

**The 6th Asian Herpetological Conference
(AHC) and the Editorial Board Meeting of
Asian Herpetological Research (AHR)**



2026.8.22-25
Chengdu, China



Hosts:

- Asian Herpetological Research Society
- Chinese Herpetological Society

Organizers:

- Editorial Office of *Asian Herpetological Research*
- China-Croatia Belt and Road Joint Laboratory on Biodiversity and Ecosystem Services, Chengdu Institute of Biology, Chinese Academy of Sciences

Co-organizers:

- Key Laboratory of National Forestry and Grassland Administration on Biodiversity Conservation on the Qinghai-Xizang Plateau, Chengdu Institute of Biology, Chinese Academy of Sciences
- Key Laboratory of Biodiversity and Environment on the Qinghai-Xizang Plateau, Ministry of Education, Xizang University

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Tianyu Xi

Welcome Speech

Distinguished guests, esteemed colleagues, ladies and gentlemen,

On behalf of the Chengdu Institute of Biology, Chinese Academy of Sciences, it is my great honor and privilege to welcome you to the 6th Asian Herpetological Conference, held here in Chengdu from August 22 to 25, 2026.

Asia itself is a global treasure trove of herpetofaunal diversity. From the flying tree frogs to the Komodo dragons, from cryptic geckos to endemic turtles, our continent harbors an extraordinary array of species. Yet this richness faces unprecedented pressures: habitat loss, climate change, wildlife trade, and emerging diseases. Nearly one-third of Asian amphibians and many reptile species are threatened with extinction. Amphibians and reptiles are keystone components of ecosystem as predators, prey, and indicators of environmental health. Their decline signals deeper ecological imbalances that ultimately affect human well-being. Protecting them means safeguarding forests, wetlands, and agricultural landscapes upon which millions depend.

Our institute is widely recognized as the birthplace of herpetological research in China and remains one of the most important centers for such studies in Asia. We have built a comprehensive disciplinary system spanning taxonomy, systematics, conservation biology, animal behavior, and evolutionary biology. Our amphibian and reptile specimen collection houses 123,000 specimens, representing approximately 80% of all known amphibian and reptile species in China. This heritage and capability place us at the heart of Asian herpetology, and we are deeply committed to advancing knowledge and conservation across the region.

This conference brings together experts in new species discovery, systematics, evolution, ecology, behavior, and biodiversity conservation. By sharing data, methods, and perspectives across borders, we accelerate understanding and refine conservation strategies.

Over the next days, I encourage you to engage deeply in presentations, workshops, and informal discussions. Let us celebrate new discoveries, debate unresolved questions, and forge lasting partnerships.

Thank you all for your dedication.

Welcome to Chengdu, and welcome to the future of Asian herpetology.

Prof. Jiatang LI

Director

Chengdu Institute of Biology, Chinese Academy of Sciences



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Asian Herpetological Research

《亚洲两栖爬行动物研究 (英文)》



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1. Contact Information

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2. Traffic information

(1) Location of Railway Station and Airport



(2) Location of Hotels

Venue & Recommended Hotels Location Map

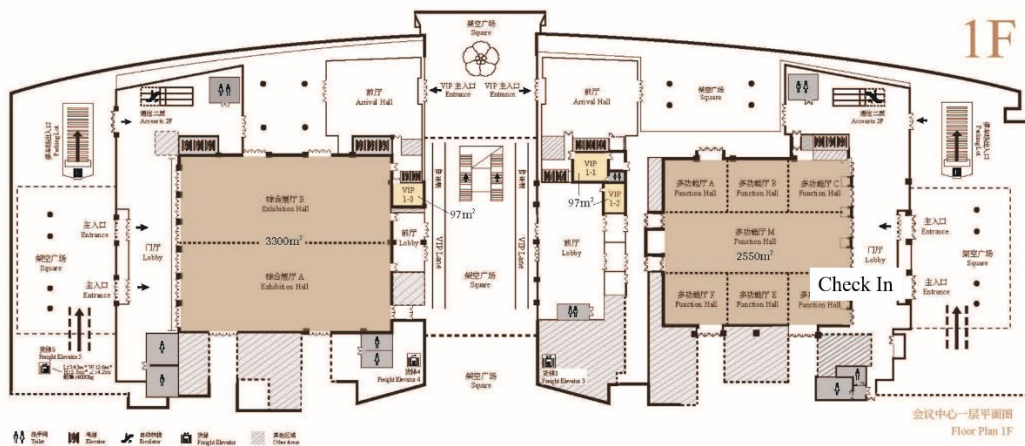
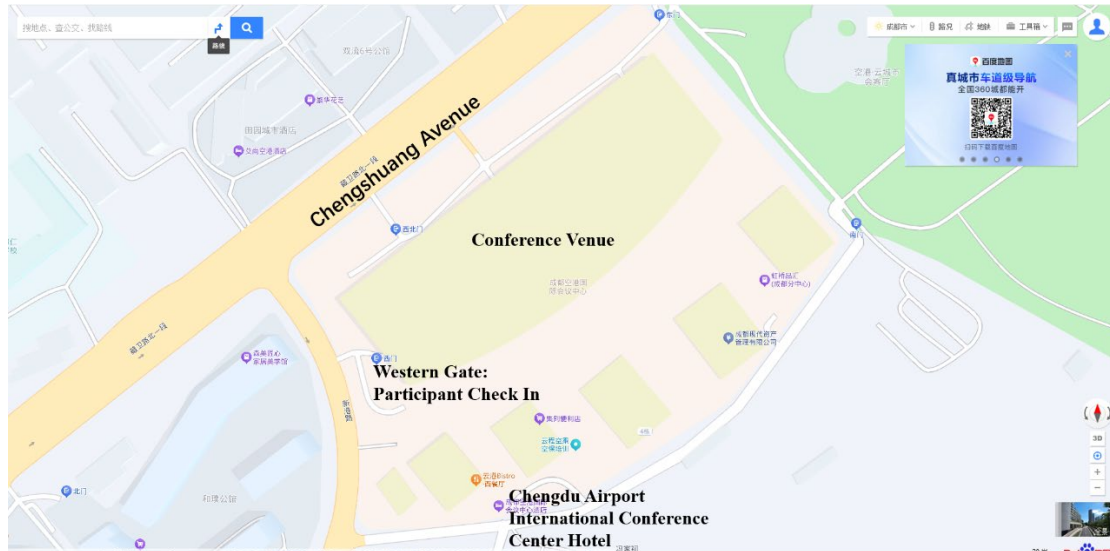
Around Chengdu Airport International Conference Center



- ★ Main Venue (Conference Center Hotel)
- ① Recommended Hotels
- M Metro Station
- ✈ Airport

3. Check-In and Meeting Room

(1) Check In: Western Gate on the first floor (1F) of conference Venue

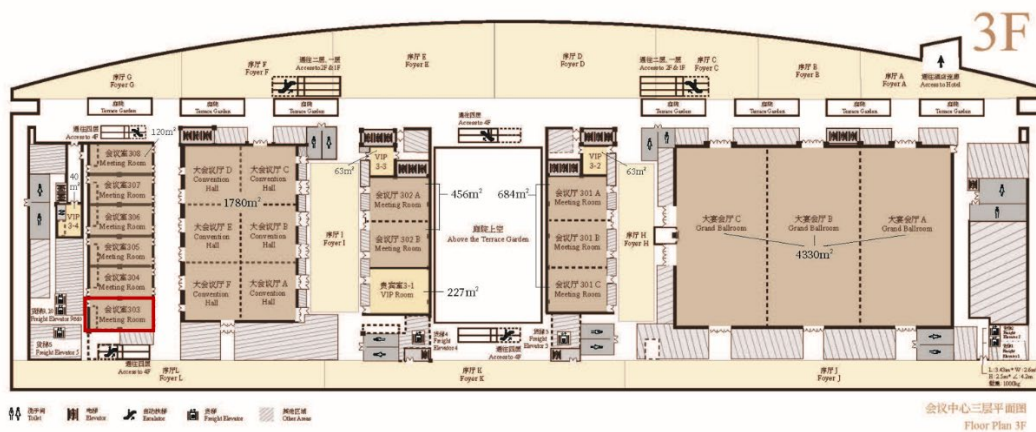


(2) Meeting Room

August 23: Room 303 on 3rd Floor (3F) of conference Venue

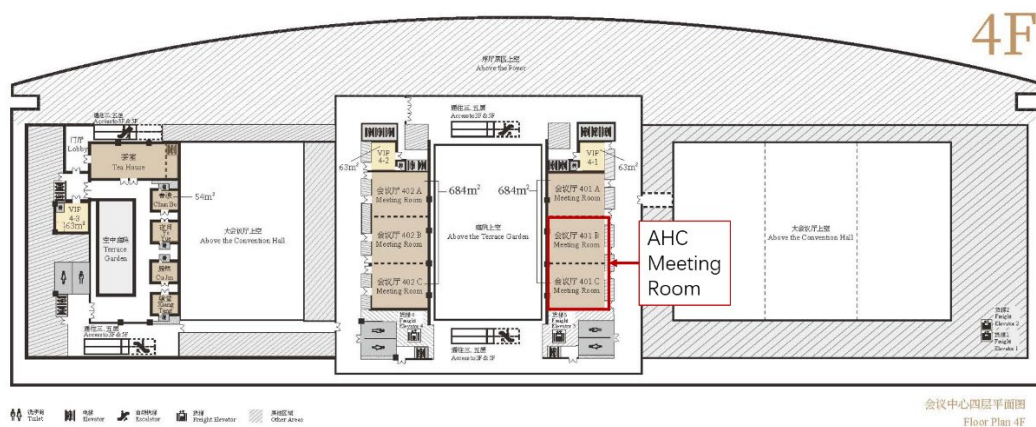
14:00-16:00 Editorial Board Meeting of *Asian Herpetological Research*

16:00-17:00 Council Meeting of the Asian Herpetological Research Society



August 24: Room 401 B and C on 4th Floor (4F) of conference Venue

Academic Conference: 08:30-12:00, and 13:00-18:30



4. Time and Place of Lunch and Dinner

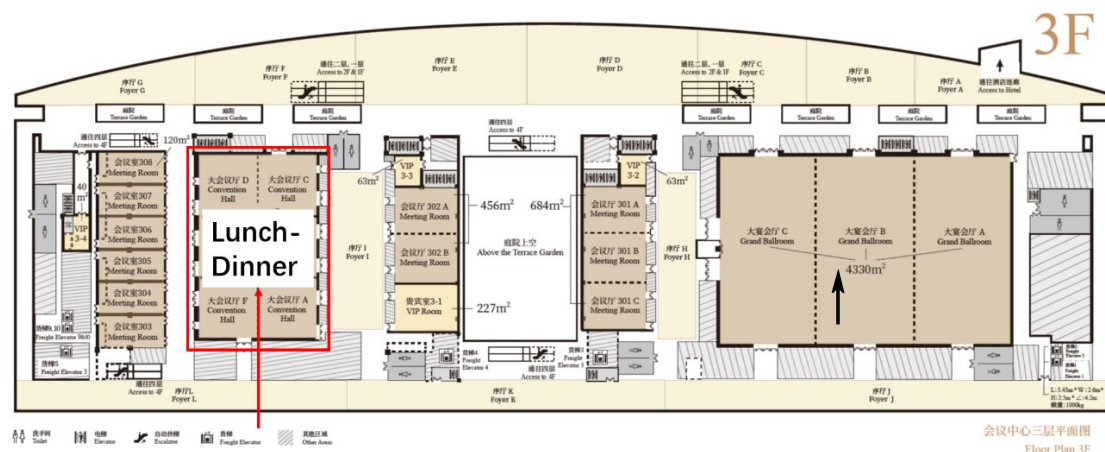
(1) Time

Lunch: 12:00 - 14:00

Dinner: 18:00 - 20:00

(2) Place

August 22, 23 and 24: Convention Hall on the 3rd Floor (3F) of Conference Venue



5. Conference Program

(1) Time Frame

August 22: Registration and Check-in

August 23:

Morning:

Visit to the Herpetological Museum of the Chengdu Institute of Biology, Chinese
Academy of Sciences

Afternoon:

14:00-16:00 Editorial Board Meeting of *Asian Herpetological Research*

16:00-17:00 Council Meeting of the Asian Herpetological Research Society

August 24: Academic Conference

08:30-09:00 Opening Ceremony

09:00-10:20 Academic Reports

10:20-10:30 Tea/Coffee Break

10:30-12:00 Academic Reports

12:00-13:00 Lunch Break

13:00-16:00 Academic Reports

16:00-16:10 Tea/Coffee Break

16:10-18:30 Academic Reports

18:30-18:45 Closing Ceremony

August 25: Departure

(2) Academic Conference

August 24, all day:

● **Opening Ceremony: 08:30 – 08:50**

Host:
Yin QI, Prof., (Chengdu Institute of Biology, Chinese Academy of Sciences) — Opening and introduction of guests
Welcome Addresses:
Jiatang LI, Prof., (Director General, Chengdu Institute of Biology, Chinese Academy of Sciences) — Welcome address
Fuwen WEI, Academician, (President, China Zoological Society; Professor, Institute of Zoology, Chinese Academy of Sciences) — Address
Natalia B. Ananjeva, Academician, (Zoological Institute, Russian Academy of Sciences) — Address
Chunyan Luo, Director General Level Officer (Grade II), (Science and Technology Department of Sichuan Province) — Address
Launch Ceremony of the reprinted edition of <i>Anurans of China</i> and Opening:
Jianping JIANG (President, Asian Herpetological Research Society; Professor, Chengdu Institute of Biology, Chinese Academy of Sciences) — Presiding over the launch ceremony, and officially declaring the opening of the 6th Asian Herpetological Conference.

● **Photography: 08:50-9:00**

Place: E part of the Pre-function Area on the third floor (3F) of Conference Venue

Organizer: Prof. Dr. Weizhao YANG

● Academic Reports: 09:00 – 12:00, and 13:00 -18:30

No.	Speaker	Affiliation	Time	Title	Session Chair
1	Natalia B. ANANJEVA	Russia: Zoological Institute, Russian Academy of Sciences	09:00- 09:20	Cryptic Taxonomic Diversity in Genus <i>Acanthosaura</i> Gray, 1831 (Sauria: Squamata: Agamidae) Species: Research History, Current Status and Perspectives	Xiang JI Prof., Wenzhou Unviversity
2	Indraneil DAS	Malaysia: Institute of Biodiversity and Environmental Conservation Universiti Malaysia Sarawak	09:20- 09:40	From Discovery, through Obscurity, to Familiarity. The Story of the Holy Grail of Herpetology, the Bornean Earless Monitor, <i>Lanthanotus Borneensis</i>	
3	Annemarie OHLER	France: Institut de Systématique, Evolution, Biodiversité (ISYEB), Muséum national d'Histoire naturelle	09:40- 10:00	What <i>Code</i> Do We Need? Some Structural Problems of Nomenclature Concerning Names of Amphibians and Reptiles	Weiguo DU Prof., Fudan University
4	Jinzhong FU	Canada: University of Guelph	10:00- 10:20	To split Or to Lump: Lessons From A Widespread Toad-Headed Agama Species	
			10:20- 10:30	Tea/Coffee break	
5	Marina A. CHIRIKOVA	Kazakhstan: Institute of Zoology of Republic of Kazakhstan	10:30- 10:50	On the Current Status of the Populations of <i>Rana asiatica</i> Bedriaga, 1898 (Amphibia, Ranidae) in Kazakhstan	Xiaobing WU Prof., Anhui Normal

6	Kornsorn SRIKULNATH	Thailand: Animal Genomics and Bioresource Research Unit (AGB), Faculty of Science, Kasetsart University	10:50-11:10	From Genomes to Reintroduction: A Decade of Crocodile Science Guiding the Recovery of <i>Crocodylus siamensis</i> in Thailand	University
7	Jichao WANG	China: College of Life Sciences, Hainan Normal University	11:10-11:30	Research on the Acoustic Communication of Freshwater Turtles	Jianguo CUI Prof., Chengdu Institute of Biology (CIB), Chinese Academy of Sciences (CAS)
8	Thitipong PANTHUM	Thailand: Animal Genomics and Bioresource Research Unit, Faculty of Science, Kasetsart University	11:30-11:50	A Systems Biology Framework for Safeguarding the Genetic Purity of the Siamese Crocodile	
9	Dong ZHANG	China: YIANWS(Qingdao) Technology Co., Limited	11:50-12:00	New Device for Monitoring Amphibians & Reptiles--Auto Camera Set on A & R	Weizhao YANG Prof., CIB, CAS
			12:00-13:00	Lunch Break	
10	Andrea CRISTIANO	Italy: Department of Biology and Biotechnologies “Charles Darwin”, Sapienza University of Rome	13:00-13:20	Assessing Amphibian Functional Resilience to Climate Change	Wenbo LIAO Prof., Western China Normal University

11	Francesco CERINI	Italy: Università degli Studi della Tuscia	13:20-13:40	Integrating freshwater conservation and Pastoral Stewardship in Mediterranean Rural Landscapes: The “Biodiversity Shepherd” Initiative	
12	Alessandra Maria BISSATTINI	Italy: Department of Biology and Biotechnologies “Charles Darwin”, Sapienza University of Rome	13:40-14:00	A Multidisciplinary Framework for Assessing Population Status and Habitat Quality in Pond-Breeding Amphibians	Baojun SUN Prof., Institute of Zoology, Chinese Academy of Sciences
13	Oleksandra OSKYRKO	China: School of Life Sciences, Fudan University	14:00-14:20	Size Matters Under Climate Change: Morphological Adaptation of Reptiles and Amphibians	
14	Jia JIA	China: Institute of Vertebrate Paleontology and Paleoanthropology, Chinese Academy of Sciences	14:20-14:40	The Evolutionary Origin and Ecological Disparities of Early Tailed Amphibians	Jun LI Prof., Central China Normal University
15	Keisuke NAKAJIMA	Japan: Amphibian Research Center, Hiroshima University	14:40-15:00	New Insight for Anuran Tail Regression	
16	Thanisha KUMAR	Hong Kong of China: Division of Science, Wu Jieh Yee School of Interdisciplinary Studies, Lingnan University	15:00-15:20	Origin of Tetrodotoxin in the Hong Kong Newt (<i>Paramesotriton hongkongensis</i>)	Zhuo CHEN Prof., Henan Normal University

17	Jie WANG	China: Chengdu Institute of Biology, Chinese Academy of Sciences	15:20-15:40	Co-Evolution of Transposable Elements and Host Silencing in the Gigantic Genomes of Salamanders	
			15:40-15:50	Tea/Coffee break	
18	Weizhao YANG	China: Chengdu Institute of Biology, Chinese Academy of Sciences	15:50-16:10	Formation Mechanisms of Lizard Diversity Across Eurasia	Baowei ZHANG Prof., Anhui University
19	Nikolay A. POYARKOV	Russia: Department of Vertebrate Zoology, Lomonosov Moscow State University	16:10-16:30	Hidden Diversity and Biogeographic History of Reed Snakes (Reptilia: Squamata: Calamariidae)	
20	Jinlong REN	China: Chengdu Institute of Biology, Chinese Academy of Sciences	16:30-16:50	Snake diversity in Eurasia: From evolution to resource utilization	Wei CHEN Prof., Anhui University
21	Igor V. DORONIN	Russia: Zoological institute of Russian Academy of Sciences	16:50-17:10	Permanent, Age-Related, and Dynamic Melanism in Caucasian Reptiles	
22	Tao PAN	China: Anhui Normal University	17:10-17:30	A Comprehensive Study on Population Demography of the Chinese Alligator and Its Habitat Succession	Jia JIA Prof., Institute of Vertebrate

23	Roman NAZAROV	Uzbekistan: Institute of Zoology, Academy of Science of Republic of Uzbekistan	17:30-17:50	Two Centuries of Herpetological Research in Uzbekistan: A Historical Overview and Analysis of Modern Diversity and Conservation	Paleontology and Paleoanthropology, Chinese Academy of Sciences
24	Elvy Quatrin DEKA	Malaysia: Faculty of Resource Science and Technology, Universiti Malaysia Sarawak	17:50-18:10	Surviving the Understory: The Ecology and Physiology of Frogs in Borneo	Guohua YU Prof., Guangxi Normal University
25	Van Chung HOANG	Vietnam: Institute of Biology, Vietnam Academy of Science and Technology	18:10-18:30	New Discoveries and Emerging Insights into Vietnam's Herpetological Diversity in the First Half of 2026	

● **Closing Ceremony: 18:30 – 18:45**

Host:
Prof. Weizhao YANG (Chengdu Institute of Biology, Chinese Academy of Sciences) — Presiding over the closing ceremony
Promotion of ACH 2027:
Dr. A. A. Thasun Amarasinghe (Chairman, Asian Herpetological Association (AHA); Postdoctoral Research Fellow, Research Center for Biosystematics and Evolution of Museum Zoologicum Bogoriense, National Research & Innovation Agency of Indonesia)— Promotion address
Closing summary:
Prof. Jianping JIANG (President, Asian Herpetological Research Society; Professor, Chengdu Institute of Biology, Chinese Academy of Sciences) — Summary on the 6th Asian Herpetological Conference and the Editorial Board Meeting of Asian Herpetological Research.

6. Abstract Book (via family name order)

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Asian Herpetological Conferences and Society: History and Development

Natalia B. Ananjeva

Zoological Institute, Russian Academy of Sciences, St. Petersburg, 1990134, Russia

A brief history of the Asian Herpetological Research Society and the Asian Herpetological Conferences is described. The Asiatic Herpetological Research Society (formerly linked with the Chinese Society for the Study of Amphibians and Reptiles) and the Association of Asian Herpetology are the most important institutions dedicated to the research and conservation of amphibians and reptiles in Asia. They collaborate extensively with the Chengdu Institute of Biology to publish the quarterly international journal *Asian Herpetological Research*.

Historically, AHR was preceded by the journal *Acta Herpetologica Sinica* which CIB began publishing in China in 1977 and stopped publishing in 1988. In 1990, *Acta Herpetologica Sinica* was renamed as *Chinese Herpetological Research*, and then was published by the Museum of Vertebrate Zoology, University of California, USA as an international journal for the Chinese Society for the Study of Amphibians and Reptiles (CSSAR). In 1991–2008, the journal was more one time renamed as *Asiatic Herpetological Research*. It was published by the AHRS and CSSAR at the same Museum, with the last issue being *Asiatic Herpetological Research* Volume 11 published by CIB and AHRS in USA. From now on, AHR quarterly published in China as a world-widely English language international journal, gradually become a journal with great influence in the herpetological research circle not only in China, but also in the world.

Asian Herpetological Research Society put forward a fruitful initiative to organize regular international Asian herpetological conferences. The first Asian conference took place in 1992 in China, followed by conferences in Turkmenistan (1995) and Kazakhstan (1998). Two subsequent conferences were successfully held in China in 2000 and 2012. This report demonstrates the available conference programs and photographs of the organizers and participants.

Keywords: Asian Herpetological Conferences, history, development

Cryptic Taxonomic Diversity in Genus *Acanthosaura* Gray, 1831 (Sauria: Squamata: Agamidae) Species: Research History, Current Status and Perspectives

Natalia B. Ananjeva

Zoological Institute, Russian Academy of Sciences, St.Petersburg, Russia

Progress in the development of research on agamid lizards of the genus is discussed. Ideas about the relationships within and between the genera of Oriental agamids have undergone significant changes during the 19th and 20th centuries (Günther, 1861; Boulenger, 1885; Smith, 1935). Interest in the problem of phylogenetic relationships within the Draconinae subfamily has increased significantly in recent years due to the use of molecular methods and the growing interest in Asian herpetological research. *Acanthosaura* Gray, 1831, Horned Tree Lizard is a genus of arboreal lizards in the taxonomically diverse agamid subfamily Draconinae Fitzinger, 1826, distributed from northeastern India, southern China including Hainan Island, through Vietnam, Laos, Myanmar, Thailand, Cambodia, the Malay Peninsula and adjacent archipelagos, to Sumatra and the Anambas and Natunas archipelagos (Uetz et al., 2026). In the second half of the 20th century, the majority of researchers accepted the validity of the genus *Acanthosaura* with only four species, i.e., *A. armata* Gray, 1827, *A. capra* Günther, 1861, *A. crucigera* Boulenger, 1885, and *A. lepidogaster* (Cuvier, 1829) (Ananjeva et al., 2008). The history and current state of research on these lizards are discussed. The results of modern studies of taxonomic diversity by Russian, Vietnamese, German, American, and other research teams using morphological and molecular methods are summarized. Data on the taxonomic position, distribution and range limits of species in this genus is contradictory, which is explained by the considerable morphological similarity of lizards within this genus and the lack of clear diagnostic characters. Currently, the genus *Acanthosaura* Gray, 1831 comprises 23 recognized species, and is typically assigned to several species groups (complexes), in addition to some species with uncertain positions for which molecular data are lacking. Thus, 17 of 23 species were described in the 21st century, a period marked by expanded opportunities for new materials and the implementation of advanced molecular methods.

Future studies should prioritize the inclusion of additional mitochondrial genes, potentially through sequencing complete mitochondrial genomes of representative lineages, to establish a well-supported phylogeny of the genus. It is equally crucial to compare mitochondrial phylogenies with those reconstructed from nuclear markers. Such an integrated approach with high-throughput next generation sequencing would help elucidate the current taxonomic challenges discussed in this study.

This research was partly supported by a grant from the Russian Science Foundation No. RSF-VAST 24-44-04004 (<https://rscf.ru/project/24-44-04004/>).

Keywords: arboreal agamid lizards, the genus *Acanthosaura*, history, current state of research

Overwintering of *Phrynocephalus Kulagini* (Reptilia: Agamidae) in the Coldest Region of Central Asia

Daniil I. Berman¹, Arcady V. Alfimov¹, Nina A. Bulakhova¹,
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Among the poikilothermic vertebrates adapted to extreme environments, the inhabitants of arid territories with cold winters are almost untouched by research.

We identified the adaptive strategies in reaction to temperatures at the overwintering sites of the common and abundant in the north of Central Asia species of lizard, Kulagin's variegated toadhead agama (*Phrynocephalus kulagini*). The cold resistance of animals and soil temperatures in the south-east of the Republic of Tyva (Russia), where the average long-term January air temperatures are -34.9°C , and the average absolute minima are -46°C , were studied. It has been established that *Ph. kulagini* does not tolerate freezing (dies), but is capable of overwintering for a long time at low negative temperatures in a supercooled state. The supercooling points (*SCP*) of *Ph. kulagini* turned out to be very low ($-12.5 \pm 1.1^{\circ}\text{C}$, $\text{min} = -17.4^{\circ}\text{C}$, $n = 20$); *SCP* of almost 60% of individuals ($n = 27$) are below the average value, and for 25% of individuals they are in the range of $-17.4 \dots -17.1^{\circ}\text{C}$. When determining the lower lethal temperature (*LLT*), it was found that mortality increases both with increasing exposure duration and with decreasing temperature. All animals successfully survived at -15°C for 7 days, but only 63% of individuals survived for 30 days. The minimum *LLT* studied was -16.3°C , at which two of the three lizards (67%) survived for 7 days. The proximity of this temperature to the minimum value of *SCP* (-17.4°C) indicates high stability of the supercooling state.

Ph. kulagini is likely the most cold resistant of the studied Lacertilia species. Only the Tibetan toadhead agamas *Ph. erythrurus* and *Ph. vlanglii* are closely related to it. Not all cold resistance parameters have been determined for the Tibetan agamas, preventing a complete comparison of these three species. *Ph. erythrurus* is the highest-altitude lizard in Central Asia, but winters in the fundamentally milder climate of the Qinghai-Tibet Plateau; it has an *SCP* value close to *Ph. kulagini* (average around -12°C) (Li et al., 2017), but *LLT* values are not known for it. *Ph. vlanglii* is similar to *Ph. kulagini* in its *LLT* value (-13°C) (Liao et al., 2026), but its *SCP* is unknown. All other studied lizard species have higher *SCP* values than the studied agamas.

A comparison of the obtained characteristics of cold resistance of *Ph. kulagini* and the vertical temperature distribution in the soils of typical habitats in the south-east of Tyva shows that overwintering of *Ph. kulagini* can be successful starting at a depth of about 50–60 cm, since the average long-term minimum temperatures at depths of 40 cm (-18°C) are lower than those tolerated by *Ph. kulagini*, and at a depth of 80 cm they are already higher than those (-12.5°C).

Thus, the adaptive strategy of *Ph. kulagini* includes both physiological and behavioral components, which allows it to successfully survive winter even in the Ubsu-Nur basin, which is probably the coldest winter region of Central Asia and the coldest area of distribution of steppes and desert steppes in the world.

Keywords: Central Asia, cold resistance, supercooling, tolerable temperatures, soil temperatures, depth of frost

The Immaculate Chinese Treefrog (*Dryophytes immaculatus*): A Silent Decline from Least Concerned to Endangered.

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The Chinese Immaculate Treefrog (*Dryophytes immaculatus*) was reported to be abundant in the plains of southern Jiangsu until the 1980s. However, the species has rarely been seen since 2000. We conducted surveys between 2017 and 2025 at more than 6000 independent sites, completed by citizen science surveys resulting in more than 1300 entries, to determine the occurrence of the species. In addition, we questioned farmers about the presence of the species. We detected *D. immaculatus* at 210 independent sites, obtained additional 12 independent sites from the citizen science data, and confirmed its local extinction at eight additional sites. Based on the accumulated data, we conducted ecological niche models, including some with putative absence, to determine the current suitable habitat for *D. immaculatus*. We also projected these models on climate change scenarios to determine the shift in suitable habitats. The current model identified the habitat to be suitable in an area marginally broader than the one where the species was found. The models of climate change scenarios highlighted a shift in the location of the suitable habitat for all scenarios and time periods tested, with a weak overlap with the current distribution of the species. Based on the data, we could apply the categories and criteria of the IUCN Red List of Threatened Species, and we suggested the species to be listed as Endangered under both criteria B2ab(i,ii,iii,v) based on geographic range, and C2a(i) based on the small and declining population size. The range of *D. immaculatus* has strongly contracted over the last decades, at a speed high enough for people who used to share their land with the species to remember them, but so fast that they are unknown by current generations. The suitable habitat for the species is further declining, and it is predicted to entirely collapse in all future climatic scenarios. While not Critically Endangered yet, *D. immaculatus* is in need of conservation actions, especially to prevent future decline in habitat quality.

Keywords: citizen science, local extinction, suitable habitat, ecological niche modelling, IUCN Red List

The European Pond Turtle *Emys Orbicularis* (Linnaeus 1758) is Tolerant to Hypoxia During Overwintering in Water

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The range of the European pond turtle *Emys orbicularis* (Linnaeus 1758) includes areas with cold winters: in the west of Russia it is distributed up to 58–59° N, in the extreme east of its range it is distributed in the south of the Urals and in Western Kazakhstan (Militov, Ananyeva, 2002; Debelov, Chibilyov, 2013). Here, it overwinters for up to six months in ice-covered, slow-flowing or stagnant water bodies, which is potentially dangerous due to the risk of a deficiency of dissolved oxygen (hypoxia). The tolerance of *E. orbicularis* to this critical winter environmental factor has not yet been studied (Ultsch, 2006).

In laboratory experiments, we determined the response of *E. orbicularis* from the Astrakhan population (Russia) to oxygen deficiency in water (hypoxia and anoxia). The experiments were conducted in sealed 10.3-L containers filled with water at 4–5°C, at dissolved oxygen concentrations of 5, 4, 3, 2, 1, 0.5, and 0.2 mg/L (i.e., from 38 to 1.5% of the normal concentration at this temperature). Oxygen concentrations were reduced by sparging the water with nitrogen gas. Survival of individuals at concentrations of 0.5–5 mg/L was determined after several days of exposure to each concentration, and maximum survival time was estimated under anoxic conditions (0.2 mg/L). Measurements were performed using a portable device HQ30D Flexi (Hach Instruments, Germany) with an LD0101 dissolved oxygen sensor (accuracy 0.1 mg/L).

Emys orbicularis at a water temperature of 4–5°C was able to survive for a long time (up to 94 days) with oxygen levels decreasing from 5 mg/L to 0.2 mg/L. Even under anoxic conditions, the turtles remained mobile, moving along the bottom of the containers. Larger individuals (weight 103 ± 5.4 g, $n = 23$) tolerated hypoxia better than smaller ones (32.4 ± 5.3 g, $n = 7$), as is the case with some other hypoxia-tolerant freshwater turtles (Ultsch, 2006). Among large turtles, the first deaths (9% of the sample) occurred only after 21–28 days at 1 mg/L. Only one of seven small turtles was able to survive at this concentration for 18 days (the rest died after 1–5 days at 3–5 mg/L). More than 55% of large individuals survived exposure to anoxia (0.2 mg/L) for 1–39 days (an average of 15 days). *E. orbicularis* proved well adapted to a sharp drop

in dissolved oxygen: 5 individuals, immediately transferred from 5 mg/L to 0.5 mg/L, then survived in the range from 0.5 to 0.2 mg/L of dissolved oxygen for 31–83 days.

Thus, *E. orbicularis* is able to tolerate hypoxia and anoxia in water bodies at low temperatures. This adaptation allows it to inhabit cold regions where overwintering ponds are covered with ice for up to six months, which increases the risk of oxygen deficiency. The turtles' continued mobility at low temperatures in anoxic water likely allows *E. orbicularis* to migrate to more oxygenated sites of water bodies, and also to move in case of low water levels in winter.

Keywords: freshwater turtles, hypoxia, anoxia, overwintering

A Multidisciplinary Framework for Assessing Population Status and Habitat Quality in Pond-Breeding Amphibians

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Amphibian declines are occurring worldwide, including within protected areas, with habitat loss and degradation representing the main drivers. Pond-breeding species associated with temporary waters are particularly vulnerable because of their dependence on small and dynamic habitats, which remain underrepresented in conservation frameworks. The Italian endemic *Bombina variegata pachypus* exemplifies this pattern, having experienced substantial declines across its range over recent decades.

Here, we developed a multidisciplinary, site- and species-focused framework in the Abruzzo, Lazio, and Molise National Park, integrating capture–mark–recapture population estimates, body condition assessment, and habitat evaluation through trophic ecology and feeding strategy analyses.

Of the 32 historically occupied sites, the subspecies was detected in 17, with most populations comprising fewer than 50 individuals, suggesting fragmented distribution and demographic fragility. Despite this, body condition remained relatively consistent among sites, whereas diet composition varied locally. The predominantly generalist and opportunistic feeding strategy, together with the alternation between active foraging and sit-and-wait tactics and the exploitation of prey with similar functional traits, suggests ecological flexibility that may support persistence under changing environmental conditions, including human-modified landscapes.

Together, these findings reveal a system in which demographic fragility coexists with relatively stable individual condition and trophic flexibility. Our results demonstrate that integrating demographic, individual-level, and trophic indicators can improve the assessment of population status by simultaneously identifying signals of vulnerability and ecological resilience. Such an approach may be particularly valuable in temporary waters and other highly dynamic ecosystems, where natural variability can obscure early warning signals of decline. From a conservation perspective, our findings emphasize the importance of preserving both aquatic and surrounding terrestrial habitats and support targeted management of natural and artificial breeding sites. More broadly, this framework provides a transferable tool for assessing population status and informing conservation strategies for pond-breeding amphibians inhabiting human-modified landscapes.

Keywords: body condition; diet composition; functional traits; population size; trophic ecology

Integrating Freshwater Conservation and Pastoral Stewardship in Mediterranean Rural Landscapes: The “Biodiversity Shepherd” Initiative

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The biodiversity crisis disproportionately affects freshwater biota, with amphibians representing the most threatened vertebrate group globally due to habitat loss, emerging diseases, and climate change. In Mediterranean rural landscapes, many aquatic organisms depend on small, shallow, often temporary water bodies increasingly vulnerable to desiccation. The Apennine yellow-bellied toad *Bombina pachypus*, an Italian endemic of high conservation concern, exemplifies this vulnerability. Although historically associated with natural ephemeral ponds, the species has long exploited artificial water bodies such as cattle troughs and traditional watering sites. These structures are built for free-ranging livestock but can function as permanent, predator-poor breeding habitats and refugia within increasingly dry landscapes, supporting *B. pachypus*, other amphibians and aquatic invertebrates. However, the ongoing abandonment of pastoral activities is leading to the disappearance or neglect of these small “safe island” habitats, exacerbating species decline. To address this, we present an integrated conservation initiative developed within the Appennino Lucano Val D'Agri Lagonegrese National Park (Southern Italy) where pastoralism and artificial watering sites remains widespread. Spatial surveys identified priority areas where drinking troughs sustain *B. pachypus* populations and associated freshwater assemblages, while genetic screenings informed the selection of source populations for future restocking. Selected troughs were restored or modified to improve ecological suitability while preserving their primary function for livestock. The key innovation is the formal recognition of the “biodiversity shepherd” role: local pastoralists who, through direct involvement and economic incentives, contribute to habitat maintenance, report ecological changes and provide continuous monitoring. This approach transforms pastoral infrastructure into conservation infrastructure and the routine, landscape-scale presence of shepherds into an effective early-warning system. Using *B. pachypus* as an umbrella species, this project delivers broader benefits for freshwater biodiversity, showing that conservation can align with rural livelihoods and that traditional pastoralism can help maintain freshwater habitats and multifunctional cultural landscapes.

Keywords: freshwater conservation, Mediterranean rural landscapes, traditional pastoralism, *Bombina pachypus*

On the Current Status of the Populations of *Rana asiatica* Bedriaga, 1898 (Amphibia, Ranidae) in Kazakhstan

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The Central Asian frog, *Rana asiatica* Bedriaga, 1898, is endemic to the Tien Shan Mountains and is classified as “Near Threatened” in China, “Vulnerable” in Kazakhstan, its conservation status remains uncertain in Kyrgyzstan. Surveys conducted in 2002 revealed the disappearance of the species from the flat part of its range in the Balkhash region, with populations persisting mainly in mountainous habitats (Dujsebaeva et al., 2002). Climate warming, increasing aridization, overgrazing, and the expansion of the (*Pelophylax ridibundus* complex) have been proposed as the main reasons for its decline (Dujsebayaeva, 2012; Dujsebayaeva et al., 2015).

To assess the current population status, we resurveyed all localities where *R. asiatica* had been recorded in July 2002 (Almaty Province, Rayimbek District) using identical observation methods. Field surveys were conducted in 2022 (April, July), 2023 (April, May, September), and 2024 (April, October) across the Karkara, Tekes, Kegen, and Shalkodesu river valleys, including Tuzgen Stream and Lake Tuzkol, using two transects per locality.

Compared with 2002, all sites exhibited marked habitat degradation and reduced frog abundance. Habitat deterioration included trampled riverbanks, degraded or weakly flowing springs, reduced water levels in temporary ponds, and decreased vegetation height and grasscover. In the Lake Tuzkol basin during 2022–2023, the only locality persisted, with an encounter rate of 2 individuals/km. In 2022, six egg clutches and juveniles were recorded; in 2023 all egg clutches had been destroyed by livestock, no juveniles were detected, while in 2024 no adults, egg clutches, or juveniles were detected. In contrast, in 2002 the species occupied the entire basin, with encounter rates ranging from 4.0 to 51.3 individuals/km. In the Shalkodesu River valley, where 4 individuals/km were recorded in 2002, the species disappeared in 2022–2023. In Sharyn National Park (Sharyn River), only a few individuals were observed in 2002, the species was absent in 2022–2023, although park staff reported occasional sightings. Relatively high densities persisted only in the Karkara River valley (up to 33 individuals/km), particularly in shrub areas (*Caragana* sp.) habitats and fenced hayfields, and within the protected zone of the Tekes Reservoir (up to 30 individuals/km), where anthropogenic disturbance was minimal. Elsewhere in the Tekes valley, the species was only occasionally recorded.

Analysis of climatic and vegetation parameters carried out with Google Earth Engine (1959–2025) showed a 1.5–2.0°C increase in air temperature, a 50–100 mm increase in average annual precipitation, stable air humidity and snow cover depth, but an increasing water deficit. SAVI change detection indicated progressive deterioration of vegetation cover between 2000 and 2025, particularly during the summer months.

Ecological niche modelling in ArcGIS Pro 3.5 using CMIP5 projections under the RCP8.5 scenario predicted a further reduction of suitable habitats for *R. asiatica*.

Although livestock numbers in Raimbek District declined between 2010 and 2025 (sheep – 46.6%, horses – 53.5%, cattle – 39.4% compared to 2010 (www.stat.gov.kz)), pasture carrying capacity and forage availability were not evaluated. Nevertheless, clear signs of overgrazing observed during field surveys indicate that livestock continue to exert pressure on *R. asiatica* habitats.

Keywords: *Rana asiatica*, population status, habitat degradation, overgrazing

Results of Kazakhstan–China Cooperation in Herpetological Research in China and Kazakhstan

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In 2013, the first Memorandum of Cooperation on herpetological research was signed between the Institute of Zoology (Ministry of Science and Higher Education of the Republic of Kazakhstan) and the Chengdu Institute of Biology (Chinese Academy of Sciences). The collaboration has continued successfully, joint research projects, academic exchanges, and training of young researchers. Field expeditions were conducted jointly by herpetologists from both institutions, resulting in extensive amphibian and reptile collections deposited in the collections of the Institute of Zoology in Kazakhstan and the Chengdu Institute of Biology in China.

Joint research surveys covered a wide range, including Mangystau and the Ustyurt Plateau, the Northern Aral Sea region and the Syrdarya delta, Moiynkum Desert, Saur and Barlyk Mountains, the Dzungarian Basin, the southern foothills of the Zhetysu Alatau, Southern Balkhash (Karatal, Aksu, and Lepsy river valleys, adjacent sandy massifs, and Ushkara Mountains), Junggar and Turpan basins, the Western, Northern, and Eastern Tian Shan ranges (Karatau, Kungey Alatau, Terskey Alatau, Borohoro, and Bogdaula), and the Ili River valley from the upper delta in Kazakhstan to the Tukai Desert in China.

These expeditions provided distributional and ecological data for more than 30 reptile species and three amphibian species. New records expanded knowledge of the ranges of *Lacerta agilis*, *Eremias vermiculata*, *E. multiocellata*, *E. stummeri*, *E. dzhungarica*, *E. velox*, *E. arguta*, *Phrynocephalus melanurus*, *P. hispidus* and *P. alpherakii*.

Molecular genetic and morphological analyses of selected *Eremias* and *Phrynocephalus* species yielded significant advances in taxonomy and phylogeography. The studies revised the intraspecific structure of *Eremias velox*, refined the phylogeographic structure of *E. vermiculata*, confirmed species-level differentiation within the *Phrynocephalus guttatus* complex, and elucidated the intraspecific structure of *P. melanurus*. Molecular dating and biogeographic analyses demonstrated the role of historical climatic changes in shaping species evolution and distribution of several species within these genera.

Ecological niche models developed for several *Eremias* and *Phrynocephalus* species identified the principal climatic variables their current distributions and provided a basis for predicting future range dynamics under changing climatic conditions.

The collaboration also included studies of the *Pelophylax ridibundus* complex, with a focus on the phylogeography in Kazakhstan and adjacent northwestern China.

Training of young specialists was another significant achievement. Daniya Ualiyeva, a graduate student from Kazakhstan, completed her doctoral studies at the Chengdu Institute of Biology and defended her PhD dissertation in 2026. Academic exchange activities included Marina Chirikova's two-week research visit to the Chengdu Institute of Biology in 2018 under the bilateral researcher exchange program, during which she examined and studied the institute's herpetological collections, contributing to subsequent joint taxonomic and biogeographic studies.

The joint research has resulted in 18 peer-reviewed publications covering these research directions. In addition, data collected during field surveys in Kazakhstan were incorporated into the latest edition of the Red Data Book of Kazakhstan.

Keywords: Sino-Kazakhstan herpetological collaboration, *Eremias*, *Phrynocephalus*, phylogeography, Central Asia herpetofauna

From Discovery, through Obscurity, to Familiarity. The Story of the Holy Grail of Herpetology, the Bornean Earless Monitor, *Lanthanotus borneensis*

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We recount the early history of discovery of what may be one of the most exciting tropical ectotherm, sometimes referred to as the Holy Grail of herpetology. Found from an unknown locality, presumably in western Sarawak by Franz Gröger, an Austrian engineer with the Borneo Trading Company, Kuching. Gröger was involved with mercury mining activities in the early 1870s, and the holotype, a part of a small vertebrate collection, was shipped to the Vienna Natural History Museum. Here, it received the attention of the then resident herpetologist, Franz Steindachner, who correctly interpreted a relationship with the Varanidae, establishing a new genus and species, and described the lizard in 1877. Thereafter, a hiatus of nearly half a century, coinciding with two World Wars, produced no specimens or field observations. However, the time was ripe for anatomists, McDowell and Bogert (1954), to examine material available in western museums, and publish a monograph on its general morphology. Tom Harrisson of the Sarawak Museum, Kuching, became aware of the species in the early 1960s, and circulated posters to find the species, and the widespread flooding across Sarawak at the time led to about the capture of about a dozen specimens by inhabitants of the Sibuan region, and sent to Harrisson, who, published on its discovery. Some specimens made their way to the Field Museum, others were given to specialists in Europe. One such worker was Robert Mertens of the Senckenberg Museum in Frankfurt, who successfully maintained individuals live and published a number of notes on its morphology and captive behaviour.

Interest in the species waned in the 1970s, and no new specimens were encountered, and none exhibited in zoos subsequently, till in the year 2008, when a group of botanists accidentally unearthed a resting specimen in Kalimantan. This was an extension of its range further south, and a new record for Indonesia. The discovery led to searches by mostly private or zoo-led investigators, and indeed, large numbers were illegally taken out to zoological gardens in eastern Asia and eastern Europe. While novel information of their captive care and reproduction were added to the scientific literature, rather disturbingly, specimens continue to be illegally trafficked from Indonesia and perhaps elsewhere on Borneo. One report remarked how western zoos are consenting to illegal trade in the species, bypassing local and international conservation laws.

Field work commenced in Sarawak on its field ecology by a team from Universiti Malaysia Sarawak, supported by Sarawak Energy Berhad. At the remote Baleh region,

individuals were fitted with radio-transmitters and tracked to understand its biology, primarily, thermal and spatial ecology, diet, movement, and interactions with humans.

Current researches have included genomic studies, as well as one that attempts to use eDNA to rapidly detect populations, particularly appropriate for a cryptic species that inhabits structurally complex where inventories are challenging, population densities are low, and their lowland rainforest habitats under threat.

Keywords: *Lanthanotus borneensis*, discovery, ecology.

Surviving the Understory: The Ecology and Physiology of Frogs in Borneo

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Frog communities in Borneo are very diverse. This delicate group of amphibians possess very thin skin, thus are vulnerable to be disrupted when the surrounding water quality and vegetation in the habitat are heavily modified by anthropogenic activities and bioclimatic changed. Due to excessive habitat fragmentations and habitat degradations to cater for agricultural, urbanization, and enhancing economic growth of the Sarawak State, several major concerns arose on the fate of Bornean frogs, that are at high risks of population declines in the wild. Despite the known population trend of the frog species in the wild and different traits to adapt well in the changing habitat, the interaction of their physiological characteristics with different environment remains poorly understood. Therefore, extensive studies had been conducted on frogs of Sarawak, Malaysian Borneo to understand the species' response and adaptation strategy towards the potential threats on the frog's genetic structure, diet, skin physiology and microbiome community, call character variations which influenced by the vocal apparatus structure and physical anomalies. This integrative research evaluates the genetic, ecological, and physiological resilience of Sarawak's amphibians against anthropogenic and climatic pressures. Molecular analysis of the Bornean horned frog (*Pelobatrachus nasutus*) identifies significant population subdivision dating back to the late Miocene, with western populations evolving independently from those in the north-east. This divergence is primarily attributed to Isolation-By-Distance (IBD) and the Lupar gap geographical barrier. While *P. nasutus* retains ancient traits for dry-environment tolerance, habitat fragmentation in regions like Suai and Kapit threatens gene flow, highlighting a critical need for enhanced landscape connectivity. While seasonal weather play role ecologically to the endangered *Limnonectes cintalubang* which was identified as an opportunistic "sit-and-wait" forager with a strong preference for Formicidae (ants). Notably, males exhibit significant seasonal shifts, consuming higher prey volumes and abundance during the wet season to support energetic demands, whereas female diets remain consistent year-round. Further investigation showed a decadal assessment (2015–2025) of Sarawak's calling ranids reveals significant temporal variations in vocal apparatus morphometrics. Ambient humidity, rather than temperature alone, emerged as a critical driver of these shifts, specifically affecting the CPEP (distance between cricoid processes), which serves as an early indicator of climate sensitivity. Furthermore, the study provides the first record of skin lesions in Bornean frog, suggesting increased susceptibility to desiccation and

microbial invasion due to habitat loss. Morphological examinations also identified skeletal abnormalities, such as oligodactyly and syndactyly, in a majority of examined specimens. The findings underscore that Bornean frogs especially in Sarawak are highly sensitive to microclimatic fluctuations and landscape changes. To ensure their long-term conservation, it is recommended to (1) prioritize habitat connectivity by establish forest corridors between fragmented sites to facilitate gene flow; (2) implement integrated monitoring by using spatial distribution models and temperature-corrected acoustic baselines to track population health; (3) mitigate developmental stressors by investigate the impacts of environmental contaminants and parasites to address the high frequency of skeletal abnormalities; and (4) protect microclimates by preserve High Conservation Value (HCV) areas to maintain the humidity and temperature thresholds essential for reproductive success and skin health. These habitable remnants would provide optimal ecological requirements for the frogs to survive.

Keywords: Bornean frogs, habitat connectivity, skin lesions, anomalies, microbiome, genetic structure

Genetic Variability, Phylogeography and Systematics of *Lacerta Agilis* Linnaeus, 1758 (Lacertidae, Sauria)

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Lacerta agilis Linnaeus, 1758 is a species with one of the largest ranges in reptiles. This species is the most morphologically variable species among the green lizards and with a number of morphologically and genetically distinguished subspecies. We analyzed 345 mitochondrial DNA *cytb* gene sequences (1143 bp) and 24 nuclear DNA β -fib intron 7 sequences (483 bp) from 234 localities of *Lacerta agilis*. All twelve currently recognized subspecies were included in genetic analysis. Two types of dendrograms of possible phylogenetic relationships were reconstructed, revealing identical topology and the presence of 11 supported clades. Eleven groups are distinguished on the median network of *cytb* haplotypes. Two clades/groups recorded in the Caucasus, both – in the North Caucasus and Transcaucasia. New data allowed us to expand our understanding of the genetic diversity and phylogeography of the species. Two valid subspecies-level taxa confirmed for the Caucasus: *L. a. boemica* Suchow, 1929 (species level status is not supported) and *L. a. exigua* Eichwald, 1831. Another currently recognized subspecies, *Lacerta a. ioriensis* Peters et Muskhelischwili, 1968 syn. nov. should be considered as junior subjective synonym of *L. a. boemica*, and three other transcaucasian subspecies, *L. a. brevicaudata* Peters, 1958 syn. nov., *L. a. grusinica* Peters, 1960 syn. nov. and *L. a. mzymtensis* Tuniyev et Tuniyev, 2008 syn. nov. should be considered as junior subjective synonyms of *L. a. exigua*. The role of the Caucasus as important center of haplotype diversity is supported based on our results. Based on genetic and morphological data, populations from the Carpathians are proposed to be considered as valid subspecies. Two subclades of mtDNA are distributed in the Tatra Mountains and the Eastern Carpathians are indicated within this new taxon. One endemic subspecies has been identified for the Caucasus, the Carpathians, the Crimean Mountains, and the Pyrenees, and there are potentially three subspecies (*L. a. bosnica* Schreiber, 1912, possible subspecies 1 and 2) in the Balkans. This study was supported by the Russian Science Foundation (grant No. 25-24-00013).

Keywords: phylogeography, subspecies taxonomy, genetic diversity, Caucasus biodiversity

The Editorial Board of A Scientific Journal Dealing with Zoological Taxonomy Should Include at Least One Nomenclatural Editor

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Many taxonomic publications include new scientific names and nomenclatural acts (which modify the status of names). To be appropriate, these acts require not only competence in evolutionary biology, phylogenetics and taxonomy, but also in nomenclature. The latter is a complex technical domain, which cannot be properly mastered by “common sense”. This requires a good knowledge and practice of the Rules of the *International Code of Zoological Nomenclature*. Unfortunately, many taxonomists have only a superficial knowledge of this text, as can be easily observed through a study of recent publications. Examples of rather common nomenclatural errors include the confusion between the concepts of nomenclatural availability and nomenclatural validity, the creation of invalid junior homonyms or synonyms of scientific names, the ignorance of the system of typification of scientific names, or the publication online of taxonomic papers introducing new names and nomenclatural acts but failing to comply with the conditions for their nomenclatural availability. A good solution to these problems is for each periodical or company liable to publish nomenclatural novelties to include in its Editorial Board one or several editors having a recognised competence in this domain, and empowered to reject a work as long as it does not respect the *Code*.

Keywords: zoological nomenclature, nomenclatural errors, International Code of Zoological Nomenclature, taxonomic publication quality control

To Split or to Lump: Lessons from A Widespread Toad-Headed Agama Species

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Molecular data from the last three decades have revolutionized taxonomy. Many cryptic species have been recognized; however, the opposite trend, taxonomic inflation, has also emerged. Toad-headed agama lizards (genus *Phrynocephalus*) have highly plastic and highly variable morphology, and several widespread species have recently been split into multiple species. I evaluate the taxonomic status of one widespread species complex, the *P. frontalis-przewalskii-versicolor* complex, with a particular focus on molecular data. Mitochondrial gene sequences grouped populations into five or six deeply diverged lineages, which may or may not correspond to traditional species/subspecies names, such as *frontalis*, *hispidus*, *kulagini*, *przewalskii*, and *versicolor*. Microsatellite DNA data revealed a clear pattern of male-mediated gene flow, and finally whole genome sequence data divided the complex into three geographic populations with substantial gene flow among them. Species delimitation tests based on whole genome sequences resulted in the whole complex being one species. There are several lessons to be learned. 1) In determining species boundaries, samples with comprehensive geographic coverage are essential. 2) Mitochondrial data are an excellent first step, but insufficient to make conclusions on their own. 3) Frequency-based data and data analyses are important to assess gene flow. Finally, a species is a scientific hypothesis and as such, a simpler hypothesis is always preferred. **Keywords:** *Phrynocephalus* species complex, species delimitation, taxonomic inflation, multi-locus molecular data, taxonomic hypothesis evaluation

New Discoveries and Emerging Insights into Vietnam's Herpetological Diversity in the First Half of 2026

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The first half of 2026 has yielded significant advances in the discovery and understanding of Vietnam's Herpetological diversity. Based on recent taxonomic studies, six new species were described from distinct ecological regions of Vietnam: *Leptobrachella deocaensis* from the coastal forest of Deo Ca Mountain, Dak Lak Province; *Amolops minhleii* from the montane evergreen forests of Vu Quang National Park, Ha Tinh Province; *Odorrana nagao* from limestone karst forests of Cham Chu Nature Reserve, Tuyen Quang Province; *Occidozyga nishikawai* from the puddle in the forest near a residential area of Khanh Hoa, Quang Ngai, Gia Lai Provinces; *Tylototriton vietnamirabilis* from Phu Xai Lai Leng Mountain, Nghe An Province; and *Scincella ngati* from the evergreen forest of Krong Trai NR, Dak Lak Province. These discoveries were supported by an integrative taxonomic approach combining morphological comparisons, morphometric analyses, molecular data, phylogenetic reconstruction, and ecological evidence. The six species exhibit substantial genetic differentiation from their closest relatives and occupy geographically restricted habitats, highlighting the presence of previously overlooked and potentially micro-endemic Herpetological lineages. Their discovery also demonstrates the importance of diverse habitats—including coastal forests, high-elevation montane forests, and limestone karst systems—for maintaining Herpetological diversity in Vietnam. Collectively, these findings emphasize that Vietnam's Herpetological fauna remains incompletely documented and that continued field surveys, integrative taxonomy, molecular research, and conservation assessments are essential for revealing and protecting the country's hidden biodiversity.

Keywords: Vietnam herpetological diversity, integrative taxonomy, micro-endemic species, karst and montane habitat conservation

The Evolutionary Origin and Ecological Disparities of Early Tailed Amphibians

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Hynobiid salamanders are a group of primitive tailed amphibians that are distributed mainly in East Asia. Hynobiids have a number of plesiomorphic characters that are absent in derived salamanders but are commonly seen in early tetrapods, and hence are important in understanding the origin of modern amphibians and the fish-to-tetrapod transition. Starting from 1990s, tens of thousands of fully-articulated salamander specimens were found from the Mesozoic strata in northern China, and many Mesozoic salamander species named based on these materials are hynobiid-like in osteology. However, their interrelationships and relationships with crown-group salamanders remain unsolved. Our comparative studies on living cryptobranchoid salamanders and fossil salamanders based on micro-CT scan reveal evolutionary patterns for a number of morphological characters. Cladistic analyses show that the total group hynobiids, Panhynobia, originate no later than the Middle Jurassic (Bathonian), and the earliest known crown-group hynobiids are recently found from the Upper Cretaceous strata in Jilin Province. Shape and non-shape multivariate analyses of the palate show that metamorphosis and biphasic life cycles (aquatic larvae and terrestrial adults) are the life history strategy employed by the last common ancestor of salamanders, and all life history strategies seen in modern salamanders are already in place by the Early Cretaceous.

Keywords: Hynobiid salamanders, Mesozoic fossil amphibians, Panhynobia origin, amphibian life history evolution

Do Toxin-Sequestering Snakes Recognize Their Own Nuchal Gland Toxin Reserve? Insights From *Rhabdophis subminiatus*

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Animals that rely on chemical defenses may modify their defensive responses according to the amount of toxins available in their bodies. However, it remains unclear whether toxin-sequestering animals are capable of directly sensing changes in their stored toxin levels. Here, we examined this possibility in the red-necked keelback (*Rhabdophis subminiatus*), a snake that sequesters bufadienolides from toads and stores these compounds in specialized integumentary structures known as nuchal glands. We experimentally assessed defensive behavior under two conditions: before and after the depletion of nuchal gland contents through mechanical extraction. The effectiveness of toxin depletion was supported by significant decreases in both the mass and coloration of the extracted glandular fluid. Among 23 individuals examined, we found no significant changes in the frequency of defensive behaviors, including displays involving the nuchal glands, between the toxin-retained and toxin-depleted conditions. These findings indicate that *R. subminiatus* may not directly assess the amount of toxin currently stored in its nuchal glands when regulating its defensive behavior. Instead, toxin-related behavioral responses in *Rhabdophis* may be influenced indirectly by factors associated with previous feeding experiences involving toxin-producing prey. This study contributes to a better understanding of how chemical defenses are regulated and how such mechanisms may have evolved in toxin-sequestering snakes.

Keywords: defensive behavior, *Rhabdophis*, toxin, toxin sequestering

Origin of Tetrodotoxin in the Hong Kong Newt (*Paramesotriton hongkongensis*).

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Tetrodotoxin (TTX) is a potent neurotoxin that blocks voltage-gated sodium channels and has attracted broad interest both in neurobiology and as a candidate therapeutic for pain and anaesthesia. In marine taxa such as pufferfish (family Tetraodontidae), TTX is now understood to originate from symbiotic bacteria and accumulate through the food chain. Whether the same holds for terrestrial vertebrates, however, remains unresolved. The Hong Kong newt, *Paramesotriton hongkongensis*, exhibits marked spatial and temporal variation in skin toxicity, the mechanisms of which are poorly understood. Recent work on the North American rough-skinned newt *Taricha granulosa* has demonstrated that symbiotic skin bacteria belonging to the genera *Aeromonas*, *Pseudomonas*, *Shewanella*, and *Sphingopyxis* are capable of producing TTX, implicating the host microbiome as a key component of the toxin system. Given that at least 25 bacterial species from these same genera have been previously reported from the skin of *P. hongkongensis*, we hypothesize that similar symbiotic bacterial activity is the primary source of TTX in this species. This study investigates the origin of TTX in *P. hongkongensis*, with a specific focus on the role of the skin microbiome in generating and modulating toxin levels. To date, we have collected skin microbiome samples from 32 individuals across three localities and established pure cultures of isolated bacterial symbionts from these animals. Taxonomic identification of bacterial isolates was performed by colony PCR using universal 16S rRNA gene primers, followed by phylogenetic analysis of 16S rRNA gene sequences in the SILVA ribosomal RNA reference database to assign genus-level identifications. This yielded seven isolates belonging to genera previously reported as TTX-producers in the literature, indicating the presence of putative TTX-associated biosynthetic capacity within the skin microbiota of *P. hongkongensis*. Future work will employ high-performance liquid chromatography (HPLC) to confirm whether these gene-positive isolates actually synthesize TTX and to quantify toxin concentrations *in vitro*, followed by experimental manipulation of skin microbiota composition to study toxin dynamics.

Keywords: Tetrodotoxin, skin microbiome, symbiotic bacteria, amphibian

Genomic Evidence Links Environmental Harshness and Relaxed Sexual Selection to the Reversal of Sexual Dimorphism in the Taliang Knobby Newt

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Sexual dimorphism arises from the interplay between sexual and natural selection, yet how extreme environments shift this balance to reverse dimorphic traits remains poorly understood. Taliang knobby newt offers an exceptional opportunity to investigate the molecular basis of these phenomena, exhibiting marked variations in body size and tail height—not only between sexes but also among alternative, habitat-cued morphs within each sex. Here using population genomic analyses of 152 individuals from 16 populations across different altitudinal gradients, we estimate genetic structure and reconstruct population history dynamics. Then we integrated genome-wide association studies (GWAS), selection scans (XP-EHH), genetic islands analysis (F_{ST} and π ratio) dissect the genetic architecture of body size and tail height dimorphism. Venn diagram showed four genes associated with body size that were under recent positive selection and within the regions of genetic divergence. We also found more male-biased expression genes identified by sex-stratified GWAS analysis. Strikingly, nearly half of the loci associated with body size overlap with those regulating tail height in males, revealing a pleiotropic genetic architecture that constrains independent evolution. At high altitudes, intensified natural selection and

relaxed sexual selection on tail height from its correlational bounds and permitting its reversal. We also found the genetic basis of intensified natural selection to shifts in sexual dimorphism trait. These genes mainly related to DNA repair pathways, inflammatory responses and skeletal muscle development. Our findings established a mechanistic framework linking extreme environmental stress to the reversal of sexual dimorphism through the disruption of genetic constraints and the attenuation of sexual selection, offering general insights into how ecological forces reshape the evolution of complex traits.

Keywords: reversed sexual dimorphism; natural selection; sex selection; secondary contact; GWAS; XP-EHH

Herpetofaunal Diversity of the Russian Far East: Current Knowledge and Research Priorities

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The Russian Far East, characterized by significant meridional extent and widespread permafrost, exhibits a mosaic of natural zones reflected in its amphibian and reptile fauna. The northeastern boundary of amphibian distribution in Eurasia passes through this area. Currently, the regional herpetofauna comprises 47 species. There are 16 amphibian species, with two introduced on the Kamchatka Peninsula (*Pelophylax ridibundus* and *Rana temporaria*), and 31 reptiles, including one invasive species (*Trachemys scripta elegans*) and two species of sea snakes and four species of sea turtles entering Russia's waters. Species richness declines northward, where only three species are found: *Salamandrella keyserlingii*, *Rana amurensis*, *Zootoca vivipara*.

Of the 45 national-level Far Eastern nature reserves, the greatest diversity of herpetofauna is found in the southern protected areas, primarily in Land of the Leopard National Park (18 species) and Anuysky National Park (15 species). One amphibian species and seven reptile species are included in the Red Data Book of the Russian Federation (2021).

Vast uninhabited territories, a low percentage of studied areas, a small number of researchers, and often extreme fieldwork conditions are the reasons why the number of far eastern herpetological studies is low. However, in recent years, positive dynamics have been observed at the regional, national, and international levels.

Recent studies have addressed multiple directions: cryotolerance research on amphibians and reptiles (*Salamandrella keyserlingii*, *Rana amurensis*, *R. arvalis*, *Vipera berus*) at the Institute of Biological Problems of the North FEB RAS (Magadan); long-term comprehensive surveys of growth, reproductive traits, and age structure of amphibians across all Far Eastern federal subjects by Russian State Agrarian University (Moscow); Holocene herpetofaunal dynamics in the Sikhote-Alin region based on cave deposits (Voronezh State University (Voronezh) and the Federal Scientific Center for Biodiversity (FSCB) FEB RAS (Vladivostok); genetic diversity assessments of the genus *Takydromus* by FSCB FEB RAS (Vladivostok); and faunistic studies yielding new regional species (*Glandirana emeljanovi*, *Dryophytes leopardus*, *Eretmochelys imbricata*).

Research on rare and endangered species included: the first description of breeding sites with egg clutches for the endemic *O. fischeri*; collaborative molecular studies on evolutionary divergence and phylogeny of *Onychodactylus* and *Salamandrella* (FSCB FEB RAS and Nanjing University, China); and a captive-breeding program for *O. fischeri* at Leningrad Zoo (Saint Petersburg). For *P. maackii*, whose numbers are declining across East Asia, monitoring continues at Lake Khanka (>ten years) and the Amur River (three years); artificial nesting sites have been developed for extreme

climatic conditions in the lower Amur; and an isolated population of disputed origin on the Razdolnaya River was surveyed.

The invasive turtle species *T. s. elegans* is being monitored on an ongoing basis. In Northern Asia, the only reliably confirmed wintering area for this species is southern part of the Russian Far East. Research continues on socio-infrastructural factors in envenomation epidemiology caused by *Gloydius*.

There are a number of small studies on the histology of Caudata, on snake reproduction, on amphibian nutrition, etc.

Expanded systematic surveys and cross-border collaboration are needed to address knowledge gaps and preserve the region's unique herpetofauna.

Keywords: herpetofauna, biodiversity, researches, Russian Far East

New Insight for Anuran Tail Regression

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Tail regression during anuran metamorphosis is a drastic and well-known phenomenon. In 1912, German scientist Joseph Frederick Gudernatsch fed several mammalian tissues to tadpoles of two anuran species, *Rana temporaria* and *Rana esculenta*, and he found that horse thyroid most strongly induced metamorphosis in them. The active substances in the thyroid are now known as thyroid hormones. In 1972, Australian scientist John Foxton Ross Kerr defined apoptosis, a form of programmed cell death. In 1974, he demonstrated that the tail epidermal and muscle cells of eastern dwarf tree frog tadpoles (*Litoria glauerti*) showed typical apoptotic characteristics during metamorphosis. More than 50 years of studies focused on tail epidermal and muscle cells have revealed many molecular mechanisms underlying apoptotic cell death and thyroid hormone signaling cascades. Nevertheless, the central mechanism driving tail regression remains unclear. In this presentation, I will demonstrate the importance of notochord degradation during anuran metamorphosis. Notochord degradation has long received little attention in studies of the mechanisms of tail regression.

Thyroid hormone is known to be necessary and sufficient for amphibian metamorphosis. Inhibition of thyroid hormone synthesis prevents metamorphosis, whereas exogenous thyroid hormone treatment induces precocious metamorphosis in premetamorphic tadpoles. *Xenopus tropicalis* has two thyroid hormone receptors, alpha and beta (TR α and TR β). These receptors have similar amino acid sequences. They are nuclear receptors and recognize the same thyroid hormone response elements. They form heterodimers with retinoid X receptors and activate or repress target gene expression in the presence or absence of thyroid hormone, respectively. I generated TR α and TR β knockdown and knockout frogs to clarify their respective roles. Unilateral TR α knockdown induces precocious hindlimb growth on the injected side in premetamorphic tadpoles. This phenotype indicates that one of the roles of TR α during premetamorphosis is to prevent the initiation of metamorphosis. TR β knockout tadpoles at metamorphic climax show delayed degradation of tadpole organs such as the tail and gills. This phenotype indicates that one of the roles of TR β during metamorphic climax is to accelerate metamorphic processes and ensure the timely completion of metamorphosis. Interestingly, the tails of TR β knockout tadpoles show loss of muscle while retaining intact notochords. This phenotype indicates that notochord degradation is necessary for tail resorption. To clarify the molecular mechanisms of notochord degradation, I established a notochord organ culture system. A physiological concentration (10 nM) of thyroid hormone triiodothyronine induced shrinkage of the cultured notochord and increased approximately 2,000-fold in the expression of several matrix metalloproteinase (MMP) genes. Thyroid hormone-induced notochord shrinkage was inhibited by the pan-MMP inhibitor doxycycline. These results

demonstrate that thyroid hormone-induced notochord degradation is autonomous and strongly suggest the involvement of MMPs. This notochord organ culture system will shed light on the molecular mechanisms of notochord degradation and its role in tail regression.

Keywords: metamorphosis, notochord, tail regression, *Xenopus tropicalis*

Two Centuries of Herpetological Research in Uzbekistan: A Historical Overview and Analysis of Modern Diversity and Conservation.

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The herpetofauna of Uzbekistan has been studied for exactly two centuries, beginning with Eversmann's expedition in 1821–1822. Despite this long history, the region is still often described as a "white spot" or "poorly studied" in modern literature—a perception likely reinforced by the language barrier, as 90% of relevant publications are in Russian.

This presentation reviews the history of studies of Uzbekistan's herpetofauna, highlights the key researchers who shaped current knowledge, and discusses modern perspectives on research and conservation of the country's reptile diversity.

Four main stages can be distinguished: the foundational work of E.A. Eversmann (first half of the 19th century), the extensive collecting of N.A. Zarudnyi (early 20th century), the ecological and faunistic school established by D.N. Kashkarov (mid-20th century), and the prolific post-war research led by O.P. Bogdanov. Their influence is evident in the fact that 14 out of 60 reptile species in Uzbekistan are named after these researchers and collectors.

From a zoogeographic standpoint, Uzbekistan's landscape is relatively young and formed in the Quaternary period, with arid plains and sandy deserts (e.g., Kyzylkum) bordered by the Tien Shan and Pamir-Alai mountains. The herpetofauna was shaped by dispersal from the more ancient continental areas of Central Asia following the Paratethys regression.

Current research employs modern integrative approaches to clarify species-level diversity and phylogeny of the herpetofauna. Our ongoing study of the miniature gecko genus *Alsophylax* exemplifies this direction. These poorly known species exhibit a mosaic distribution associated with major river basins, with two species found exclusively in anthropogenic landscapes, often on medieval fortress ruins. Using molecular, acoustic, and morphological analyses, this project aims to resolve phylogenetic relationships, identify potential new species, and test hypotheses about the influence of the Silk Road on their biogeography. This modern work demonstrates that while the historical foundation of Uzbek herpetology is solid, new methods continue to reveal the region's rich and still incompletely understood biodiversity, as well as open new avenues for research at the ecological and evolutionary levels.

Keywords: Uzbekistan herpetofauna, Central Asian arid zone reptiles, *Alsophylax* gecko phylogeny, herpetological research history

What *Code* Do We Need? Some Structural Problems of Nomenclature Concerning Names of Amphibians and Reptiles

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Nomenclature regulates the attribution of scientific names to taxa. Whereas the taxonomic concepts and methods have changed in an important way in the last decades, the *International Code of Zoological Nomenclature* did only change for a few specific points in the last 25 years. When introducing in 2012 Rules that should allow electronic publication of new names and nomenclatural acts, the *International Commission of Zoological Nomenclature* opened Pandora's box which induced a series of nomenclatural errors concerning these names and nomenclatural acts. I will discuss examples of old and recent nomenclatural cases that have impact on the names to be used as valid, and discuss concerns of stability in particular points, notably regarding databases and electronic devices necessary for the development of nomenclature in the future. The presentation will focus on the importance of giving due attention to nomenclature in the frame of publication.

Keywords: International Code of Zoological Nomenclature, electronic publication
nomenclatural errors, taxonomic name stability, zoological nomenclature rules

Size Matters: Morphological Adaptation of Reptiles and Amphibians to Climate Change

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Climate change poses significant threats to global biodiversity, driving shifts in species distributions, phenology, and morphology. Understanding how reptiles and amphibians adapt to these rapid environmental changes is critical for conservation planning. Here, we synthesize evidence across multiple spatial and temporal scales to examine morphological responses of reptiles and amphibians to climate change, focusing on three key questions: (1) the effect of latitude and temperature on morphology (Bergmann's rule), (2) the ecological predictors driving morphological change, and (3) how morphological data from museum collections elucidate species' responses over time.

To test Bergmann's rule in reptiles and amphibians, we examined species- and population-level data. Our findings demonstrate that Bergmann's rule—the tendency for larger body sizes at higher latitudes—is not supported in ectothermic groups at the interspecific level. Contrary to patterns observed in endotherms, no consistent relationship between body size and latitude was found across amphibians and reptiles. At the population level, around 20% of species showed Bergmannian clines, indicating that this rule is weaker in ectotherms than in endothermic vertebrates.

To identify the ecological drivers moderating Bergmann's rule in reptiles and amphibians, we integrated climate data with life-history trait information. Body size evolution in these groups is shaped by a combination of ecological factors rather than a single predictor. Temperature also did not correlate with body size along latitudinal gradients. However, non-tropical species and terrestrial habitats showed stronger support for Bergmann's rule, suggesting that geographic context and habitat type are important moderating factors. These findings indicate that Bergmann's rule is not a universal ecological principle but a context-dependent pattern influenced by ecology and evolutionary history.

To detect morphological changes driven by climate change over time, we leveraged Chinese museum collection specimens as a historical baseline. We compiled morphological data from more than 14,000 individuals across more than 300 species of amphibians and reptiles, applying rigorous quality control. Linear models were used to assess temporal trends and climate relationships. Generalized additive models (GAMs) were further employed to test for nonlinear associations between body size and temperature over time. Results revealed a significant overall decrease in body size over time and a significant negative relationship between body size and mean annual temperature across all years. GAM analysis identified significant nonlinear relationships between body size and temperature in more than 80% of studied species.

Specifically, in warmer years, we observed a decrease in body size, whereas in cooler years, body size increased in most species.

As global temperatures continue to rise, our findings predict continued body size reductions in many reptile and amphibian lineages, with potential cascading effects on ecosystem functioning. This study emphasizes the need for taxon-specific and context-aware approaches in predicting biodiversity responses to ongoing climate change.

Keywords: Bergmann's rule, climate change, body size, reptiles, amphibians, morphological adaptation

Assessing Amphibian Functional Resilience to Climate Change

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This project aims to develop an operational framework to assess how biodiversity–ecosystem function (BEF) relationships shape the climate resilience of amphibian communities within long-term biodiversity monitoring networks. Functional diversity is a key determinant of ecosystem functioning, stability, and adaptive capacity under environmental change, yet it is still rarely integrated into spatially explicit assessments of climate vulnerability that inform biodiversity monitoring, conservation priorities, and ecosystem management.

Amphibians represent an ideal model system due to their high sensitivity to climatic variation and their pivotal functional role in both terrestrial and freshwater ecosystems. However, responses to climate change are highly heterogeneous: species and communities differ markedly in functional traits related to thermal tolerance, habitat dependence, and dispersal ability. As a result, communities with comparable species richness may differ substantially in their capacity to maintain ecosystem functions and ecological stability under future climate conditions.

Leveraging species occurrence records, ecological trait data and distribution maps of amphibians in China, the project will focus on the analysis, harmonization, and integration of existing data from long-term monitoring networks and consolidated trait and distribution databases. We will identify climate-relevant functional traits directly linked to ecosystem functioning to establish a functional classification of amphibian species into climate vulnerability and resilience groups, based on traits linked to ecosystem functioning. Using Area of Habitat modelling, we will also produce high-resolution maps of community-level functional diversity across the study area (China). Finally, we will integrate a suite of spatially explicit BEF indicators combining functional diversity and climate exposure, suitable for identifying functionally at-risk species and establishing monitoring sites to be integrated in existing monitoring infrastructures.

By explicitly linking functional diversity, climate sensitivity, and spatial monitoring data, this approach will enable the identification of monitoring sites and communities potentially at risk of functional erosion, supporting more informative biodiversity assessments and climate-smart conservation and monitoring strategies.

The project will advance current understanding of the relationships between biodiversity, ecosystem function, and climate resilience, providing quantitative and spatially explicit tools to integrate BEF into long-term monitoring frameworks. By moving beyond species richness alone, the project will support the identification of ecologically critical communities where climate change may threaten the persistence of key ecosystem functions and the services they underpin.

Keywords: amphibians, biodiversity-ecosystem function, climatic vulnerability, functional diversity, monitoring infrastructure

Comprehensive Study on Population Demography, Habitat Succession, and Genomic Conservation of the Chinese Alligator (*Alligator sinensis*)

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The Chinese alligator (*Alligator sinensis*) is a critically endangered species endemic to China, with a wild distribution now restricted to fragmented wetlands in Anhui Province. Over the past 2,000 years, its range has contracted sharply, closely mirroring human population expansion, land-use changes, and climate fluctuations. Historical records and paleoclimate data indicate that habitat loss, deforestation, agricultural intensification, and direct human persecution have driven a sustained decline, with climatic shifts further exacerbating range fragmentation.

Recent landscape ecology studies using UAV-based remote sensing, UNet deep learning, and Random Forest models reveal that only 4.62% of the current protected area is highly suitable for alligator activity. Habitat connectivity remains poor due to barriers such as settlements, farmland, and topography, leading to frequent human–alligator conflicts when individuals disperse beyond core zones. Carrying capacity estimates suggest that supporting 2,500 wild individuals would require tripling the current core habitat area, while 10,000 individuals would necessitate a ninefold expansion—underscoring the urgent need for targeted habitat restoration and corridor planning.

At the genomic level, our team has assembled a chromosome-level reference genome (2.26 Gb, 2n=32) and conducted whole-genome sequencing on 244 individuals, including wild, captive, and F1 populations. Results show that wild individuals possess significantly lower genomic heterozygosity than captive populations, and exhibit higher inbreeding coefficients, longer runs of homozygosity (ROH), and elevated genetic load. Kinship analysis reveals that 79.6% of individuals are closely related, indicating persistent inbreeding risk. However, demographic reconstruction indicates that the wild population hit its lowest point between 2005 and 2010, and has since rebounded due to effective captive breeding, reintroduction programs, and improved hatchling survival. Mitochondrial genomics further confirms extremely low maternal diversity (16 haplotypes from 325 individuals), with amino acid variations confined to only four protein-coding genes.

Encouragingly, artificial breeding has demonstrably enhanced genetic diversity and reduced inbreeding coefficients compared to wild cohorts, highlighting the success of ex situ conservation. These integrated findings—spanning historical demography, landscape suitability, and genomic erosion—provide a scientific foundation for future germplasm management, precision breeding, and habitat restoration. While challenges remain in microhabitat selection and post-release adaptation, the recovery trajectory of

the Chinese alligator offers a compelling case for the efficacy of long-term, multi-disciplinary conservation strategies.

Keywords: Chinese alligator, population demography, habitat fragmentation, genomic erosion, inbreeding, conservation genetics, captive breeding, landscape ecology

A Systems Biology Framework for Safeguarding the Genetic Purity of the Siamese Crocodile

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The critically endangered Siamese crocodile (*Crocodylus siamensis*) is severely threatened by extensive hybridization with the saltwater crocodile (*Crocodylus porosus*), compromising the genetic integrity of captive breeding and reintroduction programs. Reliable identification of genetically pure individuals is therefore fundamental to effective conservation management and long-term species recovery.

This study aimed to develop a robust genomic framework for distinguishing purebred Siamese crocodiles from hybrid individuals and to establish a rapid molecular assay suitable for routine

Genome-wide sequencing was performed on representative populations of *C. siamensis* and *C. porosus*, including a reference population of Australian saltwater crocodiles, to identify species-specific diagnostic genetic markers. Multiple population genomic approaches were applied to characterize hybridization patterns and detect advanced backcross individuals. Candidate diagnostic loci were subsequently validated and used to develop a polymerase chain reaction (PCR)-based assay for rapid genetic identification.

Among twenty candidate loci evaluated, three diagnostic markers consistently discriminated purebred Siamese crocodiles, purebred saltwater crocodiles, and multiple hybrid classes. Integrating maternally inherited, biparentally inherited, and species-specific nuclear markers substantially improved the accuracy of hybrid detection compared with single-marker approaches. The developed PCR assay provides a rapid, reliable, and cost-effective tool for routine genetic screening of captive populations and supports evidence-based selection of genetically suitable individuals for conservation breeding and reintroduction.

This integrated genomic framework enhances the accuracy of hybrid identification and provides practical molecular tools for conservation management of the Siamese crocodile. By strengthening genetic monitoring and improving breeding decisions, the proposed approach contributes to maintaining species genetic integrity, increasing the effectiveness of reintroduction programs, and supporting biodiversity conservation through the application of genomic technologies.

Keywords: Siamese crocodile; hybridization; conservation genomics; diagnostic markers; PCR assay

Of Cows and Frogs: Cow Dung Concentration Impacts Amphibian Early Life Stages

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Livestock manure can enter freshwater habitats via surface runoff, yet its concentration-dependent effects on amphibian early development and landscape-scale exposure risks remain poorly understood. We combined controlled exposure experiments with spatial modelling to assess the effects of cow dung on *Rana dybowskii* and identify potential exposure within suitable habitats in the lower Tumen River Basin. Four cow dung concentrations (0.8, 1.2, 2.5, and 3.5 mL/L) and a control were used to monitor development from eggs to froglets, metamorphosis timing, and mortality. Higher cow dung concentrations were generally associated with earlier development. Although mean time to first froglet did not differ significantly among treatments ($P = 0.235$), the ultra-high concentration group reached this stage 4.80 d earlier than the control. Cox models showed that its hazard of first froglet appearance was 2.73 times that of the control (HR = 2.73, 95% CI: 1.20-6.21, $P = 0.017$), increasing by 27 per 1 mL/L increase in cow dung concentration (HR = 1.27, 95% CI: 1.03-1.57, $P = 0.026$). This acceleration mainly occurred during the tadpole to limb stage: first limb appearance was 3.50 d earlier and this stage was shortened by 3.74 d, whereas the subsequent limb-to-froglet stage did not differ significantly. Cumulative mortality reached 50.5% in the ultra-high concentration group, suggesting a stress-related developmental response rather than simple growth promotion. Spatial modelling revealed extensive overlap between potential cow dung exposure and suitable habitats, with relatively high exposure across different suitability levels. Integrating controlled experiments with landscape-scale modelling provides a cross-scale framework for grazing management, non-point source pollution control, and amphibian conservation prioritization.

Keywords: *Rana dybowskii*; cow dung exposure; spatial modelling; habitat conservation

Hidden Diversity and Biogeographic History of Reed Snakes (Reptilia: Squamata: Calamariidae)

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The reed snakes of the family Calamariidae are an insufficiently studied group of colubroid snakes endemic to Southeast and East Asia. Until recently the reed snakes were regarded as the subfamily Calamariinae within the family Colubridae; however, recent molecular studies demonstrated that they represent a deeply divergent lineage within the Colubroidea with an unclear phylogenetic position. At present the reed snakes encompass over 100 species grouped into 7-8 genera, with the majority of this diversity assigned to the genus *Calamaria* (over 71 species). The taxonomy of the family is still poorly understood largely due to fossorial or semi-fossorial lifestyles and small body size; no comprehensive molecular studies of the Calamariidae diversity have been presented to date. We present the first assessment of diversity and phylogenetic relationships of the Calamariidae based on extensive sampling (over 192 specimens) with the major focus on the Indochinese species. Phylogenetic relationships were reconstructed based on analyses of three mitochondrial DNA (16S rRNA, cyt b, and COI gene fragments; total length up to 2350 b.p.) and three protein-coding nuclear DNA (BDNF, CMOS, and RAG1 gene fragments; total length up to 2467 b.p.) genetic markers. Our results confirm the monophyly of the family Calamariidae and reveal five major clades (A-E) within it. The comparatively large-bodied genera *Oreocalamus* and *Macrocalamus* are sister taxa and together form the clade A. The genus *Rabdion* (clade B) from Sulawesi forms a sister group with respect to all remaining Calamariidae taxa (with the exception of clade A). Clade C includes the Sundaic genera *Pseudorabdion* and *Collorhabdium*, with the first being paraphyletic with respect to the latter; this requires further studies. Our results confirm the monophyly of the genus *Calamaria*, which includes two major clades, representing the Sundaic (clade D) and the

Indochinese (clade E) radiations. Molecular dating suggests that the Calamariidae likely originated in the middle Eocene; all early stages of the family radiation likely took place in Sundaland, from where the ancestors of *Rabdion*, *Calamaria*, and *Pseudorabdion* independently and repeatedly colonized the Philippines, Sulawesi, and certain Wallacean islands, crossing the Wallace Line via oversea dispersal, most likely via rafting. The genus *Calamaria* originated in the late Eocene, most likely from Borneo, from where, starting with the Oligocene, the genus dispersed northwards to mainland Southeast Asia using the Thai-Malay Peninsula and Tenasserim as a ‘stepping stone’ facilitating its dispersal. From the Oligocene to the Miocene, two centers of secondary radiation of *Calamaria* were formed in Indochina and southern China. Our data suggest that the actual diversity of the family Calamariidae remains largely underestimated, with at least 17 revealed lineages likely representing undescribed or currently synonymized species. Based on our estimates, most species-level lineages of Calamariidae are older than 5 mya; further integrative studies of Calamariidae taxonomy will undoubtedly result in the discovery of numerous new species of these elusive snakes. This study was carried out with financial support from the Russian Science Foundation (RSF grant № 22-14-00037-P).

Keywords: *Calamaria*, taxonomy, Southeast Asia, Sundaland, Indochina

Snake Diversity in Eurasia: from Evolution to Resource Utilization

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Of the approximately 4,000 extant snake species (35 families) distributed across all continents and oceans except Antarctica, over one quarter (~1,000) occur in Eurasia, particularly Southeast Asia, highlighting this region as a focal area for squamate evolutionary and ecological research. Snakes originated in the Early Cretaceous from lizard-like ancestors with limb reduction, and their exceptional ecological adaptability has enabled colonization of plateaus, oceans, deserts, and polar regions, generating numerous unique lineages that serve as valuable models for studying adaptive evolution.

Through systematic global sampling, we reconstructed the global distributional dynamics of representative groups such as Natricidae. Focusing on extreme environmental adaptation, we elucidated the genetic mechanisms underlying the adaptations of hot-spring snakes to high-altitude environments and sea snakes to marine habitats, and further demonstrated the profound impacts of glacial historical events and the Yadong-Gulu rift tectonic activity on the genetic diversity differentiation of hot-spring snakes. Targeting distinctive traits including limb loss, vertebral elongation, asymmetric organ development, visual and auditory degeneration, infrared sensing, and venom systems, we employed large-scale comparative genomics and gene-editing functional assays to systematically uncover the evolutionary genetic mechanisms governing complex phenotypes such as sensory systems, body elongation, lateralized organ development, toxin gene evolution, color polymorphism, and parthenogenesis. In addition, we conducted research on screening bioactive components from snake venoms and infrared-sensing biomimetics, obtaining several candidate molecules and biomimetic principles with potential application value.

Our findings provide a fundamental basis for a deeper understanding of snake origins and evolution, offer critical scientific support for evolutionary developmental biology of reptiles and even vertebrates, and yield new insights for the development of venom-derived pharmaceuticals and biomimetic technologies.

Keywords: snakes; genetic diversity; distinctive traits; evolutionary patterns

Does Call Complexity Increase with Latitude? A Study of the *Leptobrachella oshanensis* Species Group

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Although species diversity generally increases from the poles toward the equator, speciation rates do not necessarily peak in the tropics. In amphibians, particularly in the order Anura, speciation rates tend to increase with latitude. Calling is an important means of communication for frogs and a key basis for species identification, yet the relationship between lineage divergence and call characteristic divergence remains unclear. Previous studies and literature have revealed that species of the genus *Leptobrachella*, which exhibit relatively conserved morphology but high species diversity, display a high degree of diversity in bioacoustic characters. We found that the calls of *L. oshanensis* Species Group around 30°N are more complex than those of lineages in their ancestral low-latitude distribution areas, and the rates of species and lineage divergence in this region are also the highest. This suggests that lineage divergence may be associated with the complexity of their calls. The study could provide a view for understanding why speciation rates tend to increase with latitude in Anura. Here, we propose to build an international collaboration on this study.

Keywords: speciation, vertebrates, advertisement call, trait evolution, *Leptobrachella*

From Genomes to Reintroduction: A Decade of Crocodile Science Guiding the Recovery of *Crocodylus siamensis* in Thailand

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The Siamese crocodile (*Crocodylus siamensis*) is one of the world's most critically endangered crocodilians, with fewer than 1,000 mature individuals remaining in the wild yet more than one million held in Thai commercial farms. This paradox, near-extinction in nature alongside genetically rich captive stock, makes species recovery both a scientific and a governance challenge. Reintroduction to protected areas such as the Ang Rue Nai Wildlife Sanctuary in eastern Thailand requires (i) resolving the taxonomic identity of source animals, (ii) ruling out cryptic hybridization with the saltwater crocodile (*C. porosus*), and (iii) placing living populations within a robust evolutionary framework.

Over the past decade, our group has assembled an integrated genetics-to-algorithms pipeline addressing each of these bottlenecks and translating it into national policy. This talk synthesises four converging lines of evidence and outlines their application to the Ang Rue Nai reintroduction programme.

Comparative cytogenomics across Crocodylia shows that diploid numbers vary only between $2n = 30$ and $2n = 42$, while the fundamental number remains fixed at $NF = 56 - 62$ — every difference is a Robertsonian centric fusion or fission with no net change in arm content. Fertile F_1 and F_2 offspring between *C. siamensis* ($2n = 30$) and *C. porosus* ($2n = 34$) confirm that karyotype plasticity does not erect postzygotic barriers, which is a critical constraint for interpreting molecular hybrid signals.

Analyses of 22 microsatellite loci and mitochondrial D-loop sequences across captive stocks in Thailand detected high haplotype diversity (0.924–0.971) but M -ratio values below 0.68, consistent with a historical bottleneck, and revealed bi-directional introgression between the two species. DArT-seq subsequently identified 8,051 species-diagnostic SNP loci for *C. siamensis* and 1,288 for *C. porosus*, three of which were converted into a rapid PCR assay for pre-release screening.

Farm surveys documented 2–6 post-occipital scutes in crocodiles that were genetically confirmed pure *C. siamensis*, prompting a revised identification guideline: individuals with fewer than four scutes need not be dismissed as hybrids, correcting a long-standing source of source-population loss.

To operationalize identification at scale, deep metric learning combined with convolutional neural networks classified 30 captive individuals from ventral- and head-scale images with 99.75% and 92.93% accuracy, respectively, offering a photograph-based tool for lifetime tracking of released animals.

Integrating chromosomal, genomic, phenotypic and AI evidence, we now have (a) a defensible protocol for selecting non-hybrid founders, (b) individual traceability post-release, and (c) a genetic-baseline archive for the Ang Rue Nai reintroduction cohort. We propose this framework as a transferable model for Asian herpetofaunal recovery and invite collaboration across the AHC community to extend it to *C. porosus*, *Tomistoma schlegelii* and other regionally threatened crocodilians.

Keywords: *Crocodylus siamensis*; conservation genomics; karyotype evolution; deep learning; reintroduction; Ang Rue Nai

Permanent, Age-Related, and Dynamic Melanism in Caucasian Reptiles

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The phenomenon of melanism is known for 28 reptile species in the Caucasus region (bout 25% of the species diversity of the herpetofauna of the region). Two types of melanism have been described: permanent melanism, characterized by black coloration throughout life (as an example, these are the populations of snakes of Western Transcaucasia, *Natrix megalcephala* and *Zamenis longissimus*), and age-related melanism, a change in coloration toward black in adults (It is known for *Pelias dinniki*, *P. magnifica*, *P. orlovi*, *P. renardi*, and *P. tuniyevi*, but is most characteristic of *P. kaznakovi*). A hypothesis of dynamic melanism has been proposed, in which coloration changes from normal protective to melanistic and then returns to normal (using the example of a *Lacerta agilis boemica*). The ecological and physiological causes of melanism in reptiles of the Caucasus and other regions are discussed. Melanism is most common in reptiles inhabiting Pleistocene-Holocene refuges in the Caucasus. Melanistic coloration was an adaptation to lower temperatures and high humidity. The humid and cool climate of the mountainous landscape also explains the high prevalence of melanists in the population.

This study was supported by the Russian Science Foundation (grant No. 25-24-00013).

Keywords: Caucasus reptile melanism, dynamic coloration pattern, Pleistocene-Holocene refugium adaptation, viper age-related melanism, reptile thermal adaptation

Co-Evolution of Transposable Elements and Host Silencing in the Gigantic Genomes of Salamanders

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Most vertebrates boast relatively compact genomes, typically less than 10 Gb in size. However, the genomes of lungfish and salamanders, which represent a crucial water-to-land evolutionary stage, are exceptions, surpassing 120 Gb and harboring independent events of genome expansion. The evolution of genome size involves substantial gains or losses of DNA sequence amounting tens of gigabases, and the primary elements driving these massive changes are repetitive sequences—transposable elements (TEs). TEs are segments of DNA capable of “jumping” and replicating within the genome. Their insertions have the potential to rearrange exons within host genes and disrupt native regulatory elements, thereby driving the evolution of gene regulatory networks. However, the expansion of TEs often disrupts the normal expression of functional genes, reducing host fitness. As a result, the host have evolved corresponding silencing mechanisms, such as DNA methylation, chromatin remodeling, and small RNA-mediated silencing, with piRNA silencing being the most important mechanism in animals. Additionally, due to the high similarity of TE copies at different locations, homologous recombination can lead to the deletions of DNA fragments.

To explore the evolutionary interplay between TEs and their hosts in this “arms race”, we selected gigantic genomes as an extreme case. Specifically, we examined six species of salamanders with genome sizes ranging from 12 to 49.9 Gb, encompassing a variety of phylogenetic lineages.

Our approach involved low-coverage genome sequencing, transcriptomic analysis of gonads during the reproductive phase, and small RNA sequencing to examine the landscape, diversity, historical dynamics, deletion rates, expression levels, and silencing mechanisms of TEs across different genome sizes. Additionally, we compared the variations in TE silencing levels during gametogenesis between males and females.

Our findings revealed that the transcription of salamander TEs exhibited significant sexual dimorphism, which correlated positively with their genomic content. In the male testes, KRAB-ZFP-mediated silencing was relatively weak, resulting in higher TE activity compared to that in the female ovaries. Unexpectedly, no correlation was found between genome size and TE deletion rates, historical dynamics, transcriptional activity, piRNA pathways, or KRAB-ZFP-mediated suppression of TEs. Contrary to most theoretical predictions, the diversity of salamander TEs increased with genome size.

These results suggest that when genome expansion reaches a certain threshold (e.g., 6–16 times the size of the human genome), the accumulation and landscape of TEs may be driven by random events rather than by the proliferation of specific TEs or host silencing mechanisms.

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Keywords: salamander gigantic genome, transposable element evolutionary, genome size expansion mechanism, TE silencing sexual dimorphism

Research on the Acoustic Communication of Freshwater Turtles

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From insects to mammals, acoustic communication is crucial for survival, successful reproduction, and many other life history strategies, particularly for species inhabiting dark environments or underwater where light is scarce. Chelonians are considered the least vocally active group of extant reptiles and known to have poor hearing sensitivity. More than 300 turtle species have been identified worldwide; however, vocalizations have been documented in only a limited number of tortoises and sea turtles. Currently, research on acoustic communication in freshwater turtles has been neglected. We recorded and analyzed the underwater sounds of *Trachemys scripta elegans*, *Pelodiscus sinensis*, and *Mauremys sinensis*. The peripheral hearing sensitivity of these three species was also measured using auditory brainstem responses. We identified at least 10 distinct underwater call types produced by these freshwater turtles. The underwater sounds and hearing sensitivity differed significantly between individuals of varying ages and sexes. Hearing sensitivity is affected by temperature and exhibited seasonal variation. Furthermore, the hearing sensitivity of freshwater turtles was readily impaired by airborne noise but demonstrated strong recovery ability. These studies refine our understanding of the adaptation and evolution of the vertebrate auditory system. In the future, we will focus on investigating the ecological functions of underwater sounds produced by freshwater turtles. Additional technical approaches from anatomy, endocrinology, and molecular biology will be employed to elucidate the mechanisms underlying auditory plasticity in freshwater turtles.

Keywords: acoustic communication, underwater vocalization, hearing sensitivity, freshwater turtles

A New Species of the Newt Genus *Tylototriton* (Amphibia: Urodela: Salamandridae) from China, with A Report of First Known Sexually Dimorphic Skeletal Structure of the Genus

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The genus *Tylototriton* (Amphibia, Caudata, Salamandridae) comprises a group of rare and threatened salamanders characterized by prominent dorsolateral bony ridges on the head, rough skin covered with granules and warts, and a longitudinal series of knob-like warts along each side of the body. Species of this genus are mostly restricted to montane forest habitats in East, Southeast, and South Asia, with narrow ecological niches, limited dispersal abilities, and a high degree of endemism. Most species of the genus are currently listed in the appendices of CITES. Despite the increasing number of newly described species in recent years, accumulating molecular and morphological evidence suggests that the cryptic diversity within this genus remains substantially underestimated. During recent field surveys in southwestern Hunan Province, China, we encountered a *Tylototriton* population that could not be assigned to any known species. Based on phylogenetic analyses of mitochondrial 16S rRNA and ND2 genes, morphological comparisons, and micro-CT skeletal scanning, we identified this population as the sister species of *T. lizhenchangi* (Mangshan crocodile newt) and describe it herein as a new species.

Previous studies have generally shown that most *Tylototriton* species exhibit allopatric distribution patterns, with their ranges often separated by geographic barriers such as river valleys and lowland plains, and each species tends to be locally endemic. However, in the present study, we found that the new species co-occurs sympatrically with *T. guilinensis*, a species recently described from Quanzhou County, Guilin, Guangxi, in 2026.

Micro-CT scanning was performed on the new species and its closely related congeners. A peculiar sexually dimorphic skeletal structure embedded in the abdominal musculature was observed exclusively in males of the new species. Comparative examinations of skeletal data across other species of the genus revealed that a similar structure has only been documented in *T. maolanensis*, while it is entirely absent in its sister species *T. lizhenchangi*, the sympatrically distributed *T. guilinensis*, and nearly all other congeners examined. The presence of this structure may imply potential differences in reproductive strategy between species. This discovery not only provides robust morphological evidence supporting the independent species status of the new taxon, but also offers valuable supplementary data for understanding the species diversity of the genus *Tylototriton*.

Keywords: *Tylototriton*, new species, sexually dimorphic bone, Micro-CT scanning, sympatric distribution

Formation Mechanisms of Lizard Diversity Across Eurasia

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Lizards are among the most diverse groups of terrestrial vertebrates in Eurasia, yet the mechanisms underlying their diversification remain an unknown question. In the past years, we integrated phylogenomic and population genetic approaches to investigate the diversification process by focusing on two representative lizard groups. In Europe, we reconstructed the history of wall lizard (genus: *Podarcis*) and found that the Messinian Salinity Crisis at the end of the Miocene coincides closely with the rapid speciation, suggesting that this major geological event triggered an explosive diversification of the group. Meanwhile, widespread interspecific hybridization across lineages further contributed to the accumulation of species diversity. In central Eurasian, we first delineated the colonization route of viviparous *Phrynocephalus* from low elevations to the extreme high-altitude environments of the Qinghai–Tibetan Plateau, and found that interspecific gene flow facilitated the transfer of high-altitude adaptation genes among lineages, providing the genetic basis for their colonization of the plateau. Phylogenomic analyses across the entire genus further revealed that *Phrynocephalus* originated in the Iranian Plateau and Turan Lowland of central Eurasia, and subsequently diverged into three major clades: an Arabian Peninsula clade, a Central Asian oviparous clade, and a viviparous clade. In addition, we found that the largest-bodied species of the genus, *P. mystaceus*, is of hybrid origin — another line of evidence for the role of hybridization in agama diversification. Together, our results indicate that major geological events together with interspecific gene exchange, have jointly promoted the diversification of lizards across Eurasia. However, existing studies remain fragmented, each focusing on a single lineage or region, which prevents us from addressing the overarching question of how Eurasian lizard diversity was formed as a whole. Extensive international collaboration is therefore needed to integrate the entire Eurasian continent — particularly the key regions from the Alps to the Himalayas — into a unified research framework, so as to systematically unravel the evolutionary history of Eurasian lizards and its underlying mechanisms.

Keywords: lizards; speciation; hybridization; gene flow; Messinian Salinity Crisis; Qinghai–Tibetan Plateau; high-altitude adaptation; *Podarcis*; *Phrynocephalus*

New Device for Monitoring Amphibians & Reptiles--Auto Camera Set on A & R

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Current field surveys of amphibians and reptiles rely heavily on on-site manual work, which are labor-intensive and hinder continuous observation of animal natural behaviors. This report presents a novel automatic monitoring device for amphibian and reptile surveys. The device can work independently in the wild without on-site human presence, substantially lowering labor costs and field-work burden. It enables continuous recording of natural behaviors of amphibians and reptiles under undisturbed field conditions, yielding behavioral data hardly obtainable via conventional manual survey methods. Multiple field trials across different sites validated the stability and performance of this device, and various amphibian and reptile species were recorded. It offers a new technical tool for amphibian and reptile monitoring and facilitates higher automation in wildlife resource surveys.

Keywords: amphibians and reptiles; automatic monitoring device; wildlife survey; field trial; behavioral data; new tool

7. Note Sheets

