B. arietans*, *C. cerastes*, *D. mauritanica* and *E. leucogaster* in the isothermality of the soil, for *D. mauritanica* and *E. leucogaster* in the average temperature of the air, and for B. arietans and *C. vipera* in the minimum temperature of the air. Extensive areas of potential sympatry were found between some of these species pairs (e.g. *B. arietans – C. vipera*, *C. cerastes – E. leucogaster*), suggesting that ecological mechanisms, other than spatial segregation, must occur to allow vipers to partition niches and coexist. Our microclimate ENM approach stands as a promising way to pinpoint biologically-relevant processes and enhance the study of ectotherms' distributions.

Key words: microclimate model, North-West Africa, niche segregation, spatial coexistence, Viperidae

Anthropogenic and genetic impacts on stress-related traits in the Italian wall lizard (*Podarcis siculus*)

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With the increase of anthropisation, the environmental landscape has undergone major changes, leading to loss of biodiversity. Urbanisation stands out as one of the primary factors affecting the fitness of populations. This process involves land use changes that modify the structure and reduce the quality and quantity of natural habitats. These habitat conditions can induce phenotypic changes due to developmental constraints. Fluctuating asymmetry is a good proxy for developmental instability associated with environmental factors such as habitat disturbance. Additionally, the fragmentation of populations increases inbreeding, which can also affect fitness-related traits. In this study, we quantified the asymmetry of two morphological traits in island populations of the Italian wall lizard, *Podarcis siculus*, in order to assess the impact of resource availability (ecosystem productivity), anthropogenic disturbance (urbanisation) and genetic factors (inbreeding) on the expression of suboptimal phenotypes. We included the degree of asymmetry of femoral pores; as femoral pores are involved in chemical communications; they can therefore provide insights about fitness alterations. Ventral scale asymmetry was also measured to evaluate whether individuals display asymmetry in multiple traits, which would indicate organism-wide perturbations. Generalised linear models revealed a higher asymmetry of traits in urbanised areas with low resource availability. On the contrary, there was no effect of population isolation, although we expected higher inbreeding due to genetic drift in islands distant from the continent to increase population disturbance. We conclude that lizards are likely facing developmental instability in low-resource environments where competition is higher, as a consequence of habitat anthropisation.

Key words: Fluctuating asymmetry, Urbanization, Inbreeding depression, Wall lizards, Aeolian Islands

Does the glucocorticoid stress response make toads more toxic? An experimental study on the regulation of bufadienolide toxin synthesis

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Chemical defence is a crucial component of fitness in many organisms, yet the physiological regulation of defensive toxin synthesis is poorly understood, especially in vertebrates. Bufadienolides, the main defensive compounds of toads, are toxic to many predators and other natural enemies, and their synthesis can be upregulated by stressors including predation risk, high conspecific density, and pollutants. Thus, higher toxin content may be the consequence of a general endocrine stress response in toads. Therefore, we hypothesised that bufadienolide synthesis may be stimulated by elevated levels of corticosterone (CORT), the main glucocorticoid hormone of amphibians, or by upstream regulators that stimulate CORT production. To test these alternatives, we treated common toad tadpoles with exogenous CORT (exoCORT) or metyrapone (MTP, a CORT-synthesis inhibitor that stimulates upstream regulators of CORT by negative feedback) in the presence or absence of predation cues for 2 or 6 days, and subsequently measured their CORT release rates and bufadienolide content. We found that CORT release rates were elevated by exoCORT, and to a lesser extent also by MTP, regardless of treatment length. Bufadienolide content was significantly decreased by treatment with exoCORT for 6 days but was unaffected by exposure to exoCORT for 2 days or to MTP for either 6 or 2 days. Presence or absence of predation cues affected neither CORT release rate nor bufadienolide content. Our results suggest that changes in bufadienolide synthesis in response to environmental challenges are not driven by CORT but may rather be regulated by upstream hormones of the stress response.

Key words: stress response, poison, phenotypic plasticity, corticosterone, HPA axis

The impact of anthropogenic changes on amphibians

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Urbanisation and habitat modification are among the major causes of biodiversity decline worldwide. Urban environments are characterised by changes in land use, the construction of physical barriers, pollution, high density of humans and a particular microclimate (heat island effect). These features are likely to exert selective pressures on species living in urban areas. Morphological traits often reflect adaptations to habitat use because of their impact on performance. Amphibians are particularly vulnerable to landscape modifications because of their reduced dispersal capacity and biphasic life cycle. Here, we used the Common toad *Bufo bufo* and the Palmate newt *Lissotritons helveticus* to study the impact of three types of environments - urban, agricultural, and natural - in the Paris region (France) on morphology, locomotor performance, and immune responses. Our results show significant changes in morphology between habitat types that were associated with changes in locomotor performance No differences in immune responses were observed, however. Our results suggest that habitat modifications impact the morphology and performance of amphibians, likely due to their small size and limited dispersal capacity.

Key words: Urbanisation, amphibians, morphology, performance, immunity

Chemical pollution and oxidative stress in amphibians across life stages

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The release of anthropogenic chemical pollutants into the environment is one of the main stressors driving the global decline of amphibians. Chemical pollutants can disrupt the antioxidant machinery in amphibians, negatively affecting their health and survival. In species that metamorphose, the antioxidant response to pollutants may be life-stage dependent. In this study, we conducted a comprehensive meta-analysis with 85 studies published between 1998 and 2021, aiming to assess the effect of pollutants on the oxidative stress response in amphibians. We evaluated the effect of pollutants on the antioxidant responses across different life-stages (pre-metamorphic and post-metamorphic). Our metaanalysis revealed that pre-metamorphic amphibians produce antioxidant responses in response to pollutants, avoiding oxidative damage. On the other hand, pollutants do not appear to induce antioxidant responses in post-metamorphic amphibians, resulting in oxidative damage. The different types of pollutants (pesticide, metallic element, herbicide) had varying effects on the antioxidant responses across different life-stages. Our findings suggest that the pre-metamorphic stages have evolved a stronger antioxidant response to pollutants compared to the post-metamorphic stages, and these differences may be driven by the different conditions of each life-stage. These findings are important for conservation efforts protecting amphibians. Further research is required to understand the effect of pollutants on amphibians with different life-stages.

Key words: pollutants, amphibians, metamorphosis, oxidative stress, adaptation

Where and When? Determinants of pesticide concentrations in a threatened freshwater turtle (*Emys orbicularis*) in the Camargue wetland, France

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Exposure to contaminants can alter physiological functions of animals, and even their survival, and thus potentially contribute to population declines. Contaminant concentrations, however, are poorly known in freshwater reptiles. We aimed to evaluate the exposure to pesticides and its potential fitness effects in a long-lived freshwater reptile with high site fidelity: the European pond turtle (*Emys orbicularis*). Five populations of turtles were monitored in the Camargue wetlands (France) in semi-natural or agricultural habitats. From 2018 to 2022, we searched for 40 currently-used or recently banned pesticides in plasma samples (330 individuals), as well as in water bodies, sediments, and prey at each site to assess potential contamination pathways. Twenty five pesticides were detected at low frequency and low levels in the plasma of turtles, except for bentazone, an herbicide widely used for rice production, that was prevalent. Bentazone occurrence and levels in plasma depended mainly on the site of capture of the individual turtle, possibly reflecting the hydrologic characteristics and environmental contamination of the site. We also found a strong effect of day of sampling and year: we found consistently higher concentrations in plasma during the period of bentazone application. Overall, water appears to be the main route of contamination for this hydrophilic pesticide for these turtle populations. We also examined the potential correlation between bentazone levels and behaviour, coloration, and physiological state, notably oxidative stress balance and cell blood count.

Key words: Reptile, blood, bentazone, water contamination, ecotoxicology

The impacts of ophidiomycosis on the survival and detection of the barred grass snake (*Natrix helvetica*), at a site in Eastern England

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The emerging infectious disease ophidiomycosis was detected in free-living snakes in Great Britain and the Czech Republic in 2016. This was followed by further detections in mainland Europe, although the impacts of this disease on snake populations within the continent are currently unknown. A population of the barred grass snake (*Natrix helvetica*) in Eastern England has been the subject of a long-term monitoring project since 2015, through the standardised use of artificial cover objects (ACOs). Capture-mark-recapture methods were used alongside disease surveillance, in order to estimate survival, detectability and population size, as well as the impacts of ophidiomycosis. From 2019 until 2021, skin lesions were detected in 29% of snakes, with 86% of these testing rtPCR positive for *Ophidiomyces ophidiicola* DNA. Over the same time period, trauma was observed in 14% of snakes with skin lesions, and 3% without. Using skin lesions as a proxy for ophidiomycosis, on the basis of supporting laboratory diagnostics, from 2015 to 2021 there was a significant negative association between lesions and the apparent annual survival of snakes. Additionally, snakes with lesions had a higher detectability under ACOs than those without lesions. Since the apparent severity of the skin lesions in affected snakes was mild, and there was no evidence of associated debility, the mechanism for the disease to impact snakes may be indirect. We hypothesise that snakes may spend more time basking in the open as a response to ophidiomycosis, which increases their likelihood of predation, compared to clinically healthy snakes. This is also reinforced by the higher occurrence of trauma in those snakes with skin lesions.

Key words: Ophidiomycosis, Reptiles, Snakes, Population monitoring, *Natrix helvetica*

Understanding disease risk in the UK pet trade of reptiles and amphibians

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The wildlife trade is a complex, controversial, and emotive topic that impacts a variety of stakeholders across several sectors and a wide range of species, with one study estimating that it affects one quarter of all extant terrestrial vertebrate species on earth. Despite it being an important component of the wildlife trade, limited research has been conducted on the impact of the exotic pet market. A substantial number and diversity of species, many directly sourced from the wild, are transported around the world as part of this industry every year. Furthermore, there are major concerns associated with the trade of wildlife for pets, with critics viewing it as encouraging poor animal welfare, as a driver of biodiversity decline and a vector for the spread of pathogens and invasive species. Diseases spread through the trade can have serious consequences in terms of welfare and conservation, as observed by the fungal disease such as *Batrachochytrium dendrobatidis* (*Bd*), which has been spread via the wildlife trade, including the pet trade, and it is thought to be responsible for global amphibian declines. Other pathogens such as *Bactrachochytrium salamandrivorans* (*BSal*) in amphibians and adenovirus in reptiles are known to spread via the pet trade. These two diseases have been detected in the UK pet trade and are thought to pose a significant risk to native species if they spread into the wider environment Despite this, there does not appear to be much formal research investigating disease management behaviours and attitudes of reptile and amphibian pet keepers in the UK, though this is vital for planning disease prevention. This PhD research aims to better understand the structure of the pet trade in reptiles and amphibians in the UK, identify disease risks and suggest preventive measures, based on work with key stakeholders.

Key words: disease, captive, pet, biosecurity, trade

Agent-based models to explore Ranavirus infection outcomes in UK common frog populations

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Ranavirus has severely affected Common frog (*Rana temporaria*) populations in the UK. However, mass mortalities and drastic declines are not inevitable, with diverse outcomes to disease introduction documented. One likely reason is a genetic basis to the variation in defence mechanism evolution between populations and individuals. Multigenerational studies into defence mechanism evolution in frogs are limited by both time and feasibility. In the 'real world' we are restricted to comparative studies or laboratory–based evolutionary research using organisms with very short generations. This allows us to study evolutionary changes over quick generational turnovers, however, these short lived organisms are not representative of the relatively long generation time of amphibians, nor their complex immunogenetics and adaptive immunity pathways. One method to gain deeper insight into the causes of varied disease outcomes in UK common frogs is the use of agent-based models (ABMs). To investigate the role ABMs could play in unpicking the drivers behind infection outcomes, I developed a model to simulate UK common frog populations undergoing ranavirosis. These theoretical populations were subjected to a range of host-dependent fitness costs, disease mortalities and transmission rates. The model ran over 400 generations and was able to replicate the patterns seen in nature. Under the range of simulated conditions, populations experienced distinct outcomes; population crashes and population maintenance both with and without disease persistence. These patterns were replicated in the absence of any specific environmental drivers. Given this, the model re-enforces the notion that a host-dependent genetic component is influencing the outcome of ranavirus exposure. The model also shed light on several potential new hypotheses that warrant investigation. Of particular interest is how varying fitness costs of resistance between host populations exert influence over the direction and ultimate outcome of adaptive selection.

Key words: Ranavirus, Agent-based modelling, Amphibians, Disease outcomes

Impact of the Russia’s war of aggression against Ukraine on nature and herpetology

[VIRTUAL]

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Prior to the large-scale aggression against Ukraine, Russia had already occupied territories in Crimea and Eastern Ukraine with rich biodiversity and a number of protected habitats and endemic species, being responsible for all negative processes there. Since the onset in February 2022 the large-scale aggression against Ukraine, because of dense shelling, burning, building of fortifications, pollution by fuel, explosives, and other chemical compounds associated with military activities, has affected natural habitats on nearly quarter of the territory of Ukraine, mainly in the South and East, but also North of the country, including the protected areas and Chernobyl exclusion zone. The most catastrophic event so far took place in the lower course of the Dnipro River, where due to explosion of the Kakhovska HPP Dam ca 18 km3 of the discharged water temporarily flooded approximately 600 km2 of marshes, sandy dunes, steppe, and floodplain

forests, including the territory of the Black Sea Biosphere Reserve, several Natural Parks, an entire range of the relict populations of the Danube crested newt and the pool frog in the Dnipro delta. The resulting discharge of fresh water has brought a never-seen-before amount of rafting individuals of frogs, newts, turtles and snakes to the North-Western shore of the Black Sea. While the full consequences of it are yet to be evaluated - drastically changed hydrological regime will impact at least 5,000 km2 of land ecosystems (including the flooded and dried-up zones), we urge that lack of funding, deterioration of the scientific collections, disruption of conditions in research centres, especially on the occupied territories, hamper monitoring and mitigation measures as well as careful accounting of losses. We call SEH to take leadership among specialised zoological scientific communities to employ authority of its committees and fellow members in assisting Ukraine in i) documenting consequences of war on herpetofauna and ii) herpetological collections' preservation.

Key words: War, herpetofauna, Ukraine, conservation

Swiss reptile Red List - monitoring of 303 square kilometres to evaluate the decrease of species distribution

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A revision of the Swiss Red List for reptiles was conducted after a first publication in 1994 and a second version in 2005. In order to provide comparable data, a study design consisting of three visits (2 hours per visit) over 303 square kilometres was repeated between the last two Red lists. Consequently, we were able to directly assess the loss of species occurrence over a 14-year period. Moreover, the regular observation conducted by volunteers all over Switzerland allowed us to estimate the surface of occupancy (EOO). Additionally, the impact of global warming was evaluated on the most cold-tolerant species. We detected a strong reduction in species detection for most snake species, even more marked for the smooth snake (*Coronella austriaca*: -62.2% corrected over 3 generations), the Grass snake (*Natrix helvetica*; -56.3%) and the Asp viper (*Vipera aspis*: -58.6%). The observed reduction is broadly similar in all biogeographical regions. Overall, the threat levels of the new Red List are very similar to the previous ones, with about 80% of the species being considered as threatened in Switzerland, expected for the Grass snake and the smooth snake which display a more severe level (VU instead of EN). The common lizard is also now considered as near threatened (NT) due to future reduction of its population induced by climate warming. However, the relative stability in Red List status cannot be regarded as stability in population size or species distribution, but as stability in the rate of reduction. In our opinion, the reduction is mainly due to habitat loss and a reduction of the quality of the remaining habitats. We hope that these results will encourage the Swiss Confederation and the local authorities to take action to improve the remaining habitats and connectivity for future recolonisation.

Key words: Swiss Red List, Conservation, threatened species, population reduction, global warming

Four decade decline of a widespread amphibian in Britain and Switzerland

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Common species are disproportionately important for ecosystem functioning due to their biomass and trophic chain contribution, but are inherently difficult to monitor at sufficient spatial and temporal scales. As a result, widespread species, especially small-bodied ones such as amphibians, can suffer undocumented declines for decades. We used volunteer collected data as part of Toads on Roads initiatives that have long been operating across Europe including Britain and Switzerland to verify multi-decadal population trends for the two most recorded amphibian species. Previous analyses up to 2013 indicated severe declines in both countries but since then common toads have attracted conservation attention. In 2013–2021, volunteers moved an average of 80,000 common toads *Bufo bufo* across the road every year in Britain and 88,000 in Switzerland as well as 74,000 common frogs *Rana temporaria* and smaller numbers of newt species, in an effort to protect them from road traffic mortality. Overall, we included over 1.5 million records from Britain spread across an average of 80 populations per year and over 4 million across 86 populations in Switzerland. Despite some significant regional recoveries since 2013, toads declined in all decades since 1985 in both countries, with estimated overall 41% and 33% reductions since these counts began. Such profound declines threaten the viability of smaller populations as well as the metapopulation structure at the landscape level. The impacts generated by such large-scale and ongoing declines in a common species remain poorly understood in terms of cascade effects but require urgent attention.

Key words: amphibian decline, common toad, citizen science, *Bufo bufo*, volunteers

Shedding light on diel patterns: extinction risk and daily temporal activity of European amphibians

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Sympatric species, despite coexisting in the same geographical location, are still capable of exploiting resources differently from one another by concentrating their peak activity across a specific section of Earth's diel cycle. In fact, species have evolved activity patterns that can be diurnal, nocturnal, crepuscular or cathemeral, with the latter defining those that can be active both at day and night. Consequently, species have selected physiological and behavioural traits to withstand environmental conditions in each diel niche. The implications of these adaptations on extinction risk of vertebrate species are gradually gaining importance in the literature, although ectotherms, specifically amphibians, have remained neglected in comparative studies of extinction risk. Here, I predict that correlates of extinction will differ among diurnal, nocturnal and cathemeral species of 58 European amphibians, also providing a ranking of the most threatened diel group based on IUCN assessments. Seven life-history traits were obtained together with environmental parameters and indicators of human activity. Using phylogenetic comparative methods, I tested these factors to identify correlates of extinction risk for European species and for each diel group. Nocturnal species were ranked as the most threatened across Europe, followed then by diurnal species. In the comparative analyses, European species resulted generally threatened by small geographic ranges, with solely aquatic species resulting as the most vulnerable. Diurnal species status depends on habitat fragmentation and small size, although investigations were limited by small sample size. Extinction of nocturnal species is instead determined by higher UV radiation and temperatures. Finally, declines of cathemeral species are linked to low fecundity and higher annual precipitations, the latter implying a connection to rising *Batrachochytrium dendrobatidis* infections. Diurnal and nocturnal amphibian species should receive conservation priority. Species may shift towards cathemeral habits as threats linked to human activity increase, although limited ranges and infections may still cause declines.

Key words: amphibians, extinction risk, diel activity, phylogenetic comparative method, cathemerality

The unique forest and montane herpetofauna of Ethiopia

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Sometimes called the Roof of Africa, Ethiopia has extensive areas of land above 2000 m altitude and large rainforests in the south. However, the herpetofauna of these areas is unlike anywhere else in Africa. This presentation will give a glimpse of this unusual fauna, suggest how it has formed and briefly discuss its problematic future. The author was resident for 12 years in Ethiopia, and travelled widely, visiting and collecting in a range of habitats, under the auspices of, and with a permit issued by, the University of Addis Ababa. In most areas, collecting was by general herpetological searching, occasionally involving local help. However, in one specific highland area, a team of local enthusiasts was trained and equipped with collecting equipment and visited every few weeks to examine the specimens collected. This enabled a picture to be built up of the local reptile fauna, and a new snake species was found and described. This project ran for eight years. A representative spirit collection was deposited at the University of Addis Ababa.

Key words: Ethiopia, forest, montane, herpetofauna

Spot(s) on: Are larger spots more effective against predation in an aposematic amphibian?

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The interactions between predators and prey often give rise to an ongoing arms race, which can be further influenced by environmental factors. The European fire salamander (*Salamandra salamandra*) is known to possess a distinct black and yellow warning coloration, along with toxic skin secretions, serving as an aposematic signal that protects them from predator attacks. Previous research using clay models has revealed that individuals with a higher proportion of yellow coloration on their dorsal area experience fewer attacks. Building upon this knowledge, we conducted an experiment using clay models of juvenile fire salamanders, being a more vulnerable lifestage. Each model had an identical amount of yellow coloration but differed in the distribution of the yellow colour (3 large spots vs. 12 small spots). The objective was to investigate how the distribution of yellow dorsal coloration influenced predator attack rates. We deployed these models in two distinct forest zones within the Biosphere Reserve Wienerwald, which varied in terms of protection status and human impact (protected vs. managed zones). The models were left along a transect for a duration of four days. We meticulously recorded all "predation" attempts based on the marks left on the models and made note of the predator type (bird/mammal/rodent) whenever possible. Our data indicate that neither colour distribution nor forest type significantly impacted overall predation rates. However, we found a higher occurrence of bird attacks in the managed forest zones as opposed to the protected zones. Thus, our results suggest that the distribution of yellow coloration does not influence predator attack rates in juvenile fire salamanders and that predator communities differ between the two forest zones likely due to variations in disturbance regime.

Key words: predator-prey, aposematism, fire salamander, clay models

Different body size, sexual size dimorphism, and reproductive strategy in two populations of the smooth snake *Coronella austriaca* Laurenti 1768

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The smooth snake is widely distributed in Europe. This species shows regional differences in body size, being smaller in southern and western populations and larger in northern and eastern populations. Morphometric and reproductive data were collected in the Oslo area, Norway and in the Northern Pindos Mountains, Epirus, Greece. Mean total length of reproducing females is nearly 50% larger and mean body mass is 300% larger in Norway than in Greece. Mean litter size is 200% larger in the Norwegian population. Females outgrow males in Norway, but no sexual size dimorphism is seen in the Greek population. Norwegian females show delayed sexual maturation and continued growth in adult animals. The significance of potential environmental factors explaining the observed body size differences will be briefly discussed during the presentation. Neither genetic clade affiliation nor any single environmental factor seems to explain the substantial difference in body size. Most likely the observed body size difference is a result of different life-history strategies.

Key words: Colubridae, intraspecific variation, morphology, smooth snake, body size differences

Individual behavioural variation of juvenile Hungarian meadow vipers (*Vipera ursinii rakosiensis*)

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The Hungarian meadow viper (*Vipera ursinii rakosiensis*) conservation program started captive breeding of the species in 2004. Over the past years altogether over 4300 vipers were born in the Hungarian Meadow Viper Conservation Centre and over 700 vipers were released to ten habitats in Kiskunság and Fertő-Hanság National Parks in Hungary. As captive environments affect development of individual behaviour and through future survival of reintroduced vipers, we decided to test different variables with the intention to fine-tune future captive breeding techniques. In a controlled study post-release behaviour in seminatural enclosure, origin and sex of the vipers and structural diversity of the captive environment was tested on 48 juvenile vipers, representing 12 families. Vipers were kept in small or large indoor terraria, or small outdoor terraria individually after birth in August 2021. Those in indoor terraria were continuously fed over the winter. In the end of May 2022 they were translocated to large outdoor terraria individually. The vipers' behaviour was observed in a standardised way: recording their position, posture, external body temperature every hour over the whole day at least once a week over a four week period. Consistency of individual behaviour was tested by using R-statistic. We detected differences between sexes and various origins, showing slower adaptation to new environments by those who spent their early life stages in indoor conditions, and females tending to be slower in reacting to changing environmental conditions.

Key words: Hungarian meadow viper, captive breeding

A ‘telescopic’ perspective on amphibian behaviour through the use of bioacoustics: A case study of the harlequin tree frog (*Rhacophorus pardalis*) from Borneo, Malaysia

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Acoustics are the primary mechanism through which amphibians communicate amongst themselves, and early amphibians are considered the pioneers in vocalisation. A variety of behavioural contexts may be conveyed through often subtle variations in bioacoustic patterns. Recording and subsequent analysis of sound can thus yield proof of species-specific traits. In this study, an analysis of the vocal repertoire of the Harlequin tree frog (*Rhacophorus pardalis*) from Borneo, Malaysia was conducted. The study encompassed two focal objectives. The first aim was to represent a detailed account of the vocal behaviour of the species, a tree frog distributed across south-east Asia (from Thailand, Malaysia, Indonesia, the Philippines and Brunei Darussalam). The second objective was to document individual variation in calling behaviour and possible effect of temperature, as well as frog mass and body condition. A total of 471 calls from 10 males were analysed for this study. The males showed a complex vocal repertoire and produced three distinct call types, two non-pulsatile calls (Type I and II) and one was pulsatile call (Type III). These three call types can be distinguished based on temporal as well as spectral call properties. The call spectra of the three call types can be characterised by 2–3 dominant frequency peaks. The spectral properties of Type I, Type II and Type III calls were correlated with mass and body condition, while temporal properties (call duration and call rise time) of only Type III calls were found to be correlated with temperature. Despite its Least Concern threat category according to the IUCN Red List, the population of this species is in rapid decline due to habitat fragmentation and other anthropological disruptions. Given the scenario, bioacoustics can act as a non-invasive tool for prompt species identification and population monitoring, aiding in their conservation and management.

Key words: Anura, Behaviour, Communication, *Rhacophorus*, Borneo

Independent origin or single dispersal? phylogenetic study supports early Cenozoic origin of three endemic Indo-Sri Lankan lygosomine (Reptilia, Scincidae) skink genera

[VIRTUAL]

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The Western Ghats-Sri Lanka biodiversity hotspot is home to three endemic Lygosomine skink genera- *Kaestlea*, *Ristella*, and *Lankascincus*. Phylogenetic reconstructions in the past have suggested a sister relationship between the Western Ghats endemic *Ristella* and the Sri Lankan endemic *Lankascincus*, while the placement of *Kaestlea* has been uncertain. We reconstructed a global, genus-level, multi-locus phylogeny of the sub-family Lygosominae using six genes (three mitochondrial and three nuclear) to ask if these endemic genera share an immediate common ancestor, i.e., did they arise from a single dispersal event? Furthermore, to understand the possible centres of origin and dispersal routes of these three genera of Indo-Sri Lankan skinks, we construct a time-calibrated phylogeny and perform ancestral area reconstruction. We find that *Kaestlea* does not share an immediate ancestor with *Ristella* + *Lankascincus*. Therefore, their presence in the Indian subcontinent results from two independent events. The lineage leading to *Ristella* and *Lankascincus* likely originated during the early Eocene in a landmass comprising India + Southeast Asia, while that of *Kaestlea* had its centre of origin in the Southeast Asia + Sino-Japanese landscape, during the late Paleocene. Our molecular dating and ancestral area reconstruction analyses add further evidence of Eocene land connections between the Indian subcontinent and Asia. It also reveals that these skinks were some of the earliest lizards to disperse into the Indian subcontinent.

Key words: Indian subcontinent, endemic, Lygosominae, multi-locus phylogeny, early Cenozoic

Diversity and biogeography of South American mud turtles elucidated by multilocus DNA sequencing (Testudines: Kinosternidae)

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Kinosternon is the most speciose genus of extant turtles, with 22 currently recognized species, distributed across large parts of the Americas. Most species have small distributions, but the ranges of *K. leucostomum* and *K. scorpioides* span from Mexico to South America. Previous studies have found discordance between mitochondrial and nuclear phylogenies in some kinosternid groups, with the current taxonomy following the nuclear-based data. Herein, based on extended molecular, geographic and taxonomic sampling, we explore the phylogeographic structure and taxonomic limits for *K. leucostomum* and the *K. scorpioides* group and present a fossil-calibrated nuclear time tree for *Kinosternon*. Our results reveal contrasting differentiation patterns for the *K. scorpioides* group and *K. leucostomum*, despite overlapping distributions. *Kinosternon leucostomum* shows only shallow divergence across its range, whereas the *K. scorpioides* group is polyphyletic with up to 10 distinct taxa, some of them undescribed. We support the elevation of *K. s. albogulare* and *K. s. cruentatum* to species. Given the deep divergence within the genus Kinosternon, we propose the recognition of three subgenera, *Kinosternon*, *Cryptochelys* and *Thyrosternum*, and abandon the group-based classification, at least for the *K. leucostomum* and *K. scorpioides* groups. Our results show an initial split in *Kinosternon* that gave rise to two main radiations, one Neartic and one mainly Neotropical. Most speciation events in *Kinosternon* occurred during the Quaternary and we hypothesize that they were mediated by both climatic and geological events. Additionally, our data imply that at least three South American colonizations occurred, two in the *K. leucostomum* group, and one in the *K. scorpioides* group. Additionally, we hypothesize that discordance between mitochondrial and nuclear phylogenetic signal is due to mitochondrial capture from an extinct kinosternine lineage

Key words: Biogeography, Central America, Kinosternon, Molecular clock, Reptiles, South America

Recurrent introgression and multiple waves of colonization: the puzzling biogeographic history of a North Palearctic disjunction in *Salamandra salamandra*

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The climatic oscillations of the Quaternary have often produced biogeographic histories marked by cycles of range contraction/expansion and local extinctions, but also complex distributional patterns shaped by recurrent introgression. Disjunct distributions (closely related taxa occurring on both sides, but not within, a geographically intermediate area) allow unpuzzling the biogeographic history of a particular region by providing clues on ancestral ranges and relationships between geographically distant populations. In this work we reconstruct the biogeographic history of a disjunctly-distributed clade of the European Fire Salamander (*Salamandra salamandr*a). This clade is represented by two subspecies in the Iberian Peninsula (*S. s. bernardezi*/*fastuosa*), continuously distributed across the Cantabrian Mountains, and one disjunct subspecies (*S. s. gigliolii*) in the Apennine Mountains of the Italian Peninsula. This clade constitutes a remarkable biogeographic model due to its high reproductive, morphological and colour variability. Conversely, a single lineage, *S. s. salamandra*/*terrestris*/*gallaica*, from a sister clade, occupies all intermediate regions in Central and Eastern Europe and most of the northern and western Iberian Peninsula. By integrating phylogenomic relationships with high spatial resolution sampling of mitochondrial diversity and paleoclimatic distribution modelling, we reconstruct the biogeographic history that led to the current Cantabrian-Apenninian disjunction. Molecular and paleoclimatic evidence suggest expansion out of Iberia and colonisation of the rest of Europe via multiple waves. Ancient processes of stepwise colonisation drove the Cantabrian-Apenninian disjunction, followed by local extinction of intermediate populations and subsequent diversification of Iberian and Italian populations over time. Conversely, the colonisation of Central and Eastern Europe was found to be the result of rapid, recent expansion, which likely started during the early- to mid-Holocene, associated with low levels of diversification. Recurrent introgressive processes between both clades likely shaped the diversification in the Cantabrian-Apenninian clade of *S. salamandra*, highlighting the need for complementary sources of information when addressing complex biogeographic processes.

Key words: Salamandra, biogeography, disjunct distributions, paleoclimatic oscillations

Populating a continent: phylogenomics reveal the timing of Australian frog diversification

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The Australian continent's size and isolation make it an ideal place for studying the accumulation and evolution of biodiversity. Long separated from the ancient supercontinent Gondwana, most of Australia's plants and animals are unique and endemic, including the continent's frogs. Australian frogs comprise a remarkable ecological and morphological diversity categorised into a small number of distantly related radiations. We present a phylogenomic hypothesis based on an exon-capture dataset that spans the main clades of Australian myobatrachoid, pelodryadid hyloid, and microhylid frogs. Our time-calibrated phylogenomic-scale phylogeny identifies great disparity in the relative ages of these groups which vary from Gondwanan relics to recent immigrants from Asia and include arguably the continent's oldest living vertebrate radiation. This age stratification provides insight into the colonisation of, and diversification on, the Australian continent through deep time, during periods of dramatic climatic and community changes. Contemporary Australian frog diversity highlights the adaptive capacity of anurans, particularly in response to heat and aridity, and explains why they are one of the continent's most visible faunas.

Key words: Anura, Gondwana, phylogenetics, biogeography

Diversification patterns of the Palearctic True Frogs (*Rana*): climatic and morphological evolution of two parallel radiations

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True frogs of the genus *Rana* comprise more than 100 recognized species widely distributed across Eurasia and America. This group is divided in two sister clades that are geographically separated, constituting two independent parallel radiations. Although the spatiotemporal dynamics of lineage diversification of *Rana* species are currently well described, little is known about how and to what extent phenotypic traits have evolved in each radiation. Here we gathered phylogenetic, morphological, climatic, micro- and macrohabitat data for 74 species of *Rana* to compare phenotypic and ecological evolution between the two radiations. We then used phylogenetic comparative methods to identify which factors have played a major role in the phenotypic diversification patterns between the two radiations across large spatial and temporal scales. We found that, coupled with their faster lineage accumulation, American species showed higher overall morphological disparity through time and accelerated rates of body size evolution in some subclades. By contrast, Eurasian subclades followed a general pattern of Brownian Motion phenotypic evolution, with slower and constant rates of body size diversification through time. In addition, both radiations exhibited contrasting patterns of climatic niche evolution: American species seem to be ecologically more uniform, while Eurasian ones have accumulated higher diversity, in an apparently random manner. Shared ancestry does not explain the morphological differentiation within American species but, since several climatic descriptors were significantly associated with all morphological variables, the greater diversification of this clade could be the result of adaptive radiation. This was not the case of Eurasian species, where phenotypic variation was distributed as expected by their phylogenetic relatedness. Overall, contrasting patterns of lineage diversification, morphological diversity and climatic niche evolution highlights the different evolutionary trajectories that the two parallel radiations have undergone over distinct geographical areas at the same temporal frame.

Key words: parallel radiations, true frogs, morphological disparity, phenotypic diversification, climatic niche

Slithering across the Wallace Line into Australia and Melanesia: a new phylogeny and a biogeographic scenario for groundsnakes, genus *Stegonotus*

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A classic premise of biogeography is that groups of organisms may diversify on islands after colonisation from the mainland, as in the famous case of Darwin's Finches. Whereas in the case of those birds mainland South America was the only option for the larger landmass where they could have originated, there are several possible pathways for organismal colonisation and diversification in Melanesia: where did the seed populations of New Guinea's impressive vertebrate radiations originate? Groundsnakes of the genus *Stegonotus* are one such radiation, with 11 of 25 species present on the western side of the Wallace Line in the Philippines and Borneo, within Wallacea but west of the Lydekker Line in the Lesser Sundas, and beyond these regions even across the Timor Sea in Australia, and the remainder in New Guinea. Given that *Stegonotus* is likely the sister taxon to the South and Southeast Asian genus *Lycodon,* each of its non-Melanesian populations might have seeded New Guinea and its outlying islands, where 14 species occur. Our preliminary phylogeny of *Stegonotus* based on the mitochondrial *ND4* gene supports a Southeast Asian origin of the radiation, followed by stepping-stone dispersal across the Wallace Line into the Lesser Sundas, followed by additional dispersal across the land bridge between Australia and New Guinea that existed at various times with low sea levels in the region now occupied by the Arafura Sea and the Gulf of Carpentaria. This scenario is supported by the existence of one *Stegonotus* population that ranges from Cape York in Australia across the Torres Strait to Milne Bay Province at the southeastern end of Papua New Guinea. Recent taxonomic work shows that several clades identified in previous phylogenetic work are unnamed and require recognition at the species level. Refinement of this hypothesis is currently underway with additional nuclear genes.

Key words: *Stegonotus*, Wallacea, New Guinea, phylogeny, biogeography

Three new species of flat geckos (*Afroedura*) from the Eastern Cape Province of South Africa

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Flat geckos of the genus *Afroedura* are a group of at least 34 species of small to medium-sized, nocturnal, mostly rupicolous lizards distributed widely in southern Africa, especially in montane habitats. Since 2014, various genetic studies have uncovered considerable cryptic diversity within the genus, almost doubling the number of known species. The *A. nivaria* group consists of at least five species, with three morphologically similar geckos (*A. halli*, *A. amatolica* and *A. tembulica*) found in high elevation areas in the Eastern Cape Province of South Africa, the last two taxa being endemic to the region. Flat geckos were collected in several areas in the province with the aim of expanding our knowledge of the phylogeny of the group. Relationships between various populations in the Eastern Cape were investigated using sequence data for two mitochondrial genes (16S, ND4) and one nuclear gene (RAG-1), together with a detailed morphological evaluation (scalation and size characteristics) of a sample of about 150 museum specimens. We confirm the current status of the three known high elevation species, and report the existence of three new species, two of which occur in the Cape Fold Mountains. It is likely that future surveys for flat geckos in southern Africa will uncover further cryptic diversity, but a fuller understanding of their biogeography will require a great deal more sampling, especially in relatively inaccessible mountainous regions.

Key words: Sauria, Gekkonidae, *Afroedura*, Taxonomy, South Africa

Untangling the Bootlaces: New eyes and ideas for solving an old problem in the Papuan elapid genus *Toxicocalamus* (Elapidae, Hydrophiinae)

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The elapid genus *Ultrocalamus* was described in 1913 by the German herpetologist Richard Sternfeld with two component species, *U. preussi* and *U. buergersi,* both from north of New Guinea's Central Cordillera. The taxa were distinguished by their distinctive head scute arrangement, including a pair of large, fused preocular-prefrontal-internasal scutes, and their dorsal scale counts, 13-13-13 and 15-15-15, respectively. In 1945 Charles Bogert and Bessy Matalas described a new taxon from south of the Central Cordillera, which appeared morphologically closest to *U. preussi* and which they erected as a subspecies, *U. p. angusticinctus*, so called because of bold but narrow nape-bands. Subsequently, Samuel McDowell reduced *Ultrocalamus* to subgeneric status within *Toxicocalamus* Boulenger, 1896. Since then, numerous additional specimens of *Toxicocalamus* with 13-13-13 dorsal scales have been collected, but these have not yet been used to inform the taxonomy of these snakes: populations living north of the Central Cordillera are allocated to *T. p. preussi* and those from south of the range to *T. p. angusticinctus*. We examined all 62 available specimens and determined that not only does *T. p. angusticinctus* deserve recognition as a full species, but that there is a species complex hidden within *T. preussi* consisting of at least seven and possibly as many as nine operational taxonomic units that can be distinguished statistically and by unique combinations of morphological characteristics. One of these exists north of the Cordillera, with the others to the south.

Key words: *Toxicocalamus*, New Guinea, phylogeny, biogeography, hidden biodiversity

Poster Presentations

Snakes living in urban habitats: effects of urban environment on the developmental stability, condition and size of dice snakes (*Natrix tessellata*) living in a human-modified shoreline

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Animals living in urban environments are facing novel environmental factors which may cause developmental disturbances in individuals. Fluctuating asymmetry means random deviation from symmetry and it is a useful tool in biological conservation which indicates the environmentally-induced developmental instability of a bilaterally symmetric creature. The aim of our study was to investigate how dice snake (*Natrix tessellata*) populations differ in their fluctuating asymmetry levels, condition (residuals from the linear regression of body weight against snout-to-vent length) and size around a highly modified lake which is characterized by intensive urban land use and human disturbance. Our survey was carried out at 25 sampling sites around Lake Balaton in Hungary. We determined two asymmetry indices and the average size, condition of each population. We characterized the urban environment by land use and local variables and we also estimated the risk of roadkill. Our major findings is that snake populations living near to main roads and living in areas with higher road density have more asymmetric traits. It is possible that pollutants from traffic may cause developmental disturbances which manifests in asymmetric individuals. Furthermore, we found that snakes living in bigger harbours have lower condition which may be the consequence of intensive boat traffic and human disturbance. Finally, populations living in more urbanized areas have larger body size which indicates that urban environments with human-made structures may provide ideal habitat for dice snakes. Although urban artificial surroundings may function as suitable habitats, our results confirm that urban environmental stressors have negative effects on the developmental stability of dice snakes.

Key words: urbanization, fluctuating asymmetry, developmental stability, *Natrix tessellata*

How to standardise fire salamander research: get the help of citizen scientists but minimise the risk of spreading the “salamander plague”

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The European fire salamander (*Salamandra salamandra*) is — at present — still a fairly common amphibian species throughout much of its range. In central and western Europe, it typically inhabits old broadleaf forest in low mountain ranges with first-order streams; utilised for the deposition of larvae by females. However, the emergence and spread of a novel fungal disease, caused by *Batrachochytrium salamandrivorans* (“*Bsal*”) — which can lead to mass mortality in fire salamanders — in tandem with other threats, could cause the fire salamander to become an at-risk species. Despite its remarkable appearance and general popularity, the fire salamander is not particularly well monitored throughout Europe, and local population declines may well go unnoticed. At the same time, there is great potential for involving citizen amphibian-enthusiasts in monitoring, especially given the charismatic nature of the fire salamander. To adequately tap into this potential, but avoid accidental spread of *Bsal*, standardisation of field procedures and best-practice guidance are urgently required. Here, we present considerations on how to standardise and efficiently communicate hygiene and field-work regulations, and give some impressions on our fire-salamander monitoring activities in 2023.

Key words: *Salamandra salamandra*, *Bsal,* Field hygiene, Sampling standards

Effect of continuous winter activity on body condition in *Triturus ivanbureschi*

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Natural populations have been shown to respond to climate change in various ways. As the fastest declining vertebrate taxa, amphibians are of high conservation concern in the face of global warming due to their limited mobility and strong dependence on ambient conditions. Recently, we discovered a Buresch's crested newt (*Triturus ivanbureschi*) population in Bulgaria that exhibits unusual winter activity. To assess the consequences of ceasing winter hibernation, we conducted a mark-recapture study looking at the change in body condition (proxy for fitness) from December 2021 to July 2022. Using funnel traps, we captured a total of 208 unique newts (121 males and 87 females) in 11 trapping sessions. We identified recaptures using images of the ventral pattern; 49.52% of all individuals were captured more than once. Since body condition correlates with stored energy reserves, we asked if it predicts individual recapture rate (proxy for activity). Results indicate that temperature had a non-linear effect on capture success (newts per trap), which initially increased but then decreased after 15°C and 13°C for air and water temperature, respectively, which is likely associated with the advance of the summer drought. Body condition decreased during and after the breeding season (beginning of March to end of July), but not during the winter (mid-December to end of February). Winter feeding might compensate for the increased energy expenditure associated with remaining active and explain the absence of a decline during the winter months. We did not find a relationship between body condition and activity levels (Poisson GLM, z1,205=0.22, p=0.83), but female newts were less likely to be recaptured than males (Poisson GLM, z1,205=2.83, p=0.005). This study contributes to the mounting evidence suggesting sex differences in capture probability and may be the first step in evaluating the consequences of a change in behaviour associated with rising temperatures.

Key words: amphibians, capture probability, climate change, crested newts, winter hibernation

Modelling the distribution of the natterjack toad, *Epidalea calamita* (Laurenti, 1768), in Europe: accounting for connectivity suitability and dispersal

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Assessing species home range is fundamental in biogeography and requires decades of field data to implement standard distribution models (SDMs). These modelled distributions are interpreted as maps of suitable environments based on general maps of actual species presence. Two main factors are commonly used to consider species presence: biotic favourability, and accessibility to dispersal from an original region. In this study we explored a recent Connectivity-Suitability-Dispersal plot to extend the results of conventional niche modelling for understanding the effects of dispersal on the distribution of a common species in Europe, the Natterjack Toad. SDMs were generated using Bayesian additive regression trees based on predictors from the CMCC-BioClimInd, WorldClim and Global Soil datasets. The model showed high performance (AUC=0.81) and proved the importance of soil temperature, precipitation seasonality, and minimum temperature of the coldest month on the species distribution. Using a 10-percentile threshold, the model predicted habitat suitability for the toad from the Iberian Peninsula to Latvia and North-Western Ukraine, but also in Britain and Ireland. The model predicted few occurrences in Ukraine compared to the literature suggesting that the toad population may have decreased in its most eastern range. Indeed, recent field monitoring reported only 16 vocalization sites on the territory of Shatskyj district, Ukraine, with a mean of only 3 ind./site (range = [1-8]). However, the model also predicted the species to occur in Italy despite its actual absence. Using the 'BAMM' package in R, we obtained estimates of connectivity suitability and dispersal diagrams throughout Europe that permitted us to identify geographic clusters. The resulting map shows that the species can travel two steps per unit time, giving the best fit while excluding Italy from the home range. The study shows the importance of GIS-modelling for species' conservation in changing climate. We thank for cooperation the projects "EMYS-R" and Nr.lzp-2021/1-0247.

Key words: natterjack toad, GIS-modelling, distribution, climate, Europe

Using museum specimens to understand ecological and evolutionary consequences of local extinction in salamander communities

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As species declines and extinction rates increase, understanding the consequences of species/population disappearance is critical in describing ecosystem functioning. For instance, the extirpation of a dominant species may benefit competitors by creating opportunities for niche expansion. Multiple species of salamanders occur syntopically along the Gulf Coastal Plain of the southeast of North America. Widespread enigmatic declines of the most historically abundant species (*Desmognathus auriculatus*) have been documented. Here, we examined ecomorphological diversification of stream-breeding plethodontids in the Florida Panhandle by comparing communities with and without local extirpation events. We characterized time to local extinction of the declining species, disease prevalence and trophic niche of the salamander communities, and morphological variance of a target species (*Eurycea cirrigera*). We sampled salamanders from four localities during the Spring 2022. These localities were previously sampled in the 1970's and specimens stored in the Florida Museum of Natural History, providing the opportunity to assess temporal changes. All individuals were measured and swabbed to detect two amphibian pathogens (*Batrachochytrium dendrobatidis* and Ranavirus). We collected tail-tips and abdominal skin to conduct stable isotope analysis. Finally, extant individuals of E. cirrigera were Nano-CT scanned to describe skull morphological variance. In communities with local extirpations, we expect that extant target species will show increased disease prevalence, wider trophic niches, and higher morphological variance of skeletal traits related to feeding. This study establishes a research framework to study salamander trophic ecology and diversification in the aftermath of species extirpations.

Key words: Emerging infectious diseases, Extinction models, Geometric morphometrics, Plethodontids, Stable isotopes

Preliminary results indicate localised adaptation in the duration of unken reflex in fire-bellied toads (*Bombina bombina*, Bombinatoridae)

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The unken reflex (UR) is a deimatic behaviour in certain toad species, such as the European fire-bellied toad. These toads are cryptically coloured on their backs; however, when they feel threatened, they arch their backs and raise their limbs, revealing the brightly coloured ventral side of the body. This sudden appearance of bright colour has a startling effect and warns potential predators that the toad is poisonous. As an antipredator behaviour, UR should be under selection and adapt to different types of predators/predation pressure. We examined the occurrence and duration of UR in 106 individuals from three populations of the European fire-bellied toad (*Bombina bombina*). We gently tapped the toads' heads (5 times) and grabbed them with rubber forceps to entice them to perform UR. We noted the occurrence of UR, whether the toads entered UR by tapping or grabbing and the duration of UR. We observed no significant differences in the occurrence of UR between the localities, but there was a significant difference in the duration of UR between localities. In the locality where UR lasted the longest, toads entered UR more often by grabbing than by tapping. UR was longest in the locality in an urban environment where there are far fewer predators (except cats and dogs) than at the other two localities (natural wetlands) where natural predators are abundant (snakes, water birds and small mammals). Our results may indicate potential local adaptations to different predators/predation pressures and deserve further attention. Future studies of UR should also include features such as belly colour, pattern, and contrast, as these features are also likely crucial to the occurrence and duration of deimatic displays in these toads.

Key words: antipredator response, deimatic display, amphibians

Using expert elicitation to estimate habitat suitability for the translocation of a newly described skink species

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The Kapitia skink, *Oligosoma salmo*, is a cryptic lizard endemic to the South Island of Aotearoa New Zealand. Listed as Critically Endangered, the species current range consists of c.1ha of exotic grasses threatened by extreme weather events and ongoing coastal erosion. Conservation translocation will be a key tool in preventing extinction, however limited ecological understanding is a significant barrier to translocation planning. *Oligosoma salmo* was formally described in 2019, and to date there are no recorded observations of the skink in native habitat and limited experimental data. Here we utilise the Investigate, Discuss, Estimate, and Aggregate (IDEA) protocol to guide an expert elicitation formalising best available evidence for the species habitat requirements. The collective experience of experts in academia, zoo husbandry, and conservation practice is developed into a refined knowledge base using questionnaires and structured discussion. Results from this study are intended to inform a distribution model identifying potential sites suitable for translocation, leading to further refinement using structured decision-making.

Key words: Decision-making, Conservation Translocation, Expert Elicitation

Buccal swabbing as a refined method for Ranavirus screening in fish

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In a world where emerging infectious diseases have been gaining more visibility for their increasing impacts on wildlife and farmed animals, the ability to confidently screen for pathogens is critical for understanding host–pathogen dynamics and informing better management. Ranavirus is an emerging pathogen of particular concern due to its severe impacts over a broad host range, by being able to infect both fish, amphibians, and reptiles. The virus has become increasingly associated with amphibian disease outbreaks worldwide in the wild, yet not enough research has been conducted on fish, which have been suffering outbreaks specifically in the farming context. Internal tissues are the primary choice for Ranavirus detection and quantification; however, such methodology imposes several limitations from ethical and conservation perspectives. This becomes even more relevant when studying non-model organisms, including endangered species. We explored the use of non-lethal sampling methods of viral detection by comparing the efficacy of buccal swabbing and fin clipping. The study focused on two Iberian, threatened freshwater fish (*Iberochondrostoma lusitanicum* and *Cobitis paludica*), and all samples were screened for Ranavirus (detection and quantification) using qPCR. The two methods performed differently between species; while they were found similar for *C. paludica*, in the case of *I. lusitanicum* buccal swabs presented significantly higher detection rates than fin clips, which yielded significant false negatives. Overall, buccal swabbing is found to be a good alternative to more invasive procedures, a result of extreme relevance, especially for studying threatened small-bodied freshwater fishes.

Key words: 3Rs, invasive sampling, pathogen, prevalence, viral load

Optimising the molecular phylogeny of Crocodylia

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Advances in genetic sequencing and phylogenetic analyses techniques have deepened our understanding of crocodylian phylogenetic relationships. Most studies have focused on increasing the number of sequences included in these phylogenetic studies, and also on addressing the incongruence between molecular and morphological data in phylogenetic studies (e.g., the ongoing discussion about the phylogenetic relationships of *Tomistoma*). However, not all sequences contain valuable information to reconstruct the evolutionary history of organisms, and since techniques such as Bayesian Inference (BI) require extensive computational resources, it is desirable to assess the phylogenetic utility of these sequences prior to analysis to optimise processing time and obtain robust phylogenetic trees. Mitochondrial and nuclear nucleotide sequences from 23 crocodylian species were retrieved to analyse their phylogenetic utility. These sequences comprise approximately 26,000 base pairs from 33 nuclear and mitochondrial genes available on NCBI GenBank, making this study one of the most comprehensive and extensive analyses of molecular sequences from all crocodylian species currently available. Each marker was aligned, evaluated for substitution saturation (protein-coding sequences), and the best nucleotide substitution model was selected for each marker. Bayesian Inference (BI, 10 million generations) and Maximum Likelihood (ML, 1000 replicates) were performed on each marker, and the phylogenetic resolution was assessed by examining the resulting trees. Sequences that produced phylogenetic trees with significant polytomies were excluded from subsequent analyses. Most of the excluded sequences were partial nuclear markers, as many failed to resolve crocodylian phylogenetic relationships, especially between crocodylids. The remaining sequences were concatenated (approximately 17,500 bp) and subjected to BI and ML analyses (25 million generations and 1000 replicates, respectively). The resulting majority rule tree shows well-resolved and supported phylogenetic relationships among crocodylians, consistent with previous studies and optimising computational resources by eliminating sequences of low phylogenetic utility.

Key words: DNA, Bayesian Inference, Maximum Likelihood, Crocodylidae, Gavialidae

Visual evolution in subterranean lizards

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Squamates (Snakes and Lizards) comprise the most ecologically diverse group of vertebrates, with lineages occupying marine, subterranean, epigeal and arboreal niches. It is widely known that transition to a particular niche will drive adaptations by natural selection, including significant modifications to sensory systems. For example, it is predominantly agreed that snakes passed through a dim-light/burrowing period in their ancestry - consistent with their visual system adaptation such as the loss of 2 visual opsin from their genomes: SWS2 and RH2. Knowing this, it would be expected that lizards occupying similar low-light niches, such as burrowing lineages like amphisbaenians, would also have lost opsin genes in their genomes. Further investigation is required to understand whether colour vision is still utilised in these species, for which it is unlikely to be a significant fitness advantage, given their subterranean lifestyles. Presenting genomic and transcriptomic data from 18 species belonging to Lacertoidea, selected based on their mixed fossorial habits. The focus will be on the functionality of the vision genes involved in the phototransduction cascade and visual cycle, to see if colour vision is actively used by these lizards. Many of the samples collected were primary specimens with the eye tissue extracted, and transcriptomes processed and sequenced, while the remaining genes were collected from GenBank.

Key words: Squamates, subterranean, phototransduction, sensory, evolution

The importance of education in herpetofaunal conservation

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According to the IUCN, 21% of the world’s reptiles and 43% of the world's amphibians are in catastrophic decline, or already extinct. This percentage is higher than declining mammals and birds combined. Atlanta, Georgia, USA is home to the Amphibian Foundation, which provides unique educational opportunities for all ages to learn about amphibians and inspire conservation — both on and offline. Besides the in-person programs, such as Critter Camp, the Amphibian Foundation hosts online programmes such as Master Herpetologist Program Husbandry and Captive Management Course and the Southeastern Master Herpetologist Program. These programs were developed in order to create (more) understanding of reptiles and amphibians, because these are animal groups that could use more positive attention and need extra understanding in order to take care in conservation, because of their decline, and because many of these species play a key role in ecology and biodiversity. Since 2023, I have been a member of the Virtual Education Department of the Amphibian Foundation and have worked to produce more regional content and accessibility for the European herpetological sphere. Currently, I am mainly working on content for the Husbandry & Captive Management Course. I am also addressing the importance of the conservation of wildlife and animal welfare of reptiles and amphibians from the perspective of successful strategies in husbandry. In this presentation, I would like to address the importance of education and its key role in Amphibian and Reptile conservation programs and especially the role and responsibility of the Amphibian Foundation. The value and natural history of these animals is often not understood, and even the agencies that typically fund conservation work overlook amphibians (and/or reptiles). As a result, these much-needed conservation efforts are rarely funded. The Amphibian Foundation is building a model where these vital educational programs can provide the much needed financial resources for such conservation programs.

Key words: Education, conservation, Amphibian Foundation

Frogs, Beavers and Wastewater

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The recolonisation of Hungary by beavers began in the 1990s, after the species had completely disappeared from the country by the end of the 19th century. Today, beavers are widespread again and their dam construction has become a significant landscape-shaping force. On the Alsó-Tápió stream (Central Hungary), a series of beaver dams create mostly stagnant ponds in the riverbed following one another like a chain and extended flooded areas along the stream. These bodies of water became breeding sites of frogs the year after their creation. During a three-year amphibian monitoring, eggs of agile frog (*Rana dalmatina*) were found at several points around the beaver dams. In addition, however, Alsó-Tápió is loaded with treated sewage or wastewater. We assumed that the beaver-created stagnant water bodies have an extremely high concentration of organic nutrients, which can significantly influence the development of eggs and tadpoles. In our experiment, we compared two treatments. We placed *Rana dalmatina* eggs in 14 mesocosms, half of them were filled with the polluted water from the Alsó-Tápió stream, while the control group contained clean water from the nearby Felső-Tápió stream. Conductivity was higher in the water of the Alsó-Tápió, indicating higher organic load. Egg mortality in polluted water was 100%, while in clean water >50% of eggs had hatched. A similarly drastic difference was observed when the experiment was repeated with hatched tadpoles. Their mortality was also 100% in the Alsó-Tápió mesocosms, while in the Felső-Tápió mesocosms the survival rate exceeded 75%. Our study resulted in high mortality of frog eggs and tadpoles in wastewater released into Alsó-Tápió although the beaver ponds provide a suitable physical environment for amphibian reproduction. To reveal the direct cause of this effect needs further investigation.

Key words: beaver ponds, frog reproduction, wastewater, mortality

Fish introduction in mountain lakes and its effect on amphibian communities

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Mountain lakes have been exposed to fish introductions during the last decades for aquaculture, fauna enrichment, or angling. Despite the expected economic benefits, these stockings have a negative impact on aquatic communities. One way of understanding the impact of fish introduction on amphibians is by looking at how species interact. This can be achieved by building biotic interaction networks, which are useful tools for inferring the predation or competition for food or habitat which might arise in mountain lakes. We conducted a systematic literature review and selected publications dealing with the impact of fish introductions in mountain lakes on amphibians. We extracted data to assess if fish presence in mountain lakes affects the diversity, abundance and development of amphibians and constructed a database focusing on the interactions established between the introduced fish and the native amphibian. The review showed that fish presence impacts amphibian population structure and density. Moreover, it determines alterations in the time elapsed in the larval stage prior to metamorphosis and decreases the number of paedomorphic individuals. The impact is either direct, through predation and indirect through habitat modification and aquatic communities changes. Fish introduction in mountain lakes should be prevented and the colonised lakes should be managed carefully for allowing renaturation of the ecosystems. To compensate for the loss of the supposed economic benefits, fish stocking may still be carried out, but limited to artificial water bodies specifically designed for aquaculture.

Key words: biotic interactions, anura, caudata, fish stocking

‘Stowaway’ data for amphibians, reptiles, and invertebrates entering the United Kingdom from 2018–23; highlighting introductions of potentially invasive species, risks to public safety, and other ecological and conservation impacts

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The National Centre for Reptile Welfare (NCRW) provides a focus for advice and educational outreach for exotic species of amphibians and reptiles in the UK. It also provides an important role in re-homing exotic animals that are ‘stray’, or where caregivers can no longer manage them. This includes those classed as ‘stowaways’, i.e., they have hidden themselves in items being shipped to the UK, or in the luggage of people who have been travelling abroad. Stowaways are typically reported by: commercial importers, customs authorities, the military, and the wider public. The NCRW data has been collated to understand which species are involved, their origins, means of transport; and to aim to put in place mitigation measures to monitor and better manage the issue. Data was collected from 2018-2023, resulting in 157 animals identified (including reptiles, amphibians, spiders, scorpions, myriapods and insects), representing 60 species, originating from 33 countries and 8 regions. Animals arrived by sea (23.6%), air (45.3%) and road (31.1%). These included 5 (3.2%) animals considered Critically Endangered (CS)/Near Threatened (NT) in the wild, 4 (2.5%) on CITES Annex A or B, and 11 (7%) listed on the Dangerous Wild Animals Act 1976. The implications of these arrivals are discussed in terms of: animal welfare and conservation concerns; public safety posed by venomous animals including: centipedes, scorpions, spiders and snakes, e.g. the saw-scaled viper (*Echis carinatus*); and ecological concerns including threats to UK wildlife through the potential escape of an invasive species, and/or disease transmission, e.g. from wall lizards (*Podarcis* spp), some species of scorpion and many of the amphibians, particularly those from a continental European origin. We also ask the question, is there any benefit to bringing these animals into captivity, e.g., to diversify the genetic base for captive collections breeding rare animals?

Key words: stowaway, reptile, amphibian, invasive, conservation

Anuran phylogeographic patterns in Congo Basin rainforests

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While the amphibian fauna of West Africa and the Lower Guinean rainforests is comparatively well studied, the central Congo Basin and particularly the area south of the Congo River (Central Congolian Lowland Forests, CCLF) remains a “black box”. Its difficult accessibility and socio-political instability have, with a few exceptions, hampered fieldwork in recent years. As a result, the known biodiversity in this area is low, which is expectedly due to low sampling intensity rather than reflecting biological reality. We performed DNA barcoding (16S rRNA) of frogs from different ecological niches (terrestrial, semiaquatic to aquatic, and scansorial) and supplemented our data with sequences obtained from GenBank to investigate intraspecific variation and phylogeographic patterns. We screened 24 species having their major distribution in the CCLF and/or the Congo Basin. Lineages were determined both by the use of species delimitation algorithms (ASAP, bPTP) and manual classification according to phylogenetic trees created with iqtree2. We introduce a selection of interesting focal taxa and present preliminary results showing endemic haplotype variants in the CCLF. We discuss the historical biogeography of Central Africa in general and the Congo Basin in particular, with the Congo River potentially serving as a biogeographic barrier for some species.

Key words: Biogeography, Central African Amphibians, Congo Basin

Unveiling hidden diversity: herpetological explorations in northeast India

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Tucked away between the Himalayan and Indo Burma Biodiversity hotspots, the northeastern part of India is regarded as a treasure trove of herpetofaunal diversity. However, this biodiversity is very likely grossly underestimated, evident from the fact that in the last two decades, ~100 species of herpetofauna were discovered in the region, constituting one-fourth of Northeast India’s total described diversity. In the last two decades, we carried out herpetological exploration in over 30 protected areas including ~150 localities spanning an elevation range of 40–3000 m asl. Our exploratory research during these years spanned all the main physiographic formations and helped us document ~330 species of herpetofauna comprising ~3000 registered voucher specimens at the Wildlife Institute of India. Our integrative taxonomic approach using morphology, molecular, acoustics and osteological data resulted in description of five new species of amphibians and six new species of squamate reptiles including two new genera (*Smithophis*, *Cristidorsa*). We also rediscovered five squamate reptiles, redescribed two amphibian species and documented 12 new country records. We revised the taxonomy and determined the phylogenetic status of natricine snakes (*Herpetoreas*, *Trachischium*, *Smithophis*, *Rhabdophis*), other reptile (*Boiga* cf. *multomaculata*, and *Calotes* cf. *jerdoni*), and anuran species complexes (*Microhyla* cf. *ornata*, and *Amolops* cf. *monticola*). A large-scale phylogenetic database of amphibians and reptiles generated from the region is being used to understand how the regions complex geography including prominent mountains and rivers, has shaped diversity and distribution across the wide Assam valley. Our integrated taxonomic approach is helping in determining species distribution crucial for conservation assessment and identifying critical habitats for conservation priority.

Key words: underestimated diversity, inventory, new species, systematics, Himalaya

Age estimation in non-avian reptiles using growth marks in skeletal and non-skeletal hard tissues

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Age and growth-related parameters are essential in population ecology, evolution and conservation biology. There is a growing body of published data on age structure studies in reptiles based on sclerochronology, a technique based on counting the growth layers deposited in bones (skeletochronology) and other hard body structures. We compiled the existing published data and information describing the current status of knowledge, combined the results of disparate sclerochronological studies, and identified patterns of research and information gaps, prioritising the needs for future research. Our database includes the results of 470 published studies covering 236 species from 38 families, (less than 2% of the total number of known extant species). Turtles and crocodiles were proportionally better studied, while snakes were the least studied group. The distribution of these studies does not reflect conservation needs, since there is an important geographic bias, with an overrepresentation of Northern temperate species, for which 16.7% of the reported species have been evaluated, compared to 3.6% in the Southern temperate or 0.7% in the Tropics. Only 8.3% of the studies checked the accuracy of age estimation using known-age individuals while 13.6% tested the periodicity of growth marks deposition by complementing sclerochronology with capture-mark-recapture. Overall, the data obtained through sclerochronology can be considered robust, especially if validation methods are employed. This is especially true since the general goal is to characterise population parameters, trends and dynamics, rather than determining the exact age of one specimen in particular.

Key words: age structure, reptiles, sclerochronology, global patterns

Age and growth-size variation in the common frog across a latitudinal gradient

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The Common Frog (*Rana temporaria*) is a widespread species in Europe that exhibits a range of variation in life history strategies related to ageing and growth. We compiled a database on age structure assessed through skeletochronology from published studies and our own unpublished data. The database includes data from 55 populations sampled between years 1958–2020, from locations ranging in latitude from 42 to 70°N and in longitude from 8°W to 62°E. Age-related parameters varied significantly between populations: age at sexual maturity ranged from 2 to 8 years, average age from 2 to 13 years, and longevity (i.e. the oldest animal found in a population) from 4 to 18 years. When combining the known age structure from 37 populations, the most frequent age class was 3 years old. Overall, the average age and longevity were higher in populations from higher latitude, with lower average annual temperatures, and higher precipitations. Altitude had no significant effect on average age and longevity, but body mass and size were larger at higher altitudes.

Key words: *Rana temporaria*, skeletochronology, life history, adaptations

The freeloaders of toads: parasite diversity in UK populations of *Bufo bufo*

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Amphibians are the most threatened terrestrial group of vertebrates on the planet, having approximately 41% of the IUCN assessed species being threatened with extinction. There are many factors that could possibly be linked to this decline including habitat loss, fragmentation, climate change, disease, and parasites. Parasites are known to have both behavioural and physical effects on their hosts, costing energy to either avoid infection or to regulate parasite loads once infected, reducing host fitness especially in breeding males. The common toad (*Bufo bufo*), has been declining in the UK since the 1980s. There are very few studies that attempt to ascertain the cause of *B. bufo* declines, and fewer still looking into the parasite dynamics of *B. bufo* and its impact on the species in the UK. The aim of this study was to determine parasite prevalence in *B. bufo* in the West Midlands, UK. Toad samples were collected, measured, and weighed to determine body condition and then dissected. Macro parasites from each individual were collected and counted to determine parasite prevalence and intensity. For identification, the collected parasites were then photographed using light microscopy and genetically identified using the commonly used 18s rRNA marker. Here, I will present the results from this study and the role parasites might play on the decline of *B. bufo* in the UK.

Key words: Amphibian conservation, Common Toad, Parasite dynamics, Morphological, Genetic identification

Turtle Tally UK Citizen Science: 5 years monitoring introduced pet terrapins in the UK

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Trachemys spp. are classed as the most invasive species globally. Due to this, in 2016, they were listed on the Invasive Alien Species Regulation (Regulation (EU) 1143/2014) which prohibited them from sale, exchange, breeding and keeping. Non-native introductions can occur due to escapes or the inability for pet owners to continue their care. Relinquishment is commonly due to the following factors: size at adulthood (up to 28cm (SCL)); larger housing requirements (min. 5ft x 4ft x 4ft); personal circumstances and individual longevity (35+ years). At present, there are estimated to be thousands living in UK waterbodies and there has been little investigation into their impacts. In Europe, many studies focus on the impacts to native European pond turtle (*Emys orbicularis*) populations and their conservation. *E. orbicularis* has been extinct in the UK for approximately 6000-9000 years. Data on distribution, demographics, behaviours, and numbers of released terrapins have been collected to gain further understanding of the impacts to both fauna and flora, welfare of the individuals and create strategies to prevent future release through education and guiding policy. Over 5 years (2018-2023), 678 sightings have been submitted to the online survey. All individuals were of adult size, no juveniles reported. The primary species seen are Yellow-bellied sliders (*Trachemys scripta scripta*), Red-eared sliders (*Trachemys scripta elegans*) and Cooters (*Pseudemys* spp.). Common snapping turtles (*Chyledra serpentina*) and Chinese softshell turtles (*Pelodiscus sinsensis*) have been reported and removed due to their potential impacts being greater on wildlife. We predict listed species will diminish over time due to mortalities transitioning from Winter to Spring and the lack of recruitment due to unsuccessful hatching in the UK climate. We also predict *Pseudemys* spp. will be more commonly seen as they are not listed on any regulations and are equally as adaptable and hardy.

Key words: Turtle, Citizen Science, Non-native, Pet

Unveiling the spatial ecology and conservation implications of *Bufotes balearicus* (Boettger, 1880) in the Balearic Islands: insights from capture, mark, and recapture studies

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Amphibian populations around the world are facing significant declines, underscoring the urgency of monitoring and understanding their life history. The use of capture, mark and recapture techniques provide essential tools for such studies, offering valuable information on the spatial ecology and movement patterns of species. This summary presents two separate studies that highlight the importance of these techniques and their implications for amphibian conservation. The first focuses on the spatial ecology of *Bufotes balearicus* (Boettger, 1880) in the island of Mallorca. Through field observations and mark-recapture studies, we investigated the spatial behaviour and population dynamics of *B. balearicus*. Surprisingly, our findings indicate the absence of apparent connectivity between the ponds. Furthermore, we do not observe a discernible pattern in the arrival of males for breeding purposes. However, the observed low survival rates raise intriguing questions about individual migration and the potential for unexplored connectivity between ponds. These findings contribute to our understanding of the life history of *B. balearicus* and have important implications for future conservation programs. Overall, the study emphasises the importance of capture, mark, and recapture techniques in unravelling the spatial ecology of amphibians. These findings provide valuable information on the conservation needs and priorities of these vulnerable species. By highlighting the importance of monitoring and understanding amphibian populations, we can pave the way for effective conservation strategies to safeguard their survival.

Key words: *Bufotes balearicus*, island populations, spatial ecology

The joint effects of mild winter conditions and two pyrethroid insecticides on the development and survival of juvenile common toads (*Bufo bufo*)

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Amphibian populations are declining globally, partly due to pollutants and climate change. During metamorphosis and overwintering, amphibians are especially sensitive to perturbation by chemicals and extreme thermal conditions, so we tested how they are affected by the combination of chemical exposure around metamorphosis and milder winter temperatures. We applied one of two pyrethroid insecticides, cypermethrin or deltamethrin, at maximal allowed concentrations to newly metamorphosed common toads (*Bufo bufo*) via spraying. We reared animals in outdoor enclosures and after measuring their body mass we overwintered them in laboratory refrigerators. We used two hibernation scenarios: we exposed half of the animals to a long and cold winter (1.5 °C for 91 days) and the other half to a short and mild winter (4.5 °C for 61 days). After hibernation we examined changes in body mass, condition of parotoid glands and visceral organs, and determined the phenotypic sex of the surviving toadlets. In the long and cold winter scenario we observed a high mortality rate, regardless of the chemical treatment (control: 82%, cypermethrin: 78%, deltamethrin: 70%). At the same time, mortality was significantly lower in the short and mild winter scenario (control: 33%, cypermethrin: 41%, deltamethrin: 26%). The decrease in body mass during overwintering did not differ among treatment groups. Although relatively few individuals survived to the end of the experiment (64 out of 162), our data suggest that mortality was not sex-biased. No significant deformations of the internal organs were found in either group. Our results suggest that milder winter conditions, in combination with exposure to the tested insecticides do not cause a significant decrease in fitness of juvenile common toads.

Key words: Anuran amphibian, climate change, ecotoxicology, overwintering

Sex ratio in the presence of the chytrid fungus (*Batrachochytrium dendrobatidis*) in a common European amphibian

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The persistence of stable and diverse amphibian communities is threatened by many factors. One of the most important threats is chytridiomycosis, a disease caused by the fungal pathogen *Batrachochytrium dendrobatidis* (*B*d). Another threat to amphibian population persistence is skewed sex ratios through sex-biased mortality or environmentally induced sex reversal whereby larvae develop the phenotypic sex opposite to their genetic sex. However whether *Bd* infection can skew sex ratios in amphibians is currently unknown. Such a hidden effect may cause another serious problem for the already declining amphibian populations. To investigate this possibility, we collected three groups of common toad (*Bufo bufo*) tadpoles from a natural habitat, and continuously treated them with sterile *Bd* culture broth (control), a liquid culture of a Hungarian Bd isolate, or a Spanish *Bd* isolate until metamorphosis. After metamorphosis, we raised the toadlets without any further treatment for another three months. After euthanasia, we dissected the individuals and determined their phenotypic sex, based on gross gonad morphology. Genetic sex was determined using sex-specific molecular markers. Survival was generally low in controls (43%), but significantly decreased as a result of *Bd* treatments (16 and 19% in the Hungarian and Spanish *Bd* treatment groups respectively), and we did not observe sex-related mortality. Individuals which survived until the end of the experiment had no detectable *Bd* load at dissection. Treatment with the Spanish Bd isolate significantly increased the frequency of sex reversal by

genetic females into phenotypic males. Based on our results, *Bd* infection may have the potential to affect the sex ratio in common toads through female-to-male sex reversal, but future research is needed to ascertain the generality of our results.

Key words: Bufonidae, Chytridiomycota, Infectious disease, Sex determination, Sexual development

Effects of water temperature on growth and development in tadpoles of red eyed tree frogs

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Several climatic models predict that Central America will experience increased temperature and reduced precipitation over the coming century. This will likely impact many species including amphibians, which are highly sensitive to changes in their environment. As ectotherms, temperature will be a key factor in the way amphibians respond to climate change. Water temperature can affect the way in which larval forms develop in both rate and size, and ultimately survivability with many tropical species already operating within the optimal temperature range. This study investigated the possible effects of four constant water temperatures on the growth and development of captive bred *Agalychnis callidryas* tadpoles kept in a controlled lab setting; a species found in Central America, northern South America and southern Mexico. Weekly measurements for head width; body, tail and total length; developmental stage reached; time till emergence from the water; and exit weight were taken. Those kept at 24 °C appeared to grow significantly larger ($P < 0.5$) than those kept at 22, 26 and 28 °C by week 4. Those kept at 22 °C exited the water significantly later ($P < 0.5$) than other groups. There was no significant difference in exit weight, however, which previous studies have suggested may be related to the level of ossification. Our results build on prior works, which have indicated a significant difference between *A. callidryas* kept at extremes of temperatures (21 and 29 °C) and other species kept at a range of warmer and cooler temperatures. These results also suggest a possible limit to phenotypic plasticity in a species which operates close to its optimal temperature in the wild. This may have impacts on future ecosystem management for anurans in response to climate change. Future works would benefit from taking measurements at more regular intervals and using true replication.

Key words: Temperature, Development, *Agalychnis callidryas*, tadpole

Comparing genetic and morphological patterns between the Western Mediterranean vipers, *V. aspis* and *V. latastei* across a hybrid zone in Northern Spain

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Morphological diagnostic traits are frequently used for taxonomic purposes. In the *Vipera* genus, morphological traits are even considered to identify putative hybrids in contact zones. However, there is no comprehensive assessment of the relationship between morphological variability and interspecific gene flow in contact zones. This study aims to uncover patterns of hybridization and how they relate to morphological variation between two Western Mediterranean vipers, *Vipera aspis* and *V. latastei*, in the contact zone of Oja-Tiron (northern Spain). A total of 87 specimens from the contact zone (35 individuals with typical *V. aspis* morphology, 34 with *V. latastei* traits, and 18 with intermediate traits) were considered. Nine diagnostic meristic traits were used to morphologically characterise them, and 18 novel microsatellite loci were used to genotype them. Clustering analysis based on morphological data identified three morphological groups, corresponding to putative parentals of each species (40 *V. aspis* and 31 *V. latastei*) and intermediate forms (16 individuals). Clustering genetic analysis, however, identified 32 specimens as pure *V. aspis*, 34 as pure *V. latastei*, and 21 as hybrids, mostly classified as F2. Six backcrosses were detected with the parental species. Most parentals were correctly identified based on morphology (97% of accuracy for *V. aspis* and 85% for *V. latastei*), while only 57% of the hybrids corresponded to intermediate vipers. The remaining 43% of hybrids were found within the parental clusters, five of which were classified as backcrosses with the species they clustered with. Morphological traits, therefore, generally distinguish parental species, but they largely fail to identify second generation hybrids and backcrosses. Other processes not related to hybridization, such as local adaptation and/or plasticity, could be also acting in this contact zone, affecting patterns of morphological variation between both species.

Key words: hybridization, morphology, diagnostic traits, vipers

Genomic phylogeography of the Iberian frog *Rana iberica*

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During the Pleistocene, Iberian refugial species had to contend with not only extreme climatic cycles but also vicariance dividing the large continental range. As such, Iberian endemic species provide an excellent opportunity to investigate the importance of geography vs demography in the development of genetic clusters and diversity hotspots. We expand on previous phylogeographic studies of the Iberian endemic refugial frog species *Rana iberica*, to investigate the genomic phylogeography of the species from a metapopulation stand-point. Previous authors identified 3 three major mitochondrial lineages, including a highly distinct lineage from the Sierra de Guadalupe. We sequenced a large genomic (RADSeq) data set comprising 308 individuals from 51 sites across the range of the species. We aimed to see if the Sierra de Guadalupe cluster could be recovered using nuclear data, and if this structuring persisted with more continuous sampling of the region. In addition, has there been recent gene-flow that can now be detected using fine-scale genomic data? We found that nuDNA data was largely concordant with mtDNA and identified a general Isolation By Distance signal in addition to confirming the distinct Sierra de Guadalupe cluster. The results here contribute to explaining the high variation in phylogeographic responses observed in refugial species: the determinants of hotspots of diversity is not only dependant on historic refugia acting as stable 'cores' for the metapopulation, but also on the contact of distinct genetic lineages after isolation.

Key words: phylogeography, genomic, ddradseq, amphibian, population

Global amphibian decline: applying a research focused mixed-method pedagogical approach to undergraduate learning

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Global amphibian decline is an introductory theoretical and hands on mixed methods undergraduate research course examining the ecology and conservation of amphibians. The global decline of amphibians is applied as a proxy for assessing large-scale environmental degradation and interdisciplinary approaches to research, management, and policy. Lecture topics include: key aspects of amphibian ecology, habitat destruction, environmental contamination, introduced species, infectious diseases, over exploitation, ethnoherpetology and climate change. Students use case studies to compare local to global responses regarding the global decline of amphibians through lectures, documentaries, readings, and media investigation. A future direction of the course hopes to include more live web-based conferencing with experts to incorporate diverse perspectives. Learning outcomes include 1. To acquire an understanding of ecological principles related to the conservation of species, as well as an awareness of the interconnectedness between the responses of nature to human activities, 2. To develop field research skills and geospatial literacy through repeat data collection and preparation of a hypothesis based written report demonstrating synthesis of spatial and temporal movements of amphibians, 3. To become familiar with basic laboratory procedures needed to test and design hypotheses associated with a standard experimental dosing and exposure study, 4. To use real-time recorded frog calls for a soundscape (bioacoustical) analysis and/or camera trapping as a tool to identify and interpret dynamic frog behaviour that can be influenced by biological processes, landscape structure, and human activity. At each of the learning outcome stages students have the opportunity to refine and develop their original research for the review process. The advantages of a mixed method experiential and research centred teaching and learning approach is in the effectiveness to develop process and an evidence-driven approach, while incorporating reflection that builds innovation and creativity in solving complex environmental problems.

Key words: undergraduate, pedagogy, experiential learning

Reconstruction and comparison of the flora of the former and existing habitats of the Hungarian meadow viper (*Vipera ursinii rakosiensis*)

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The aim of our study was to map the distribution of the endangered Hungarian meadow viper in the past on a 5×5 km scale to determine the former plant species of the areas and to compare it with the remaining habitats. To map the former distribution, we created a viper-site database using data from direct observations, literature sources, and museum specimens and determined the extent of viper habitat loss. For the reconstruction of the flora, we used herbarium, coenological and floristic data, which resulted in n=185476 plant occurrence records. We calculated the Raup-Crick's dissimilarity index to perform a NMDS to visualise differences between past and present plant communities. Subsequently, we compared the dissimilarity of past-present communities among sites where the viper became extinct or persisted using a Mann-Whitney U test. To assess the effect of dissimilarity of past-present plant communities on viper persistence we fitted generalized linear models (GLMs). In addition, we determined the plant species that mostly contribute to community differences with PERMANOVA and SIMPER. We identified former viper habitats in Austria, Hungary, and Romania, and based on the extent of habitat loss, we chose the year 1975 to separate past and present habitats. The past-present dissimilarity of plant communities was significantly lower in areas where the meadow viper survived compared to those in which it became extinct, and the dissimilarity had a significant negative effect on viper persistence probability. The past plant communities did not differ significantly among sites where later the viper became extinct or persists. However, present plant communities differ significantly among extinct and persisting habitats. This difference was explained mostly by the presence of *Stipa borythenica*, *Iris arenaria* and *Alkanna tinctoria* at current viper habitats. Our results provide a community grounded basis for more effective habitat reconstructions in the future to help protect the species.

Key words: community ecology, *Vipera ursinii rakosiensis*, former distribution, plant community, museum specimens

Classification of Marmaris lycian salamander, *Lyciasalamandra flavimembris* (Mutz & Steinfartz, 1995) (Amphibia: Urodela) and Göcek lycian salamander, *Lyciasalamandra fazilae* (Başoğlu & Atatür, 1974) by electronic nose

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In this study, we investigated whether there are differences in the odour profiles of pheromones between the Marmaris Lycian Salamander (*Lyciasalamandra flavimembris*) and the Göcek Lycian Salamander (*L. fazilae*), both of which belong to the genus Lyciasalamandra. These salamanders are distributed in the Southwestern Anatolia region and are represented by six species and eighteen subspecies in Turkey. To assess the potential variations at the species level, an electronic nose was utilised for odour analysis. Two species, which are under protection and categorised as "EN" (endangered) according to IUCN criteria, use their sense of smell to recognize each other and find their nests. Electronic noses, which do not harm the tested individuals and allow working in their natural habitats, are more effective options for classifications of species compared to other methods due to their economic and easy-to-use nature, ability to make sensitive measurements, and high accuracy results. As a result of the data analyses an accuracy rate of 86.67% was achieved. Thus, it was proven that there are pheromonal differences between species and that these differences can be distinguished through artificial intelligence. Therefore, in the future, the electronic nose method can be employed not only for species identification within the *Lyciasalamandra* genus but also for other closely related families and genera, as well as for primitive vertebrates, amphibians, lizards, and snakes. The utilisation of this method in future studies holds significant value due to its cost-effectiveness, practicality, and potential for biodiversity preservation. This method has a great importance in terms of being quite economical and practical, as well as preserving biodiversity.

Key words: *Lyciasalamandra flavimembris*, *Lyciasalamandra fazilae*, Pheromones, Electronic Nose, Artificial Neural Network

Mitochondrial phylogeography of the common toad (*Bufo bufo*) in Britain

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The common toad (*Bufo bufo*) is a widespread species occurring from Britain in the west to Russia in the east. The species is reported to have declined in many regions of Britain for unknown reasons and little is known about the genetic diversity and phylogeographic patterns observed on the island nation. Previous studies have identified low genetic variation in England; however, these were limited to only a few sites. Here, we present newly generated genetic data and infer phylogeographic patterns between *B. bufo* populations in England, Scotland, and Wales. Buccal swabs and tissue samples were collected from across Britain. Following DNA extraction of samples, sequence data were generated for two mitochondrial loci (cytochrome b (cytb) and 16s rRNA) for ca. 150 samples. We estimated phylogenetic relationships using maximum likelihood and Bayesian inference methods, and haplotype networks. In concordance with previous studies, we found very little mitochondrial variation across the UK but did identify some phylogeographic signals possibly indicative of separate colonisation routes from France into southeast England and from Scandinavia into Scotland.

Key words: Mitochondrial, Phylogeography, Decline, Diversity, Britain

How long is a snake? Comparison of different measurement methods

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A variety of techniques for quantifying animal dimensions exist. Often, scientific publications only provide the measurements taken, without detailing the employed measurement techniques. In the case of flexible organisms such as snakes, this can create difficulties in making comparisons. In order to eliminate or minimise snake handling and discomfort, we conducted a comparative analysis of various measurement techniques for live snakes. We 1) compared four methods for measuring body length in snakes, and 2) determined the difference between measurements taken by experienced researchers and inexperienced students. Preliminary calibration between researchers and students for each method was done. Measurements were taken for four snake species: *Natrix natrix*, *N. tessellata*, *Dolichophis caspius* and *Elaphe sauromates*. Snake length was measured using (i) manual stretching of the snake alongside a measuring tape, (ii) using a squeeze box and then a thread along the snake's body, (iii) digitally measuring a photograph of the snake (in the squeeze box) in ImageJ and, (iv) respectively, SnakeMeasurer. Our results indicated that both the selected techniques and individual experience had a significant effect on the resulting length measurements across all studied species. Notably, the manual method yielded the longest lengths, followed by measurements in the squeeze box, while the digital methods yielded the shortest measurements. Measurements obtained by the inexperienced students significantly differed from those obtained by the experienced researchers. The manual method was the fastest for researchers, the squeeze box method was the most challenging due to the requirement of specialised equipment, and the digital method was the most comfortable in performing the measurements for both researchers and students, with a preference for ImageJ, rather than SnakeMeasurer.

Key words: measurement, body length, snake species, digital, squeeze box

Ontogenetic development of skull shape in *Bothrops jararaca*, with special emphasis on the pit organ and the venom gland

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The venomous pit viper *Bothrops jararaca* from Brazil is known to experience a dietary shift during growth, i.e. whereas juveniles initially hunt for ectothermic prey and insects, prey preference changes towards endotherms, i.e. mammals, in the adult stage. This shift is also reflected in a change in venom composition during growth. However, it remains unknown if there are also any anatomical changes resulting from this dietary change. To investigate whether this shift can be detected in the morphology of the head we generated micro-computed tomography scans of the skulls of 85 individuals of *B. jararaca* across all growth stages and applied a geometric morphometrics approach with special focus on the imprint of the pit organ onto the maxillary bone. Also, we used Diffusible Iodine-based Contrast-Enhanced Computed Tomography Method (DiceCT) to visualise the morphology of the venom gland. Results reveal that the growth trajectory of the pit organ deviates from that of the skull, with the pit organ following a much steeper inclination and showing fast, positively allometric growth relative to the remaining skull until close to the adult stage. In addition, not only the pit organ but also the venom gland system follows its own growth trajectory. Our results suggest a relationship between ontogenetic changes in prey preference and the postnatal ontogenies of pit organ and venom delivery system in *B. jararaca*, whereas it remains to be tested if similar patterns are also found in other species of pit vipers without dietary shifts.

Key words: venom gland, ontogeny, pit organ, pit viper, DiceCT

Unravelling the disease ecology of *Ophidiomyces ophidiicola*: high genetic variability and ecological basis of the agent of snake fungal disease

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The discovery of the fungal pathogen *Ophidiomyces ophidiicola*, the etiologic agent of Snake Fungal Disease (SFD), raised a growing conservation interest in North America and in Europe's scientific community. This pathogen has been associated with the declines of several snake populations in North America and was also detected in Europe. Its ecology, distribution and phylogeography still remain largely unknown. Recent work by Gaelle Blanvillain (1) investigating the distribution of *O. ophidiicola* and its lineages in Europe highlighted a pathogen hotspot in Switzerland. In this study in collaboration with Gaelle Blanvillain, we collected skin swabs from 259 free-ranging snakes and 12 skin sheds in Switzerland across 8 different species and 13 sites. The overall pathogen prevalence detected by conventional and quantitative PCR was at least 28% with a maximum of 45% positive individuals in the swiss-german region (30/66). Sequencing of short gene sequences revealed pathogen clades consistent with both the European and two North American lineages of *O. ophidiicola* distributed across the different regions. Semi-aquatic snakes (genus *Natrix*) were more likely to be infected by *O. ophidiicola* than terrestrial snakes (means of pathogen prevalence = 35% and 7.2%, respectively), and high human disturbance (assessment of human frequentation and direct impact on snakes with the knowledge of Swiss specialists) was likely to induce a higher *O. ophidiicola* prevalence, whereas season, body condition and snake species introduction did not. This study suggests that Switzerland might represent a region characterised by high pathogen prevalence and high genetic variability in *O. ophidiicola*.

Key words: Snake Fungal Disease, *Ophidiomyces ophidiicola*, Conservation, Aquatic snake species, Human impact

Weather conditions and detection probability of reptiles in the Kiskunság National Park, Hungary

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Reptiles play a crucial role as key components of ecosystems and serve as indicators of habitat health. However, many reptile species are currently facing the threat of extinction. Monitoring programs are essential to guide evidence-based conservation efforts. Incorporating the detection probability into monitoring schemes becomes crucial when visual encounters of individuals are limited. Within the framework of the HUNVIPHAB LIFE project, we conducted a reptile monitoring study in the grasslands of the Kiskunság National Park, focusing on the Hungarian meadow viper (*Vipera ursinii rakosiensis*) and other reptile species. Reptile occurrence data were collected using 50×50-meter quadrats (n=100), while weather parameters were continuously measured by two meteorological stations. To estimate the detection probabilities, we employed dynamic occupancy models and conducted model selection for each species. Among the species studied, *Lacerta viridis* exhibited the highest occupancy, followed by *Lacerta agilis*, *Podarcis tauricus*, *Vipera ursinii*, and *Coronella austriaca*, with the lowest occupancy rates observed across the study plots. We identified a negative relationship between the detectability of all species and the number of days after 10 mm of rainfall. The detectability of lizards was positively influenced by high soil temperature and low air temperature in the 24 hours prior to the survey. Moreover, the detectability of *Podarcis tauricus* increased with high air temperature, while *Lacerta viridis* exhibited a similar response to high radiation. Increasing wind negatively affected the detectability of the latter two lizard species, whereas the activity of *Coronella austriaca* was positively influenced, particularly in autumn. *Vipera ursinii* showed a higher likelihood of detection during spring. These findings highlight the importance of considering weather conditions and detection probability in reptile monitoring programs. Incorporating detection probability information in the analysis of monitoring data enables more accurate assessments of reptile populations and enhances our conservation strategies.

Key words: occupancy modelling, weather, activity, grassland, conservation

The first molecular analysis of the Lanza’s Frog (*Lanzarana largeni*) from the Horn of Africa supports its unique position in the family Ptychadenidae

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Lanzarana largeni is known from only eleven localities in northeastern and southern Somalia. This species spends most of its life hidden underground and only comes to the surface during periods of sufficient rainfall. The author of the original description placed it in the genus *Hildebrandtia*, but not without a suspicion that it may in fact represent a different genus [*H.* (?) *largeni*]. A later study of the external morphology and osteological characters focused on African "ranid" frogs confirmed the distinctness of this species from the other representatives of the genus *Hildebrandtia* in several characters. Based on these results, *H.* (?) *largeni* was assigned to a separate monotypic genus *Lanzarana*, with the assumption that it is closely related to *Hildebrandtia*. This classification has not yet been verified using molecular phylogenetic methods as most of the available material dates to the 1970s which complicates the use of conventional molecular methods. However, recent discovery of this species in eastern Somaliland has allowed its first molecular phylogenetic analysis. The results confirm the affiliation of the genus *Lanzarana* to the family Ptychadenidae, but not as a sister lineage to the genus *Hildebrandtia*, but as a sister lineage to the species-rich genus *Ptychadena*, from which *Lanzarana* diverged about 32 Mya in the early Oligocene. We also report the first record of *Lanzarana* in neighbouring Ethiopia, where its occurrence has so far only been assumed, and a previously unnoticed observation at a locality west of the Juba River in southern Somalia. These new localities extend the known range of this species significantly to the west and suggest the possible occurrence of this species in northeastern Kenya, which is supported by our results of the species distribution modelling.

Key words: Africa, Somaliland, phylogenetics, species distribution modelling

Key informant surveys demonstrate biases and benefits for invasives species rapid status assessments

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The benefits of incorporating wide-ranging social views and values into wildlife conservation policy and strategy is being increasingly recognised. The opinions and knowledge of key stakeholders can help reconstruct poorly documented processes and can highlight conflicting views that may affect the success of conservation action. Humans are inherently biased and an understanding of how these biases inform perceptions is important for building consensus around conservation decisions. The alpine newt *Ichthyosaura alpestris* is a widespread invasive urodele for which little is understood about its impacts or invasion dynamics in the UK. Here I use an online questionnaire distributed to key informants with the aim of understanding the utility of this approach for producing a rapid status update, for providing insights into ecological impacts, introduction pathways and opinions around management, and to disentangle biases that may be informing perceptions. Previously unreported alpine newt locations were recorded, a series of introduction pathways identified and a pattern of ongoing purposeful animal release detected. Opinions towards species management were influenced by general perceptions of invasive species as well as perceived ecological impact, despite limited evidence of impact and only 16% of named populations undergoing any form of systematic monitoring. My findings show the value of key-informant surveys for rapidly assessing the status, distribution and invasion history of an understudied invasive species but also highlight its shortcomings. Those with most knowledge of specific populations were less concerned by their impacts, but wider perceptions of negative impact drove more intensive management preferences. Together with limited systematic monitoring these findings suggest that opinions of conservation relevance are largely based on gut feeling rather than evidence, which could have the potential for profound consequences for limited conservation resources. A better understanding of the ecological impacts of alpine newts are urgently required for amphibian conservation efforts in the UK.

Key words: Social science, questionnaire, invasive, perceptions, management

Photo-Identification of *Bufotes balearicus* (Boettger, 1880) using individual colour patterns for population studies

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In recent years, photo-identification has emerged as a valuable method for identifying and studying individuals. This study focuses on *Bufotes balearicus* (Boettger, 1880) and highlights the use of its distinctive individual colour patterns for photo-identification in population studies. The colour patterns present on the back of *B. balearicus* individuals offer a unique and identifiable feature for photo identification. By utilizing photo-identification techniques, researchers can effectively recognize and track individuals within populations. This non-invasive approach eliminates the need for invasive marking methods, minimizing potential stress and harm to the studied species. Through the application of Image Template Matching (ITM) using the Automated Photo Identification Suite (APHIS) software, this study achieved a high level of success in accurately identifying recaptured *B. balearicus* specimens. The results demonstrate the efficacy of photo-identification as a reliable method for population studies, with the colour patterns providing a natural and stable marker for individual recognition. The utilization of photo-identification not only facilitates population studies of *B. balearicus* but also enables broader insights into spatial ecology, population structure, and dynamics through Capture, Mark, and Recapture (CMR) studies. By combining photo-identification with other individual marking methods, such as microchipping, long-term monitoring of natural colour patterns can be conducted to assess their stability over time.

Key words: *Bufotes balearicus*, PhotoID, natural marks, CMR

Exploring climate change impact on phenotypic diversity and geographic distribution in the sand lizard (*Lacerta agilis*)

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Climate change has precipitated notable effects, including range shifts, habitat loss, and even species extinctions. Polymorphic species, with their diverse phenotypes, display distinct responses due to differences in their ecological niches and thermal physiological optima. Among these species is the Sand Lizard (*Lacerta agilis*), whose phenotypic traits, such as the colour of the back, dark side marks, markings, and colour of the vertebral region, show a broad range of diversity. The broader implications of having such diverse phenotype diversity remain poorly understood, particularly within the context of climate change. In this study, we utilised a comprehensive database, aggregated from various citizen science platforms, detailing the distribution of *L. agilis* phenotypes across its extensive range from Western and Central Europe to Siberia and Lake Baikal. Through this, we generated Ecological Niche Models (ENMs) to assess if twenty-first-century climate change impacted the distribution and diversity of the lizard's phenotypes. Our findings indicate a potential northward shift in species distribution and alterations in predicted phenotype diversity across the species' range. Notably, these effects varied across different phenotypes. By integrating phenotypic data into ENMs, we are better equipped to understand how populations in different regions will be affected by climate change. This paves the way for future research adopting a more mechanistic approach to study the different responses of phenotypes to climate change.

Key words: climate change, ecological niche models, distribution change

Speciation, hybridization and introgression as evolutionary processes in Galapagos giant tortoise

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Across the Galapagos archipelago giant tortoises are present on seven of the major islands, currently existing as 13 living populations, with at least three extinct. Previous genetic research has confirmed hybrids do exist between populations but typically as a result of human mediated movement of tortoises and not natural dispersal. Fundamental to effectively managing hybrid individuals is to understand where in the process of speciation the Galapagos giant tortoise lineage lies. We performed species delimitation models using genomic data from all extant populations to answer this question. We then sequenced the genome of 72 potential hybrid Galapagos giant tortoises from Volcano Wolf, on Isabela island, to gain a better understanding of the degree and genomic architecture of hybridization in this population. Overall this research has implications for management of the Galapagos giant tortoise lineage and highlights the potential benefits hybrids can provide in conservation.

Key words: hybridization, genomics, evolution, giant tortoise

Increasingly cautious sampling, not the black colouration of unpalatable prey, is used by fish in avoidance learning

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The efficiency of aposematic colouration of prey is based on the innate bias or facilitation of avoidance learning of predators. In many toxic bufonids, larvae are uniformly black, which is considered a warning signal. We compared fish predation on normal (black) and 'transient albino' (greyish) common toad *Bufo bufo* tadpoles that did not differ in toxicity or activity. In a two-stage experiment, each fish was presented with tadpoles of one colour in the first trial and the other colour in a subsequent trial. While tadpoles sampled by fish were typically not ingested, some died from injuries. The attack rate did not differ between tadpole phenotypes nor trials, irrespective of which phenotype was the first exposed to the fish. However, during the second trial, the sampled tadpoles, independent of colouration, were mouthed by fish for shorter periods and tadpole mortality decreased. We conclude that in single-species prey populations, the black colouration of tadpoles is not a warning signal as it did not accelerate predator learning about prey unprofitability. Our results indicate that with growing experience, predator samples potentially toxic prey more cautiously. This may explain why natural selection does not eliminate aposematic morphs even if predators continuously sample conspicuous prey.

Key words: aposematism, common toad, predation, tadpoles, warning colouration

Hidden diversity and natural history of the secretive New Guinean worm-eating snakes, genus *Toxicocalamus* (Elapidae: Hydrophiinae), revisited

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Toxicocalamus is an elapid genus represented by 526 specimens in thirty collections worldwide. It is a genus of diurnal but secretive, terrestrial, or fossorial, oviparous, vermivorous snakes, endemic to the island of New Guinea and its satellite islands. These snakes inhabit rainforest, hill and pre-montane forests, or montane grasslands, but one species is especially common in earthworm-rich highland garden systems. Most species are relatively small (< 600 mm in SVL), but one species exceeds 1.0 m. Many species exhibit distinctive head-scute fusion arrangements that greatly aid in their identification. The genus was erected in 1896 by George Albert Boulenger based on *T. longissimus* from Muyua (Woodlark) Island, a satellite of New Guinea off the southeast coast of New Guinea. During the remainder of the 19th Century additional species were described, both in *Toxicocalamus* but also in three other genera (*Apistocalamus, Pseudapistocalamus, Ultrocalamus*) that were later reduced to subgenera within *Toxicocalamus*. By the end of the 1960s, *Toxicocalamus* comprised nine species, and this number remained constant for forty years until a new generation of herpetologists started to investigate the genus. Since 2009 a further twelve species have been described and three have been resurrected from synonymy, bringing the current total to 24 species, making *Toxicocalamus* the most diverse terrestrial alethinophidian snake genus east of the Wallace Line. Since the time of the 21st SEH conference in Belgrade, when this poster was first displayed, a major paper resolving the status of the *T. loriae* complex has been published, in which we described three new species resurrected three from synonymy. In addition, the name *T. longhagen* was proposed, which we have shown to be a *nomen dubium.*

Key words: *Toxicocalamus*, New Guinea, phylogeny, biogeography, hidden biodiversity

Community-level response of reptiles to grassland reconstruction to connect isolated Hungarian meadow viper habitats

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The Hungarian meadow viper (*Vipera ursinii rakosiensis*) has experienced a significant decline in its population due to agricultural expansion and afforestation in the Carpathian Basin. With only

a few isolated populations remaining, the risk of extinction is high due to inbreeding and genetic drift. The LIFE project, aimed at conserving the viper, focuses on enabling gene flow between these isolated populations. In the Bócsa-Bugaci sandplain, two previously separated populations were reconnected through grassland reconstruction efforts in a cleared 20-hectare area. This study investigates the impact of grassland reconstruction on the reptile community by comparing sampling sites in the reconstruction area to reference grasslands nearby. The research aims to address several questions: Which reptile species have colonised the reconstruction area? Does the reptile species composition differ between the reconstruction and reference areas? How does reptile community diversity change over time since the reconstruction? To characterise the reptile communities, the study employs repeated-sampling occupancy and n-mixture models to estimate habitat occupancy indices and densities at the sample sites. Non-metric multidimensional scaling is used to analyse habitat occupancy and density estimates. Community dissimilarity between the intervention and reference sites is assessed using distance matrices, and the effect of elapsed years on dissimilarity is evaluated through linear models. Since the reconstruction, the green lizard and Balkan wall lizard were the first species observed to colonise the area, followed by sporadic appearances of the sand lizard, smooth snake, and grass snake. The Hungarian meadow viper has not been observed thus far. The habitat occupancy of reptile species shows no separation between the two sub-areas of the intervention area, with one sub-area resembling the Tolvajos reference area. However, the presence of the sand lizard and viper distinguishes the intervention area from other reference areas. Regarding reptile species density, significant differences were found between the two subdivisions of the intervention area, with one subdivision remaining most similar to the Tolvajos reference area. Over the course of the three-year study, the dissimilarity between the intervention and reference areas based on habitat occupancy estimates decreased significantly. However, dissimilarity based on reptile species density did not change significantly. Five species spontaneously colonised the intervention area affected by the reconstruction, making it most similar to the Thistle reference area, characterised by open sandy shrub grassland. Continued habitat reconstruction and monitoring are crucial for creating suitable habitats for the Hungarian meadow viper and potentially observing its spontaneous colonisation in the future.

Key words: Hungarian meadow viper, grassland reconstruction, reptile community, habitat occupancy, biodiversity change

Range reduction of *Rana temporaria* in Pilis Hills, Hungary, after 22 years of monitoring

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Regular and annual monitoring of amphibians and reptiles was initiated in Hungary in 2001. We monitor the Pilis Hills, one of the driest mountain regions in northern Hungary. The area is largely covered by forest and comprises ca. 140 ponds. These ponds are characteristically small in size, many are temporary and water levels can decrease significantly even in those that persist throughout the year. The 22-year-old monitoring program started in 3 ponds and after some conceptual changes it is currently being undertaken in 18 ponds. Regularly observed species are: *Rana dalmatina*, *Rana temporaria*, *Bufo bufo* and *Lissotriton vulgaris*. Occasional occurrences were recorded for *Bombina bombina*, *Hyla arborea*, *Pelobates fuscus* and *Pelophylax esculentus* complex. The distribution of *R. temporaria* in Hungary is limited to regions with a higher and cooler microclimate, and it has long been observed in the Pilis Hills. In the first half of the monitoring period, we observed the species in about half of our ponds, although we consistently detected a lower number of eggs than those of its close relative, *R. dalmatina, R. temporaria* choirs and egg clutches have increasingly disappeared from our ponds since 2010, with only one pond harbouring the species in 2023. The primary cause of this range reduction is quite likely the desiccation of Pilis Hills, caused by the gradual but continuous increase in average temperature and decrease and more erratic precipitation events. An observed corollary effect involves the expansion of *R. dalmatina*, which utilises the same ponds as breeding substrate in the same period as R. temporaria. In cooperation with local forestry and nature conservation authorities, we will extend the monitoring to 40–50 ponds and targeting *R. temporaria*. Further, we are implementing a microclimate measuring network and will investigate environmental conditions, along with the interspecific relationship between *R. dalmatina* and *R. temporaria.*

Key words: *Rana temporaria*, decline, climate change, monitoring

Initial toxicological characterisation of the skin secretion of Buresch's crested newt (*Triturus ivanbureschi*)

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The Buresch's crested newt (*Triturus ivanbureschi)*, distributed in Southeastern Europe and Anatolia, is one of the largest species in the genus *Triturus*, family Salamandridae. Although many salamandrids are known for their toxins, only a limited information about the toxicological profile of skin secretion in this species is available. Our study provides characterization of skin secretion from 20 adult Buresch's crested newts, captured with funnel traps in March 2023 as part of an ongoing population study in a pond near Sofia, Bulgaria. Skin secretions were obtained by a non-invasive procedure, without usage of chemicals and electrostimulation, based on direct collection. Gauze was gently rubbed against the body of each newt for approximately 1 min., after which samples were individually stored in a freezer. After sample collection, all newts were released at the site of capture. The samples were eluted from the gauze and lyophilized. Initial in vitro and in vivo characterization was performed. SDS-PAGE revealed a number of protein bands, most of which focused between 15 and 65 kDa. The secretion possesses strong hemolytic activity, as already reported in other studies, but does not affect blood coagulation in vitro. Morphological studies of human RBCs treated with the secretion displayed extreme anisocytosis (RDW-SD 140.6 fL) and hypochromic changes. The acute toxicity (LD50) of the total secretion was estimated at 3.6 mg/kg b.w. (mice, i.v.; normalised to protein content). Signs of toxicity are primarily neurotoxic – rapid onset (2-3 min after injection), apathy, tremors, convulsions, seizures, hypersalivation, as well as varying degrees of paralysis. An indirect GC-MS analysis for tetrodotoxin (TTX) was performed which detected a C9 fragment, so the neurotoxicity of skin secretion of Buresch's crested newt was definitely related to the presence of a TTX-related structure. Its exact composition, and whether TTX production in *T. ivanbureschi* is endogenous or diet-based, remains to be clarified.

Key words: acute toxicity (LD50), blood coagulation, Buresch's crested newt, hemolysis, tetrodotoxin

Natural history museum collections as an untapped reservoir for pathogen studies: a case study of snake fungal disease in Norway

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Natural history museum collections are an invaluable resource when studying pathogens or disease vectors. The use of collection material ensures test-repeatability, large-scale geographical and temporal sampling, and allows sampling among threatened, protected or even extinct populations and species. As global climate change is expected to increase the frequency of infectious disease outbreaks, the use of biological archives will represent a rapid and rigorous way of assessing, preventing, and mitigating such diseases. Snake Fungal Disease (SFD), caused by the fungus *Ophidiomyces ophiodiicola*, is a disease threatening snakes. The disease is broadly distributed in North America and has recently been discovered in several European countries, among multiple snake species. The causative fungus invades the snake's skin which leads to lesions and localised immune reactions. In Norway, SFD has not yet been studied among the three native and protected snake species, the Common European adder (*Vipera berus*), the Grass snake (*Natrix natrix*), and the Smooth snake (*Coronella austriaca*). In this study, we screened for SFD among all Norwegian snake species using 330 skin swab samples from living and dead snakes, in addition to sloughs borrowed from the herpetological collection at the Natural History Museum and Botanical Garden, University of Agder. The specimens' collection year varied from 1996 to 2023. We molecularly tested for the presence of *O. ophiodiicola* using real-time PCR and species- specific primers and probes. We will present our preliminary results.

Key words: *Ophidiomyces ophiodiicola*, real-time PCR, molecular pathology, Norway

Diversity of *Anolis* lizards in Cusuco National Park, Honduras

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Neotropical lizards within the *Anolis* genus are ecologically diverse and typically demonstrate convergent evolution and adaptive radiation. Proposed as a ‘beta’ group within Anolis based on osteological morphology, *Norops* are a complex group of understudied mainland anoles distributed across North, Central, and South America. Their biogeographic origin is often debated, and recent studies have contested previous ideas about the classification of *Norops* and thus we will refer to these as *Anolis* henceforth. Although there have been previous phylogenetic studies of the genus, there remains taxonomic confusion due to morphological similarities between candidate species especially in mainland anoles that have received less attention than Caribbean anoles. Within Cusuco National Park (CNP), Honduras, there are thought to be 13 species of Anolis including four species which are endemic to the National Park, making it an important area for Anolis biodiversity. However, their evolutionary relationships are poorly understood, and individuals may be prone to misidentification. Our study aims to (1) identify how many and what species of Anolis occur within CNP, (2) place the CNP Anolis into a phylogenetic and biogeographic context. We present data for ca. 100 individuals sequenced for two mitochondrial (16S rRNA and CO1 and two nuclear loci (RAG1 and UBN1). We identified a possible 16 lineages that each could represent candidate species (work ongoing). Within CNP there is biogeographic structuring of species possibly linked to barriers to gene flow or niche partitioning.

Key words: *Anolis*, *Norops*, Diversity, Phylogenetics, Central America

The Evolutionary and morphological constraints of arboreality in geckos

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Skull shape morphology in lizards is essential for adapting to diverse diets and habitats. Geckos (infraorder Gekkota) are distributed globally, except the continent of Antarctica, and have infiltrated most ecological niches, from being fossorial to highly arboreal in nature. Yet, there are noticeable commonalities to most geckos with exceptions of fossorial species, they have dorso-ventrally flattened body shape and are aided by structures called Setae in their lamellae to climb. Both these adaptations, in combination with the limitations imposed by gravity, are hypothesised to be evolutionary constraints to the evolution of skull shape in geckos (Losos, 2010). In this study, we test this hypothesis by comparing the ecomorphological evolution of skull shapes in geckos to other squamates which are putatively not limited by the same constraints. Using the dataset from Watanabe et al. (2019) and adding >55 new taxa most of which comprise of geckos that are ecologically, phylogenetically, and morphologically diverse, we assess and quantify the morphospaces occupied by geckos in comparison to these groups. To accomplish this, we utilise 3D geometric morphometrics on 3D meshes generated using MicroCT scanning of specimens in natural history collections and open-source datasets. We examined the role of body size, habitat, and phylogeny in the evolution of gecko skulls through multivariate analyses that incorporate phylogenetic uncertainty. Through this study, we find that geckos occupy a more narrow morphological trait space in their skull shapes when compared to other Squamates. Comparing them to other arboreal groups of lizards and chameleons we find that other groups show far more diversity in skull shape when compared to geckos, revealing the need for further research into the ecomorphology of this diverse infraorder.

Key words: Geometric morphometrics, evolution, morphospace, reptiles

Anatomical and molecular characterisation of *Strophurus ciliaris* tail regrowth

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The northern spiny-tailed gecko, *Strophurus ciliaris* (Boulenger, 1885), bears glands in its tail that are used to eject a malodorous adhesive secretion to dissuade predators. Preliminary studies have shown that tail regeneration compromises the anatomical organisation of these “tail adhesive cannons” in related species. In this study, we analysed such a hypothesis in *S. ciliaris* observing its tail anatomy through a novel combined approach of Magnetic Resonance Imaging (MRI)-and histological examination, before and after tail regeneration. We discovered that the series of paired glands identified along the original tail is replaced by two larger glands after tail regeneration. However, we observed a proximo-distal gland organisation gradient with some invaginations towards the distal part of the tail. We speculate that tissues produced in the early stages of tail regeneration might retain some of the original structuring, while at later stages the construction of only two glands is prioritised. Combined transcriptomic and proteomic analyses also provided an unprecedented overview of the repertoire of proteins secreted by these glands prior to autotomy. Future studies could reveal whether this repertoire is modified after tail autotomy and replacement by the simplified pair of glands.

Key words: Geckos, adhesives, tail regeneration, reptiles, proteomics

Within-individual variance and population-level repeatability of the voluntary thermal maximum of grassland vipers (*Vipera* spp.)

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The thermal tolerance of ectotherms is a critical factor that influences their distribution, physiology, behaviour, and ultimately survival. Understanding the factors that shape thermal tolerance in these organisms is therefore of great importance for predicting their responses to forecasted climate warming. The small size of these vipers and the open landscape they inhabit renders them particularly vulnerable to overheating and dehydration. Here, we investigated the within-individual variance and population-level repeatability of voluntary thermal maximum (VTmax) of nine grassland viper taxa and explored the factors that influence these traits. We found that within-individual variance of VTmax of grassland vipers is only influenced by the thermal landscape, as we found no effect of body length, sex, and timing of measuring during the reproductive season. By comparing taxa occupying habitats below vs. above the treeline (i.e. steppe vs. alpine), we found no difference regarding between- and within-individual behavioural variation or repeatability, however, results show that regardless of the elevation (~ climate) of the habitat, within-individual variance explain a higher amount of total variance in VTmax than differences across individuals. Our findings emphasise the importance of considering local to regional

adaptation and environmental conditions when studying thermal physiology and the evolution of thermal tolerance in ectotherms.

Key words: Ecology, Evolution, Conservation, Behaviour, Adaptation, Physiology, Reptiles

Predation pressure on the endangered Hungarian meadow viper (*Vipera ursinii rakosiensis*) in grazed and mowed grassland habitats: insights from plasticine models

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Unecological management of habitats in grassland ecosystems is a critical issue for the conservation of animals, which may be further enhanced by altered predation pressure. In this study, we investigated the effect of mowing on the predation pressure by birds on an endangered snake, the Hungarian meadow viper (*Vipera ursinii rakosiensis*), using plasticine snake models. Mowing is a common but presumably harmful management type in viper habitats. We placed snake models in mowed hayfields and grazed pastures (as controls) in two study periods, before and after mowing on hayfields, in 2021 and 2022. We found that attack rates by birds on hayfields in the first year of the study were much lower than those on pastures when averaged across study periods, but also before mowing. Furthermore, mowing did not influence attack rates on snake models by birds in hayfields, but attack rates by birds were higher in pastures before than after the dates of mowing on hayfields. We also found that attack rates by birds on snake models in hayfields were constantly low during the two years of the study, regardless of the study period. On the other hand, attack rates by birds were significantly diminished in 2022 in pastures compared to 2021. Our study highlights the importance of considering potential factors influencing predation pressure and predator-prey dynamics in grassland habitats, as well as the need for further research to provide reliable datasets for evidence-based conservation management strategies to mitigate population declines and local extinction risk.

Key words: clay models, predator-prey interactions, reptiles, habitat management, wildlife conservation

Human-snake conflict mitigation data sheds light on snake occurrence patterns in a peri-urban setting in western India

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Snakes are perhaps the only wildlife in the Indian subcontinent that extensively co-occur with people and some are capable of being life-threatening. Dedicated manpower operates for mitigating such conflicts. As snakes are very secretive animals, records of snakes encountered in human habitation could provide valuable data on snake distribution patterns. Here, we present rescue records of snakes from Navsari district, Gujarat, western India, gathered during 2021-22 by Wildlife Rescue Trust Navsari (WRTN). Rescue records for 2021 and 2022 were compared from 11 March to 31 December. The total number of snakes rescued was 798 and 1589 respectively. In 2021 WRTN rescued 796 snakes (*-venomous) including: 201 *Naja naja**, 110 *Ptyas mucosa*, 110 *Daboia russelii**, 81 *Coelognathus helena helana*, 62 *Fowlea piscator*, 48 *Bungarus caeruleus**, 47 *Eryx conicus*, 40 *Lycodon aulicus*, 36 *Python molurus*, 15 *Platyceps plinii*, 13 *Amphiesma stolatum*, 9 *Oligodon tillacki*, 8 *Dendrelaphis tristis*, 7 *Eryx johnii*, 4 *Gerarda prevostiana*, 3 *Ahaetulla oxyrhyncha*, 1 *Echis carinatus**, 1 *Sibynophis subpunctatus*. In 2022, the total number got doubled and NGO rescued reptiles also included *Boiga trigonata*, *Calliophis melanurus** and *Boiga westermanii*. The rescued snakes were regularly released, on the same or the following day in their natural habitat within a range of 500 meters to 1 Km from the rescue site. Terrestrial snakes were released in unused open areas, grasslands, and barren farms, arboreal snakes were released in shrubby or well-wooded areas, and (semi)-aquatic snakes were released near water bodies of the Purna River. These datasets add up to a growing body of literature on methodically-collected snake rescue records serving as snake occurrence datasets, with a caveat that detection probability and natural history play a role in the snakes being seen by the inmates of the house.

Key words: Conservation, Gujarat, Rescue, Rehabilitation, Serpentes

Specific diversity of Helminth parasites of the edible frog *Hoplobatrachus occipitalis* (Günther, 1858) in an agricultural environment in the south-east of Ivory Coast, Africa

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Anurans are the most diverse amphibians in the world. They include 55 families divided into 451 genera and 6968 listed species (Lecointre and Le Gouyader, 2006). However, 40% of these species are on the verge of extinction. The decline of amphibians is seen as one of the most serious threats to global biodiversity. The main reasons for this decline are the destruction of their habitats (especially wetlands), pollution and their collection for food (Gibbons et al., 2000; Kiesecker et al., 2001). In addition, Anurans are hosts for a wide variety of parasites, including Helminths (Euzéby, 2008). Indeed, these worms can cause significant abnormalities in their hosts, including slowing of growth, skeletal deformities, deterioration of sight, reduction of host fertility. Parasitic helminths impact natural populations all the more when they are confronted with a polluted environment, but could also be transmissible to humans through consumption. "The Helminth-Amphibian-Human system constitutes a relevant study model for evaluating the health of ecosystems, the consequences on animal health and on human health on the one hand". Thus, the present work aims to study the parasitic load in Helminths in a group of Anurans representative of the Amphibians of West Africa exploiting contrasting environments in terms of pollution and interactions with human populations, namely the Park National Banco and the agro-industrial zone of Toumanguié in the south-east of Côte d'Ivoire. We propose to test the hypothesis according to which the Amphibian populations of the National Park being less exposed to environmental risks, they present the lowest parasitic load.

Key words: Zoonosis, wetlands, pollution, Anurans, parasitic Helminths, Côte d'Ivoire

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Kızıl, Ü.	0000-0002-8512-3899	Wang, J.	_
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Klynova, O.	0009-0002-4282-2486	Watanabe, A.	0000-0001-5057-4772
Knapp, A.	0000-0003-4822-5623	Wenner, B.	_

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Korsós, Z.	0000-0003-1545-5086	Wilkinson, M.	0000-0002-9459-8976
Kotserzhynska, I.	0009-0006-8661-7934	Wilson, L.E.	_
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Kovács, G.	0009-0003-5561-7825	Wollenberg-Valero, K.	0000-0001-8858-1804
Kovács, T.	_	Wormald, K	_
Kowalski, K.	0000-0001-6320-8384	Wüster, W.	0000-0002-4890-4311
Kraus, F.	_	Yaryhin, O.	0000-0003-0363-2057
Kruger, N.	0000-0002-6082-3135	Young, G.	_
Kumar, M.	0000-0002-0373-0426	Žagar, A.	0000-0003-2165-417X
Kusrini, M.	0000-0003-1111-2406	Zaman, S.	0000-0001-5399-0130
Labisko, J.	0000-0001-9324-5899	Zampieri, V.	_
Lalronunga, S.	0000-0002-7542-4815	Zethof, J.	_
Lapadula, S.	_	Zieliński, P.	0000-0002-8533-6800
Lassnig, N	0009-0003-3225-4523	Zinenko, O.	0000-0001-5228-9940
Laudelout, A.	0000-0002-7358-8517	Zuazo, O.	_
Laughlin, L.	_	Zuffi, M.A.L.	_
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