ЭКОЛОГИЯ - ECOLOGY

UDC 598.1; 574.9
IRSTI 34.33.02
DOI 10.37238/2960-1371.2960-138X.2025.100(4).190

Edvárd Mizsei

Centre for Metagenomics, University of Debrecen, Debrecen, Hungary

E-mail: edvardmizsei@gmail.com

SNAKE DIVERSITY AND SURVEY BIAS IN WESTERN KAZAKHSTAN REVEALED BY OBSERVED AND MODELLED SPECIES RICHNESS

Annotation. Understanding biodiversity patterns in under-surveyed regions is essential for effective conservation planning. Western Kazakhstan, despite its extensive steppe and semi-desert habitats, remains poorly documented in terms of reptile diversity. In this study, we compiled all available snake occurrence records from field surveys and online biodiversity repositories to provide the first integrated assessment of species richness and sampling bias across the region. We recorded 16 snake species from 1,143 observations, but the spatial distribution of records was highly uneven, with more than 80% of grid cells lacking any detections. As a result, observed richness was restricted to a small number of well-surveyed locations, creating a fragmented picture of regional diversity. To complement these patterns, we generated spatially explicit predictions of species richness using ensemble species distribution models for the best-represented taxa. Predicted richness revealed broad areas of environmental suitability, particularly in the northern parts of the region, extending far beyond the locations of known records. Observed and predicted richness were moderately correlated, yet both were significantly associated with sampling effort, indicating persistent data bias. By identifying environmentally suitable but poorly surveyed areas, our results provide clear priorities for future fieldwork and highlight substantial knowledge gaps in the herpetofauna of Western Kazakhstan.

Keywords: steppe ecosystems, data-deficient regions, spatial sampling gaps, ecological suitability, reptile assemblages, distribution modeling, biodiversity mapping, conservation prioritization.

Introduction

Biological diversity exhibits pronounced spatial variation across the globe, driven by gradients in climate, productivity, habitat heterogeneity, and evolutionary history [1]. These broad-scale patterns structure how species richness accumulates and declines across landscapes and biomes, often revealing hotspots of conservation importance and coldspots where ecological processes limit diversity [2]. Global analyses have repeatedly shown that reptiles, including snakes, follow these macroecological principles, with richness frequently concentrated in environmentally complex regions or those with long-term climatic stability [3]. Understanding these diversity gradients is crucial because they offer insight into both historical biogeography and contemporary ecological functioning [4]. Moreover, variation in diversity across space provides a foundation for predicting how environmental pressures may shape future species distributions.

Reliable biodiversity data form the cornerstone of evidence-based conservation. Knowledge of species' geographic distributions allows for the assessment of threat status, the identification of priority areas, and the development of strategies for reducing extinction risks [5, 6]. This need is particularly acute for reptiles, many of which face multiple threats including habitat loss, degradation, invasive species, climate change, and emerging diseases [7,8]. Despite advances in atlas projects and the proliferation of digital repositories, distribution data for reptiles remain incomplete or spatially biased across many regions, highlighting persistent challenges for conservation planning. As demonstrated by recent syntheses, uneven sampling intensity and historical gaps in surveys can obscure true diversity patterns and hinder conservation decision-making. Consequently, improving distribution data remains a global priority for refining biodiversity assessments and enabling more accurate conservation interventions.

Snakes represent a particularly threatened component of reptile diversity worldwide [9]. Approximately one-fifth of reptile species are considered threatened with extinction, reflecting widespread pressures on their habitats and ecological communities [5]. Threatened snake taxa, including multiple viper species, face especially acute risks from habitat degradation, overgrazing, climate change, and human persecution, as documented in several recent studies from Eurasia [10, 11]. Global reviews have highlighted that snake species restricted to specialized habitats, such as high-elevation meadows, arid steppes, or fragmented landscapes, often exhibit small ranges and strong sensitivity to environmental change, increasing their extinction vulnerability. Many snake lineages also show deep phylogenetic structure and cryptic diversity, underscoring the need for detailed distributional datasets to capture true species limits and biogeographic patterns. As such, understanding snake conservation status requires integrating both global trends and region-specific ecological pressures.

Despite growing attention to reptile conservation, knowledge gaps persist across many parts of the world. On a global scale, incomplete geographical and ecological information hinders accurate threat assessments and limits understanding of species' responses to environmental change [5]. These gaps are often concentrated in regions with historically limited field surveys or logistical constraints, leading to biased biodiversity estimates. Similar limitations have been documented in several Eurasian regions, where many areas remain poorly surveyed or lack updated herpetofaunal data, resulting in distributions that are outdated or incomplete [13, 14]. Within Western Kazakhstan, the scarcity of systematic snake surveys prevents comprehensive assessments of regional diversity, potential declines, or conservation needs. Addressing these gaps is therefore essential for identifying true biodiversity patterns and highlighting areas where conservation attention is most urgently required.

Given the limited and uneven distribution of available occurrence data, this study aimed to generate a comprehensive assessment of snake diversity across Western

Kazakhstan using both empirical records and species distribution models. Specifically, we addressed the following questions:

(1) What are the spatial patterns of observed species richness, and how extensively does the current dataset represent the snake fauna of the region?

(2) How do modelled richness patterns compare to observed patterns, and to what extent do empirical and predicted richness values correlate across the landscape?

(3) Does sampling effort influence observed and predicted richness, and how strongly is spatial bias reflected in each dataset?

(4) Which areas exhibit high predicted richness but low sampling effort, indicating priority locations for future field surveys?

By integrating field observations, citizen science data, and ensemble SDMs, the study aimed to identify key gaps in current biodiversity knowledge, improve spatial estimates of snake diversity, and provide a framework for guiding targeted monitoring and conservation planning in Western Kazakhstan.

Materials and methods

Study area

The study was conducted across the four western administrative regions of the Republic of Kazakhstan: Aktobe, Atyrau, Mangystau and West Kazakhstan (Fig. 1). Together, these regions cover a broad expanse of steppe, semi-desert, and Caspian lowland environments, representing some of the most climatically variable and ecologically diverse landscapes in Central Asia. The area includes extensive open habitats known to support a variety of reptile species, including steppe and semi-desert snakes, although systematic herpetofaunal surveys remain limited. As identified in previous research from Central Asia and adjacent regions, insufficient field coverage has historically led to distributional uncertainties for several snake taxa and motivated improved regional biodiversity assessments. The boundaries of the study area were defined using official administrative region shapefiles and all spatial analyses were restricted to the polygon extent.

Occurrence data compilation

We assembled snake occurrence records from two primary sources: (1) field data collected by regional researchers and (2) online biodiversity repositories. Field observations were obtained from the WKU Herpetology Program dataset, which contains verified snake records across multiple years. To supplement these data, we queried the Global Biodiversity Information Facility (GBIF) and iNaturalist using the spocc package [15], retrieving all available records for the snake species listed in the WKU dataset. Taxonomic names were standardized to binomials, and only records with valid geographic coordinates were retained. All occurrences were projected into the WGS84 coordinate reference system and clipped to the study area using spatial containment operations. Following recommendations from previous studies that emphasize the importance of controlling data quality in reptile distribution research, duplicate records and erroneous coordinates were removed before analysis.

Estimation of sampling bias in occurrence data

To evaluate spatial variation in sampling effort, all occurrence points, regardless of species, were rasterized at a resolution of 0.5° across the study area using the terra package [16]. Each grid cell was assigned the number of occurrence records it contained. A kernel density estimate (KDE) was then calculated using a 3×3 focal window to account for spatial autocorrelation and to capture broader patterns of sampling intensity. KDE values were normalized to the range [0–1] to facilitate interpretation. Following similar approaches used in reptile conservation studies to identify survey bias and unsampled habitats, we performed leave-one-out t-tests for each grid cell to identify significantly under-sampled areas. Cells with $p \leq 0.01$ and KDE values below the regional mean were classified as survey gaps.

Observed species richness

Observed species richness was calculated using presence-only snake occurrence records compiled from field surveys and online biodiversity repositories. All species records were projected to a common 0.5° grid covering the four regions of Western Kazakhstan, and each species was converted into a binary presence–absence layer by assigning a value of one to any grid cell containing at least one observation. Following established approaches for reptile inventory analysis, this rasterization procedure reduces the effect of repeated observations and helps standardize comparisons across species with uneven sampling intensity. Species-specific presence layers were stacked to derive a total observed richness map. To visualize spatial structure and reduce noise associated with isolated records, richness values were additionally smoothed using a 3×3 focal neighborhood mean. The final observed richness layers were masked to the study-area boundary to ensure consistency across subsequent analyses.

Predicted species richness

Predicted species richness was generated by summing species distribution model (SDM) outputs for all snakes with sufficient occurrence data. To minimize spatial sampling bias, presence records for each species were thinned using spatially balanced resampling with a 0.05° buffer, ensuring that no two retained points fell within the same local neighborhood. Spatial thinning is recommended in reptile SDMs because many snake species show clustered detection patterns due to habitat structure or observer bias, which can inflate model accuracy if not addressed. Environmental predictors were sourced from the CHELSA 1981–2010 climatological dataset, representing temperature, precipitation, and related bioclimatic variables at regional scale. To avoid overfitting and multicollinearity, we applied automated variable selection, the envselect function of the chlsdm package [17], using a correlation threshold of 0.7 and 10-fold cross-validation, retaining only predictors consistently supported across resampling iterations. Species distribution models were then fitted using the sdm R package [18], combining four algorithms (GLM, GAM, RF, and FDA) into ensemble predictions weighted by algorithm performance. For each species, model-based suitability surfaces were thresholded to binary presence - absence maps using a 10% omission threshold derived from suitability values at known presence locations, a method widely applied to reduce omission errors in reptile SDMs. This approach is consistent with recent herpetological modelling efforts, which emphasize the importance of conservative thresholds when dealing with incomplete or biased datasets. Binary predictions were resampled to the same 0.5° grid as the observed richness data and stacked to produce a predicted richness map. By comparing observed and modelled estimates, we evaluated how sampling gaps and environmental suitability jointly shape snake diversity patterns across Western Kazakhstan.

Results

A total of 1,143 snake occurrence records were compiled for Western Kazakhstan, including 664 from the WKU dataset and 479 from GBIF and iNaturalist databases (Fig. 1, Table 1). These records represented 16 species, with substantial variation in data availability. V*ipera renardi*, *Elaphe dione*, *Eryx miliaris*, and *Psammophis lineolatus* accounted for most observations, whereas several species (e.g. *Hemorrhois ravergieri*, *Echis carinatus*) were represented by only one or two records. Nine species had more than 20 observations and were included in species distribution modelling (Table 1.).

Observed species richness exhibited strong spatial heterogeneity (Fig. 2). Across non-empty 0.5° grid cells, richness ranged from 1 to 7 species, with a median of 2, while 80.4% of the landscape lacked any recorded species. Local richness peaks were restricted to northern West Kazakhstan, central Aktobe, and sections of the Ural River basin, whereas most remaining areas showed only isolated detections.

Species-specific sampling coverage differed markedly (Table 1). *V. renardi* occurred in 57 grid cells, followed by *E. dione* (52) and *E. miliaris* (30). Most species occupied fewer than 10% of grid cells, and the rarest species appeared in only one cell each. Occupancy ratios ranged from 7.7% (*V. renardi*) to 0.14%.

Predicted species richness formed smooth environmental gradients across the region (Fig. 2). Modelled richness peaked in the northern part of the study area, with additional elevated values in southern Mangystau and western Atyrau, followed by moderate richness in central areas and lowest values in the southeast. Predicted richness covered a wider and more continuous area than the observed dataset.

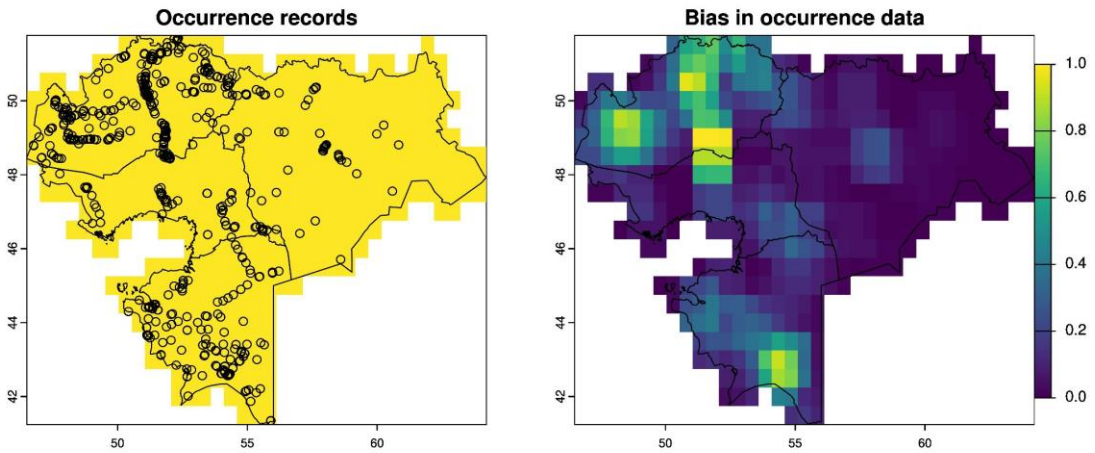

Figure 1 - Spatial distribution of occurrence records and sampling bias across Western Kazakhstan. Left: Map of all snake occurrence records from the WKU dataset, GBIF, and iNaturalist plotted within the study-area boundary. Right: Kernel-smoothed sampling effort (dark colors = low sampling effort, bright colors = high sampling effort).

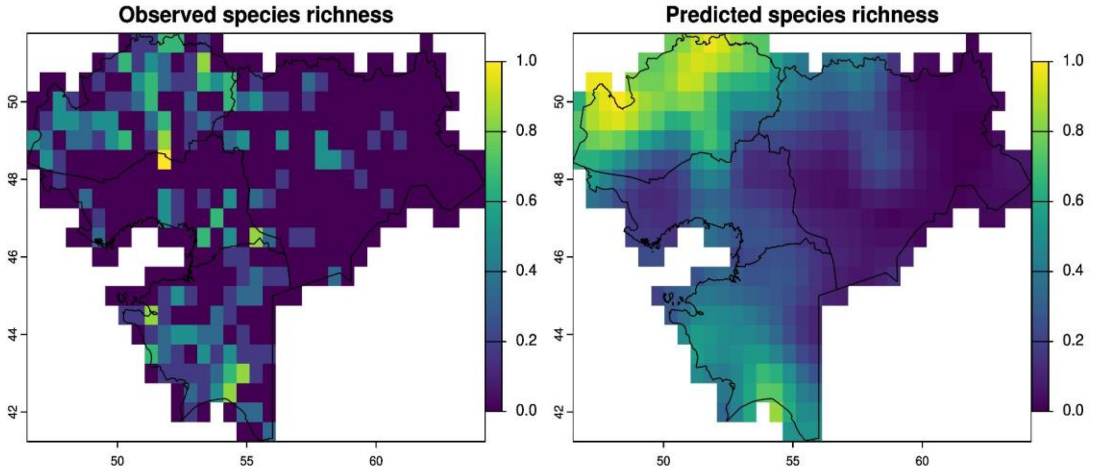

Figure 2 - Observed and predicted snake species richness at 0.5° resolution. Left: Observed species richness derived from stacked binary presence–absence rasters for all species. Right: Predicted species richness obtained by summing the normalized ensemble SDM projections for the nine modelled species and applying a focal smoothing filter. Dark shades represent lower richness and bright yellow shades represent higher richness.

Sampling effort was significantly related to both richness measures. For observed richness, effort had a strong positive effect ($\beta = 2.503 \pm 0.174$ SE; $z = 14.36$; $p < 0.001$). For predicted richness, effort also remained significant ($\beta = 1.608 \pm 0.252$ SE; $z = 6.39$; $p < 0.001$). Observed and predicted richness were positively correlated. A Pearson correlation test indicated a significant association between the two measures ($r = 0.441$, $t = 10.04$, $p < 0.001$), indicating moderate correspondence between empirical richness and model-based estimates across grid cells.

Discussion

This study provides the first integrated assessment of snake diversity patterns in Western Kazakhstan using both observed and modelled distributions. Occurrence records were highly unevenly distributed, with more than four-fifths of the study area lacking any observations. Observed richness was therefore concentrated in a small number of surveyed localities, producing an artificially fragmented diversity pattern. In contrast, predicted richness from the SDM ensemble revealed broad areas of suitable habitat, most prominently in the northern part of the region, but also in parts of Mangystau and Atyrau. The moderate correlation between observed and predicted richness suggests partial concordance between the two datasets, but also indicates that substantial areas remain biologically plausible yet unsampled. Collectively, these results demonstrate that current biodiversity knowledge for snakes in Western Kazakhstan is limited by strong spatial biases, and that modelled richness provides valuable complementary insight into regional diversity patterns and could guide future expeditions.

The results demonstrate that species observations are heavily concentrated near larger settlements and transportation corridors, with large intervening regions lacking records. This uneven coverage strongly influenced empirical richness patterns and underscores the limitations of relying solely on opportunistic or uneven survey efforts. While predicted richness captured broad environmental gradients consistent with snake ecology, it did not align perfectly with observed richness due to the patchy nature of the spatially biased input presence data. Both GLMs showed a significant positive effect of effort on observed and predicted richness, confirming that sampling bias permeates both empirical and model-derived outputs. Although the effect was weaker for modelled richness, the persistence of bias demonstrates that even robust modelling frameworks cannot fully compensate for strongly uneven occurrence datasets. In identifying undersurveyed areas, the overlay of predicted richness and sampling effort clearly highlighted regions with high environmental suitability but little or no survey effort [19]. These areas form priorities for future fieldwork aimed at improving representation of snake species across Western Kazakhstan.

Tables

Table 1 - Number of observations, number of occupied 0.5° grid cells, and percentage of occupied cells for each of the 16 snake species recorded in the study area. Species with more than 20 observations (n = 9) were retained for species distribution modelling.

Species	N of observations	N of occupied 0.5°grid cells	% of occupied 0.5°grid cells
Vipera renardi	374	57	7.8
Elaphe dione	134	52	7.1
Eryx miliaris	124	30	4.1
Psammophis lineolatus	120	34	4.6
Natrix tessellata	94	37	5
Natrix natrix	77	35	4.8
Elaphe sauromates	72	20	2.7
Gloydius caraganus	50	6	0.8
Platyceps karelini	41	12	1.6
Dolichophis caspius	20	3	0.4
Spalerosophis diadema	16	3	0.4
Coronella austriaca	12	5	0.7
Gloydius halys	6	4	0.5
Echis carinatus	2	1	0.1
Hemorrhois ravergieri	1	1	0.1

Several limitations affect the interpretation and generalisability of our results. First, the presence data are spatially biased, with clear clustering around larger settlements, major roads, and frequently visited sites. Such patterns are typical for opportunistic vertebrate datasets and can lead to inflated estimates of richness in accessible areas while underrepresenting remote habitats. Second, the SDMs were calibrated only within the WK project area rather than across the full geographic ranges of the species. This restriction likely reduced the ecological realism of the models, as many species occupy broader environmental gradients across Eurasia that were not represented in the calibration data. Third, we relied solely on climatic predictors, whereas other factors, including soil properties, vegetation structure, land use, and human disturbance, are known to influence snake distributions (e.g., meadow and steppe viper studies documenting habitat specialization and sensitivity to land-use change). Including such variables would likely improve model performance and refine predictions in ecologically heterogeneous areas.

An additional challenge concerns the accessibility of regional literature [20]. Much of the historical herpetofaunal knowledge for Kazakhstan and adjacent areas is published in Cyrillic-script sources, limiting accessibility for western researchers. This language barrier contributes to the persistence of outdated distribution information and impedes the integration of regional expertise into global biodiversity syntheses [21].

Future research should extend SDM calibration to the entire global range of each species, enabling models to capture the full spectrum of environmental conditions used by steppe and semi-desert snakes. Such broader modelling would likely yield more realistic predictions within Kazakhstan. Horizon scanning approaches could also be applied to identify species that may be present but currently unrecorded in the region, similar to the case of *Echis carinatus*, which was detected only recently. Incorporating data from all reptile taxa, not only snakes, would help resolve community-level diversity patterns and allow assessment of shared responses to environmental gradients and anthropogenic pressures. Expanding field surveys to the undersampled areas identified by our analysis would rapidly improve the completeness of regional biodiversity knowledge and strengthen future conservation assessments.

In conclusion, this study reveals strong spatial biases in snake occurrence data across Western Kazakhstan and demonstrates how these biases shape both observed and modelled richness patterns. While species distribution modelling provides a valuable tool for identifying areas of high potential diversity, it cannot fully overcome the limitations of uneven sampling. By highlighting priority areas for future surveys and identifying methodological gaps in current datasets, this work provides an essential foundation for improving biodiversity assessments and supporting evidence-based conservation planning for snakes in Western Kazakhstan.

Acknowledgements

We thank the staff and students of M. Utemisov West Kazakhstan University for their assistance, collaboration, and logistical support throughout the project. EM is grateful for the opportunity to serve as a visiting professor at M. Utemisov West Kazakhstan University within the framework of the XXX Programme of the Ministry of Education of Kazakhstan. Field data collection and related research activities were supported by the XXX Grant provided by the Ministry of Education of Kazakhstan. We also acknowledge the contributions of citizen scientists and data providers whose records, made accessible through GBIF and iNaturalist, substantially enriched the occurrence dataset used in this study. Finally, we thank colleagues who provided valuable discussions and feedback during the development of the project.

REFERENCES

[1] Willig, M. R., Kaufman, D. M., & Stevens, R. D. (2003). Latitudinal gradients of biodiversity: Pattern, process, scale, and synthesis. Annual Review of Ecology, Evolution, and Systematics, 34, 273–309.

[2] Gaston, K. J. (2000). Global patterns in biodiversity. Nature, 405(6783), 220–227.

[3] Roll, U., Feldman, A., Novosolov, M., Heath, T. A., Guralnick, R., Scharf, I., Tallowin, O., Shani, G., Fienberg, H., Weil, G., Meiri, S., & Mayrose, I. (2017). The global distribution of tetrapods reveals a need for targeted reptile conservation. Nature Ecology & Evolution, 1(11), 1677–1682.

[4] McCain, C. M. (2010). Global analysis of reptile elevational diversity. Global Ecology and Biogeography, 19(3), 293–304

[5] Böhm, M., Collen, B., Baillie, J. E., Bowles, P., Chanson, J., Cox, N., ... & Masterson, G. (2013). The conservation status of the world's reptiles. Biological conservation, 157, 372-385.

[6] Caetano, G. H. D. O., Chapple, D. G., Grenyer, R., Raz, T., Rosenblatt, J., Tingley, R., ... & Roll, U. (2022). Automated assessment reveals that the extinction risk of reptiles is widely underestimated across space and phylogeny. PLoS Biology, 20(5), e3001544

[7] Mizsei, E., Adorjáni, C., Bancsik, B., Kovács, G., Rák, G., Babocsay, G., & Budai, M. (2025). Effect of plant-related threats on lizards of open sand steppes: a snapshot at the beginning of the spread of a novel invader. NeoBiota, 104, 95-111

[8] Mizsei, E., Sos, T., Móré, A., Wenner, B., Rák, G., & Mebert, K. (2025). Restriction times on the rise: mechanistic modelling of activity time of grassland vipers (Vipera spp.) in the face of climate change. Frontiers in Zoology, 22(1), 10

[9] Gibbons, J. W., Scott, D. E., Ryan, T. J., Buhlmann, K. A., Tuberville, T. D., Metts, B. S., ... & Winne, C. T. (2000). The Global Decline of Reptiles, Déjà Vu Amphibians: Reptile species are declining on a global scale. Six significant threats to reptile populations are habitat loss and degradation, introduced invasive species, environmental pollution, disease, unsustainable use, and global climate change. BioScience, 50(8), 653-666

[10] Mizsei, E., Szabolcs, M., Szabó, L. O. R. Á. N. D., Boros, Z., Mersini, K., Roussos, S. A., ... & Lengyel, S. (2021). Determining priority areas for an Endangered cold-adapted snake on warming mountaintops. Oryx, 55(3), 334-343

[11] Mebert, K., Igci, N., Karis, M., Yildiz, M., Schmid, P., Gruenewald, J., ... & Kirschey, T. (2025). Critically Endangered Darevsky's Viper: Incisive Distribution Discoveries and Taxonomic Considerations. Herpetological Conservation and Biology, 20(2), 438-456.

[12] Mebert, K., Karis, M., Yildiz, M., Igci, N., Stumpel, N., Zinenko, O., ... & Elden, J. (2025). Taxonomy, Distribution, and Conservation of Threatened Steppe Vipers of Western Asia: Vipera anatolica and Vipera renardi eriwanensis (sensu lato). Herpetological Conservation and Biology, 20(2), 393-412

[13] Ananjeva, N. B. (2006). The reptiles of Northern Eurasia: taxonomic diversity, distribution, conservation status (No. 47). Pensoft Publishers

[14] Simonov, E., Bakiev, A., Klenina, A., Ermakov, O., & Akhmedenov, K. (2025). From the Woods to the Great Steppe: The Phylogenetic Affinities and New Distribution Records of the Smooth Snake Coronella austriaca in Kazakhstan. Diversity, 17(5), 348

[15] Owens, H. L., Barve, V., Chamberlain, S. A., Ram, K., & Hart, T. (2024). spocc: Interface to species occurrence data sources (Version 1.2.3) [Computer software]. rOpenSci

[16] Hijmans, R. J. (2025). terra: Spatial data analysis (Version 1.8-83) [Computer software]. The Comprehensive R Archive Network

[17] Mizsei, E. (2025). chlsdm: Species distribution modelling pipeline [Computer software]. GitHub. https://github.com/edvardmizsei/chlsdm

[18] Naimi, B., & Araújo, M. B. (2016). sdm: a reproducible and extensible R platform for species distribution modelling. Ecography, 39(4), 368–375

[19] Phillips, S. J., Dudík, M., Elith, J., Graham, C. H., Kodner, A. L., & Schapire, R. E. (2009). Sample selection bias and presence-only distribution models: Implications for background and pseudo-absence data. Ecological Applications, 19(1), 181–197

[20] Amano, Tatsuya, Juan P. González-Varo, and William J. Sutherland. "Languages are still a major barrier to global science." PLoS biology 14.12 (2016): e2000933

[21] Amano, T., Berdejo-Espinola, V., Akasaka, M., de Andrade Junior, M. A., Blaise, N., Checco, J., ... & Zamora-Gutierrez, V. (2023). The role of non-English-language science in informing national biodiversity assessments. Nature Sustainability, 6(7), 845-854.

Эдвард Мижей

РАЗНООБРАЗИЕ ЗМЕЙ И ПРЕДВЗЯТОСТЬ ИССЛЕДОВАНИЙ В ЗАПАДНОМ КАЗАХСТАНЕ, ВЫЯВЛЕННЫЕ НАБЛЮДАЕМЫМ И СМОДЕЛИРОВАННЫМ ВИДОВЫМ БОГАТСТВОМ

Аннотация. Понимание закономерностей биоразнообразия в малоизученных регионах имеет важное значение для эффективного планирования природоохранной деятельности. Западный Казахстан, несмотря на обширные степные и полупустынные районы обитания, остается недостаточно документированным с точки зрения разнообразия рептилий. В этом исследовании мы собрали все доступные данные о встречаемости змей, полученные из полевых исследований и онлайн-хранилищ биоразнообразия, чтобы провести первую комплексную оценку видового богатства и систематической выборки по всему региону. Мы зарегистрировали 16 видов змей из 1143 наблюдений, но пространственное распределение записей было крайне неравномерным: более 80% ячеек сетки не были обнаружены. В результате наблюдаемое разнообразие было ограничено небольшим числом хорошо обследованных мест, что создало фрагментарную картину регионального разнообразия. Чтобы дополнить эти закономерности, мы составили пространственно-точные прогнозы видового богатства, используя комплексные модели распределения видов для наиболее

представленных таксонов. Прогнозируемое богатство выявило широкие области экологической пригодности, особенно в северных частях региона, выходящие далеко за пределы известных мест регистрации. Наблюдаемое и прогнозируемое богатство умеренно коррелировали, однако оба они были в значительной степени связаны с затратами на отбор проб, что указывает на постоянную погрешность данных. Выявляя экологически подходящие, но плохо обследованные районы, наши результаты определяют четкие приоритеты для будущих полевых работ и выявляют существенные пробелы в знаниях о герпетофауне Западного Казахстана.
Ключевые слова: степные экосистемы, регионы с дефицитом данных, пробелы в пространственной выборке, экологическая пригодность, сообщества рептилий, моделирование распространения, картирование биоразнообразия, определение приоритетов сохранения.

Эдвард Мижей

БАЙҚАЛҒАН ЖӘНЕ МОДЕЛЬДЕНГЕН ТҮР БАЙЛЫҒЫМЕН АНЫҚТАЛҒАН БАТЫС ҚАЗАҚСТАНДАҒЫ ЖЫЛАНДАРДЫҢ ӘРТҮРЛІЛІГІ ЖӘНЕ ЗЕРТТЕУЛЕРДІҢ БІРЖАҚТЫЛЫҒЫ

Аңдатпа. Жеткіліксіз зерттелген өңірлердегі биологиялық әртүрлілік модельдерін түсіну сақтауды тиімді жоспарлау үшін маңызды мәнге ие. Батыс Қазақстан, кең далалық және жартылай шөлді мекендеу орындарына қарамастан, әртүрлі рептилиялар тұрғысынан құжатталмаған күйінде қалып отыр. Бұл зерттеуде біз бүкіл өңір бойынша түрлердің байлығы мен іріктеменің жылжуын алғашқы кешенді бағалауды қамтамасыз ету үшін далалық зерттеулерден және биологиялық әртүрліліктің онлайн қоймаларынан жыландардың пайда болуы туралы барлық қол жетімді жазбаларды жинадық. Біз 1143 бақылаудың 16 жылан түрін тіркедік, бірақ жазулардың кеңістіктік таралуы өте біркелкі емес және тордың 80% -дан астамы ешқандай табылған жоқ. Нәтижесінде байқалатын байлық өңірлік әртүрліліктің бөлшектелген бейнесін жасай отырып, жақсы зерттелген орындардың аз санымен шектелді. Осы заңдылықтарды толықтыру үшін біз неғұрлым ұсынылған таксондар үшін ансамбльдік түрлерді бөлу модельдерін пайдалана отырып, көрнекі байлықтың кеңістіктік айқын болжамдарын жасадық. Болжанған байлық экологиялық жарамдылықтың кең салаларын, әсіресе өңірдің солтүстік бөліктерінде белгілі жазбалар орнынан әлдеқайда тыс жерлерді анықтады. Бақыланатын және болжанатын байлық біркелкі үйлесімді болды, бірақ олардың екеуі де таңдау бойынша күш-жігерге байланысты болды, бұл деректердің тұрақты ауысуын көрсетеді. Экологиялық қолайлы, бірақ нашар зерттелген аудандарды анықтай отырып, біздің нәтижелеріміз болашақ дала жұмыстарына нақты басымдықтар береді және Батыс Қазақстанның герпетофаунасы туралы білімдегі елеулі олқылықтарды көрсетеді.
Кілт сөздер: далалық экожүйелер, деректер тапшылығы бар өңірлер, кеңістіктік іріктемедегі олқылықтар, экологиялық жарамдылық, рептилияларды жинау, бөлуді модельдеу, биоәртүрлілікті картаға түсіру, сақтауды басымдыққа алу.