ABS ACTA BIOLOGICA SIBIRICA
A journal on the biodiversity of Siberia and the adjacent lands

Acta Biologica Sibirica 11: 1261–1274 (2025)
doi: 10.5281/zenodo.17637628
http://journal.asu.ru

RESEARCH ARTICLE

Taxonomic status and phylogenetic relationships of the desert monitor *Varanus griseus caspius* (Squamata: Varanidae) from the territory of Uzbekistan

Abdurakhim E. Kuchboev[1], Oybek O. Amirov[1], Azamat A. Yuldoshxonov[1], Ruziboy K. Shapaotov[1], Baxodir A. Raxmatullayev[2], Timur V. Abduraupov[1]

1 *Institute of Zoology of the Academy of Sciences of the Republic of Uzbekistan, 232B Boshishamol St., Tashkent, 100053, Uzbekistan*
2 *Termiz State University, 43 Barkamol avlod St., Termiz, 190111, Uzbekistan*

Corresponding author: Abdurakhim E. Kuchboev (abdurakhimkuchboev@gmail.com)

Academic editor: R. Yakovlev | Received 5 September 2025 | Accepted 8 November 2025 | Published 20 November 2025

http://zoobank.org/AF008E7D-2BFC-4340-BA04-5C49C4722486

Citation: Kuchboev AE, Amirov OO, Yuldoshxonov AA, Shapaotov RK, Raxmatullayev BA, Abduraupov TV (2025) Taxonomic status and phylogenetic relationships of the desert monitor *Varanus griseus caspius* (Squamata: Varanidae) from the territory of Uzbekistan. Acta Biologica Sibirica 11: 1261–1274. https://doi.org/10.5281/zenodo.17637628

Abstract

This study investigates the phylogenetic position and genetic diversity of *Varanus griseus caspius*, a widely distributed yet understudied subspecies of monitor lizard in Central Asia, with a focus on samples collected from Uzbekistan. Using DNA barcoding based on the mitochondrial cytochrome oxidase subunit I (COI) gene, molecular phylogenetic analyses were conducted via Maximum Likelihood (ML) and Bayesian Inference (BI) approaches. In addition, genetic distance and Disparity Index analyses were employed to assess evolutionary relationships among *Varanus* species. The *V. g. caspius* specimens formed a highly supported clade with *V. griseus* sequences in GenBank, indicating a close genetic affinity and confirming its subspecies status. Genetic distance values and substitution pattern similarities further revealed minimal divergence between *V. g. caspius* and other *V. griseus* lineages, suggesting recent common ancestry and ongoing gene flow. In contrast, significantly greater divergence was observed between *V. g. caspius* and other *Varanus* species. These findings clarify the phylogenetic placement of *V. g. caspius* within the *V. griseus* complex and provide essential baseline data for future taxonomic and conservation efforts.

Keywords
DNA barcoding, herpetofauna, phylogeography, lizards, *Varanus griseus*

Introduction

Uzbekistan is located in the center of the Iranian-Turanian biogeographic region and its fauna is characterized by a high proportion of autochthonous Turanian elements. The reptilian fauna of Uzbekistan has at least 60 species. Taxonomy dependent, four amphibian (three toads and a frog) and 57 reptile species (a tortoise, 36 lizards and 20 snakes) appear confirmed as occurring within the Republic of Uzbekistan (Showler 2018; Martin et al. 2017).

In recent years, molecular-genetic research on Uzbekistan's fauna has significantly intensified, yielding important findings in vertebrates, including in fishes (Quvatov et al. 2023; Ubaydullayev et al. 2025) and mammals (Kuchboev et al. 2024, 2025; Sobirov et al. 2025). These approaches have become essential tools for clarifying species boundaries and reassessing phylogenetic relationships.

Reptiles are one of the most studied groups of animals using molecular genetic methods. One such species, the desert monitor (*Varanus griseus caspius* Eichwald, 1831), is a large predatory lizard native to Central Asia and represents one of the three subspecies of *Varanus griseus*. Its distribution range extends from the eastern shores of the Caspian Sea across Uzbekistan, Kazakhstan, Turkmenistan, Tajikistan, northern Iran, western and southern Afghanistan, and western Pakistan (Leviton and Anderson 1970; Bennett 1995). The other two subspecies – *V. g. griseus* (Daudin, 1803) and *V. g. koniecznyi* (Mertens 1942) – occur in North Africa and the Arabian Peninsula, and in India and Pakistan, respectively (Mertens 1954; Sindaco and Jeremčenko, 2008). *V. g. caspius* is well adapted to arid and semi-arid landscapes and can be found in deserts, steppes, and foothill areas. Despite its broad ecological plasticity and wide distribution, the species faced a sharp population decline in the early 20th century due to excessive hunting for its skin (Paraskiv 1956). Although hunting has since been restricted, the expansion of agricultural activities, infrastructure development, and urbanization has continued to reduce its natural habitats. In Uzbekistan, suitable habitats for this subspecies shrank by up to 40% in the second half of the 20th century, leading to its complete disappearance from the Fergana Valley and a drastic population decline in the Kopet Dag foothills and Kharsha steppe (Bondarenko 1989; Tsellarius et al. 1991). Recent studies have highlighted uncertainties in the species' northern distribution limits (Nuridzhanov et al. 2016). Species Distribution Models (SDMs) based on Maxent have predicted further contraction of its potential range in Central Asia due to climate change and anthropogenic impacts (Zima and Fedorenko 2024; Shadloo et al. 2021). Böhme et al. (2023) suggested considering *V. g. caspius* as a separate taxonomic unit based on morphological and genetic differences. Local studies emphasize the ecological, conservation, and ethnobiological significance of the species. As noted by Abduraupov

et al. (2023), it holds a prominent place in local folklore and traditional medicine. Moreover, the species is listed in Uzbekistan's Red Data Book, and several studies have addressed its ecological vulnerability, habitat degradation, and human-related threats (Khodzhaev et al. 2019; Khudirov et al. 2021; Martin et al. 2017).

To identify species rapidly, reliably, and cost-effectively, a modern molecular method-DNA barcoding can be applied (Hebert et al. 2003). Previous research on the systematics and biogeography of the (mtDNA) markers such as 12S rRNA (Fuller et al. 1998), ND4 (Doughty et al. 2014), and 16S rRNA (Ziegler et al. 2007). Ast (2001) analyzed full sequences of the ND1 and ND2 genes as well as partial sequences of 16S rRNA and COI genes. Some studies have used combinations of mitochondrial and nuclear genes (Vidal et al. 2012). However, the use of the COI marker in phylogenetic studies among *Varanus* species remains rare, and molecular-genetic characterization using this gene (i.e., DNA barcoding) is still underutilized (Nagy et al. 2012).

Molecular analyses play a crucial role in understanding the genetic structure and evolutionary relationships of *V. g. caspius*. In recent years, molecular phylogenetic approaches have been widely used as effective tools for identifying cryptic lineages and exploring biogeographic history (Stuart et al. 2006; Hekkala et al. 2011). By using the mitochondrial COI marker to assess genetic diversity among *V. g. caspius* populations, it is possible to determine the phylogenetic relationships of this subspecies with other related subspecies.

The main objective of this study is to investigate the molecular phylogenetic relationships of the subspecies *V. g. caspius*, determine its evolutionary position within the *Varanus griseus sensu lato*, and assess its genetic diversity at the population level.

Materials and methods

For this study, genetic samples were obtained from species of the *V. g. caspius* preserved in the collection of the Institute of Zoology, Academy of Sciences of the Republic of Uzbekistan (Table 1). Taxonomic identification of the tissue samples was performed based on the information provided on their labels.

Table 1. Information on genetic samples of *Varanus griseus caspius* in Uzbekistan

No	Collection parameters	*V.g. caspius*	*V.g. caspius*
1	Collection number	1675	1992
2	Date of collection	13.05.2016	02.05.2022
3	Locality	Karnabchul, Uzbekistan	Guzar region, Uzbekistan
4	Coordinates	39°43'63"N, 65°43'27"E	38°33'16"N, 66°34'43"E
5	Collector	Jumaev F.Q.	Yangiboyev E.Ch.
6	Inventory number	–	11309

DNA Extraction and PCR Amplification

DNA extraction was carried out using Diatom purification reagents, following standard laboratory protocols to ensure high-quality DNA suitable for subsequent molecular analyses. For polymerase chain reaction (PCR), the primer pair RepCOI-F (5′-TNT TMT CAA CNA ACC ACA AAG A-3′) and RepCOI-R (5′-ACT TCT GGR TGK CCA AAR AAT CA-3′) was used (Nagy et al. 2012). These primers are designed to amplify a fragment of the mitochondrial cytochrome oxidase subunit I (COI) gene, which is widely used as a "DNA barcode" (Hebert et al. 2003). The primers were applied randomly across the samples used in this study. The PCR mix had a total volume of 20 μL and included the appropriate concentration of primers. The PCR cycling conditions were as follows: initial denaturation at 94°C for 3 minutes; followed by 40 cycles of denaturation at 94°C for 30 seconds, annealing at 48.5°C for 30 seconds, and extension at 72°C for 1 minute. A final extension was performed at 72°C for 5 minutes.

The presence of DNA in the PCR products was confirmed by electrophoresis on a 1.0% agarose gel under 120 V. DNA amplification and gel purification were carried out according to the manufacturer's instructions using reagent kits provided by "Silex M" (Moscow, Russia). DNA sequencing was performed using the ABI PRISM® BigDye™ Terminator v. 3.1 Cycle Sequencing Kit, and sequencing reactions were analyzed on an ABI PRISM 3100-Avant Genetic Analyzer (Moscow, Russia).

Phylogenetic Tree Construction

For phylogenetic analysis, nucleotide sequences of the COI gene from 25 species of the *Varanus* genus were used, along with one COI sequence from *Xantusia jaycolei* Bezy, Bezy and Bolles 2008 (MH274797) as an outgroup. The obtained nucleotide sequences were manually edited using BioEdit version 7.0.5.2 (Hall 1999), and all sequences were then automatically aligned using the MAFFT program (Katoh et al. 2002). Phylogenetic trees were constructed using the Maximum Likelihood (ML) method implemented in IQ-TREE 2 (Minh et al. 2020). The best-fitting evolutionary model was selected using ModelFinder, which is integrated into IQ-TREE (Kalyaanamoorthy et al. 2017). The reliability of the tree topology was assessed using 1000 bootstrap replications (Felsenstein, 1985). Additional analyses were performed using Bayesian Inference (BI) with the MrBayes 3.1.2 software (Huelsenbeck and Ronquist 2001). The MCMC (Markov Chain Monte Carlo) algorithm was run for 4 million generations, with samples taken every 1000 generations. The first 1000 trees were discarded as burn-in. Phylogenetic tree reliability was evaluated using Bayesian posterior probabilities (PP) and bootstrap values (BS) as follows: PP ≥ 0.95 and BS ≥ 70% – high support; PP = 0.90–0.94 and BS = 50–69% – moderate support; PP < 0.90 and BS < 50% – low support (Huelsenbeck and Hillis, 1993). The final phylogenetic trees were visualized graphically using the iTOL (Interactive Tree of Life) online platform (Letunic and Bork 2021).

Assessment of Evolutionary Pattern Heterogeneity Using the Disparity Index Test

To assess differences in evolutionary patterns in COI gene sequences of *Varanus* species, a Disparity Index (DI) test was conducted. The analysis was performed using MEGA11 software (Tamura et al. 2021). Sequence alignments were generated using the built-in MAFFT algorithm with standard parameters. The test settings were as follows: Substitution type: Nucleotide; Treatment of gaps/missing data: All positions included; Number of Monte Carlo replications: 500. The output was a matrix of Disparity Index (DI) values between species pairs. These index values reflect the degree of difference in substitution patterns between sequences. Higher ID values indicate significant differences in evolutionary patterns.

Results and discussion

Phylogenetic Analysis

According to the results of the phylogenetic analysis, the *V. griseus caspius* sample collected from Uzbekistan clustered closely with other *V. griseus* genotypes available in GenBank, forming a well-supported clade. Within this clade, high bootstrap support (≈100) was observed for *V. griseus* sequences OP117173 and OP117223, indicating a high degree of genetic similarity between the *V. g. caspius* sample from Uzbekistan and these taxa (Fig. 1).

Other species included in the analysis formed several distinct clades in the phylogenetic tree. For example, *Varanus albigularis* formed a separate, well-supported clade (≈94–100) consisting of four samples. Similarly, *V. bengalensis*, *V. niloticus*, *V. salvator*, *V. flavescens*, and other species were grouped into distinct monophyletic clades, confirming species-specific genetic divergence. The placement of *X. jaycolei* as an isolated taxon in a basal position on the phylogenetic tree demonstrates its use as an outgroup in this analysis. This validates the tree's correct rooting and enhances the reliability of inferred evolutionary relationships among the ingroup taxa.

Overall, the placement of the *V. g. caspius* sample within its species-specific genetic clade, strongly supported by high bootstrap values, suggests that the sample can confidently be classified within the *V. griseus* subspecies group. These results confirm the genetic congruence of the *V. g. caspius* population with other populations represented in GenBank and support the phylogenetic integrity of the subspecies.

Genetic Distance

The analysis of genetic distances among species within the *Varanus* genus, based on the genetic distance matrix and the heatmap, revealed key aspects of their phyloge-

netic relationships. The heatmap clearly illustrated the gradation of genetic distances, with light pink colors representing close genetic similarity and dark red colors indicating greater genetic divergence (Fig. 2). According to the results, the *Varanus griseus* subspecies – including *V. griseus caspius* (Uzb), *V. griseus* (OP117223), and *V. griseus* (OP117173) – showed very low genetic distances, specifically 0.0000, 0.02507, and 0.02737, respectively. These values indicate an extremely close genetic relationship among the subspecies, supporting their classification within a single phylogenetic cluster.

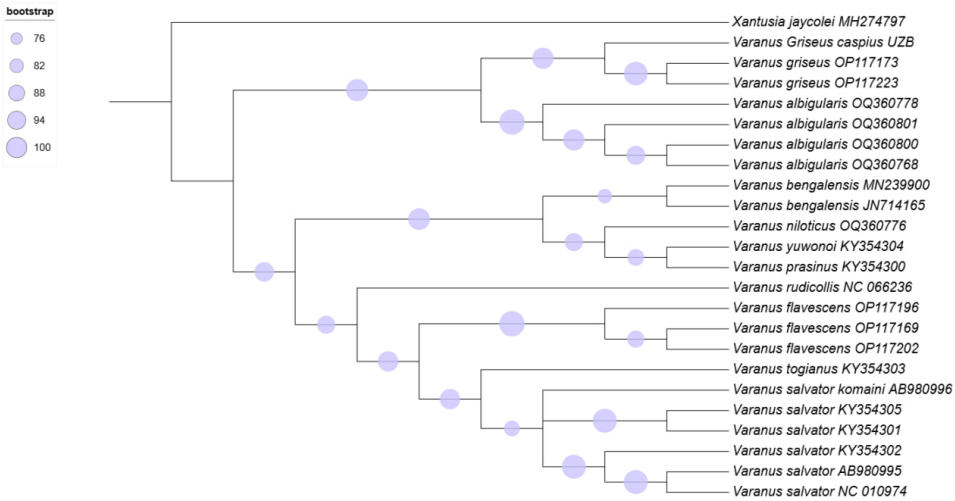

Figure 1. Phylogenetic tree of *Varanus* species based on the COI gene (genetic relationships among species). The tree was constructed using bootstrap values to ensure phylogenetic reliability and was used for species classification within the genus.

Similarly, members of the *V. salvator* group (KY354302, KY354301, KY354305) also exhibited very low genetic distances (0.0000-0.0401), confirming their close evolutionary relationships.

In contrast, species from different clades displayed significantly higher levels of genetic divergence. For instance, the genetic distance between *V. albigularis* (OQ360801) and *V. niloticus* (OQ360776) was 0.3987, while the distance between *Varanus rudicollis* (NC066236) and *V. flavescens* (OP117196) reached 0.5675. The outgroup species *Xantusia jaycolei* (MH274797) had the highest genetic distances from all *Varanus* species (ranging from 0.6296 to 0.8217), indicating that it represents a completely distinct evolutionary lineage from a phylogenetic perspective. These results suggest that complex phylogenetic and evolutionary processes have taken place within the *Varanus* genus. While some species form clusters based on close genetic relationships (e.g., the *Varanus griseus* and *Varanus salvator* groups), others represent distinct evolutionary lineages characterized by substantial genetic divergence.

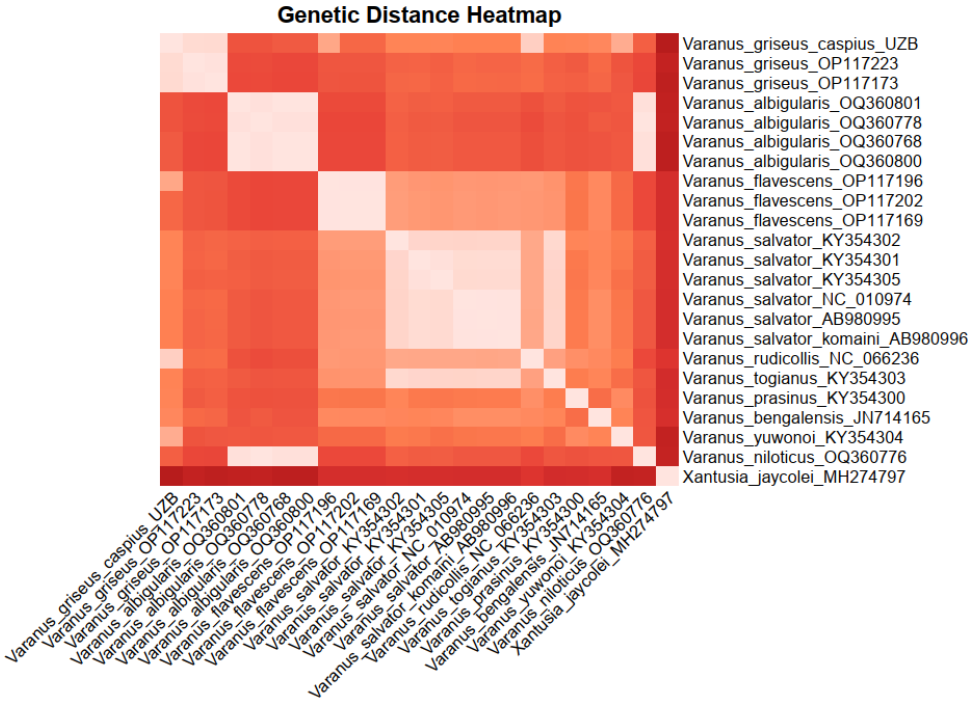

Figure 2. Genetic Distance Heatmap among *Varanus* species. This COI-based heatmap shows pairwise genetic distances among *Varanus* species. Green to yellow shades indicate high genetic similarity, while orange to red represent greater divergence. *V. griseus caspius* (UZB) clusters closely with *V. griseus* samples, whereas *Xantusia jaycolei* stands out as the most genetically distinct outgroup. The results reflect clear phylogenetic relationships within the genus.

Disparity Index analysis

The results of the Disparity Index analysis revealed a significant degree of heterogeneity in substitution patterns among species within the genus *Varanus*. The pairwise ID (Disparity Index) values ranged from 0.0000 to 1.0000, reflecting varying levels of evolutionary divergence. When comparing the focal taxon *V. griseus caspius* (UZB) with its closest phylogenetic relative *Varanus griseus* (OP117223), a very low ID value (0.0176) was observed (Fig. 3). This suggests that the two taxa share nearly identical evolutionary substitution patterns and likely diverged from a recent common ancestor.

This finding molecularly confirms that *V. griseus caspius* is closely related to *V. griseus*. Similarly, other closely related taxa, such as *Varanus salvator* specimens (KY354302, KY354301), also exhibited ID values below 0.0400, indicating strong internal phylogenetic stability. In contrast, distant relatives of *V. griseus caspius*, such as *Varanus rudicollis* (NC066236) and *Varanus flavescens* (OP117196), showed

much higher ID values (0.8924 and above), suggesting they have evolved along independent evolutionary lineages. The outgroup species *Xantusia jaycolei* (MH274797) exhibited the highest ID value (1.0000) when compared to all *Varanus* species, including *V. griseus caspius*, further confirming its distant phylogenetic position and the appropriateness of its selection as an outgroup.

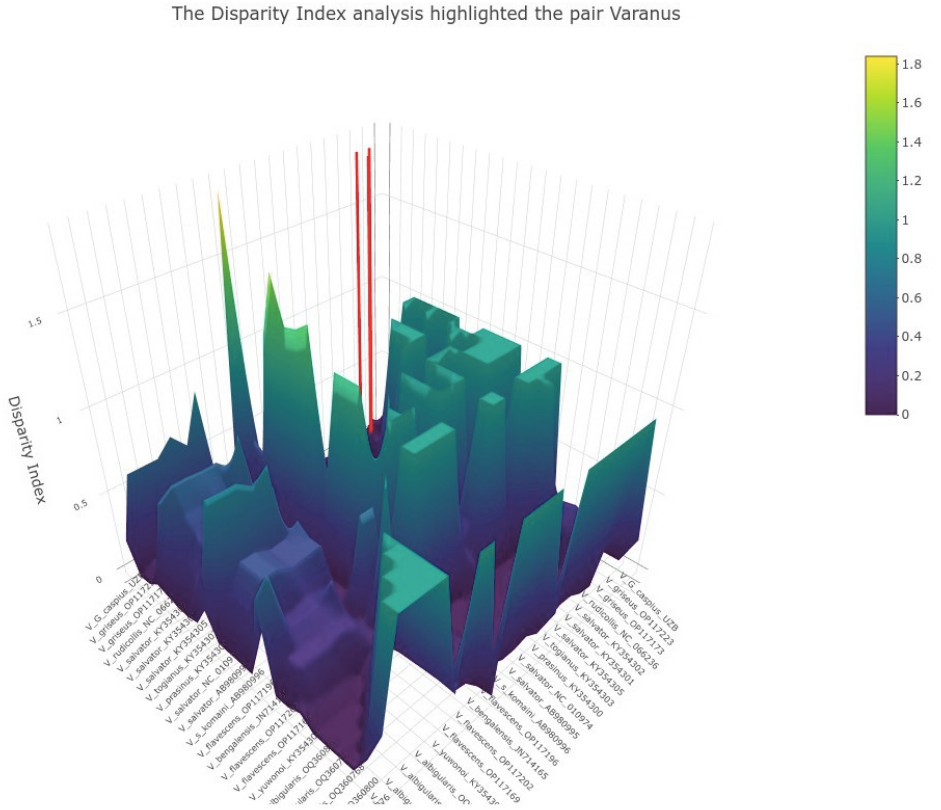

Figure 3. The 3D Disparity Index diagram for pairwise comparisons among various *Varanus* species.

The diagram displays Disparity Index values for pairwise comparisons among various *Varanus* species. Red lines indicate the connections between *V. griseus* and *V. griseus caspius* samples. As the color gradient shifts toward yellow, it reflects an increase in the disparity index, indicating a higher degree of heterogeneity in nucleotide substitution patterns and greater evolutionary divergence between species.

In this study, *Varanus griseus caspius* was selected as the main object of analysis, and its molecular-phylogenetic position as well as interspecific evolutionary relationships were comprehensively evaluated using three independent methods: a phylogenetic tree constructed using the Maximum Likelihood (ML) method, genetic

distance analysis based on evolutionary models conducted via IQ-TREE2, and a Disparity Index test carried out using MEGA11. Each of these methods produced reliable and complementary results, collectively confirming the subspecies status of *V. griseus caspius* within the *V. griseus* group on a solid scientific basis.

In the phylogenetic tree constructed using the ML method, the *V. griseus caspius* specimen from the collection of the Institute of Zoology, Academy of Sciences of the Republic of Uzbekistan, clustered closely with *V. griseus* sequences registered in the GenBank database (OP117173 and OP117223). This grouping was strongly supported by a high bootstrap value (100/1000), indicating robust statistical confidence. These results reflect the molecular-level expression of the morphological diversity previously proposed for *V. griseus* by Pianka and King (2004), as well as Koch et al. (2013). In other words, despite external morphological differences, there is considerable underlying genetic similarity between the taxa.

Unlike the commonly used Kimura 2-parameter model, the genetic distance analysis was performed using IQ-TREE2, which relies on evolutionary probability models. This approach provides more accurate and biologically meaningful results than simplified methods such as p-distance, as it accounts for the probabilities of nucleotide substitutions. The results revealed very low genetic divergence between *V. griseus caspius* and *V. griseus*, indicating that these lineages are not fully separated and are likely in close evolutionary proximity. This finding may be attributed to recent diversification or ongoing gene flow between the taxa (Hebert et al. 2003; Ast 2001). Similarly, low genetic distances within the *V. salvator* group also point to ongoing intraspecific diversification processes and may reflect ecological adaptation and gene exchange dynamics.

The Disparity Index analysis between *V. griseus caspius* and *V. griseus* yielded a very low ID value (0.0176), indicating that their nucleotide substitution patterns are nearly identical. This result is consistent with both the phylogenetic and genetic distance analyses, supporting the hypothesis that these taxa share a recent common ancestor and that there is currently insufficient evolutionary divergence to classify them as separate species. In contrast, when *V. griseus caspius* was compared to more distantly related taxa such as *V. rudicollis* and *V. flavescens*, significantly higher Disparity Index values (≥0.8924) were observed, indicating independent evolutionary pathways (Nagy et al., 2012).

The outgroup species *Xantusia jaycolei* was consistently placed on a distinctly distant branch from the *Varanus* group in all analyses, further validating the reliability of the methodologies used to test evolutionary hypotheses (Farris et al. 1979; Maddison et al. 1984).

The integrated results of these three methods provided a robust molecular identification of *V. griseus caspius* and clarified its phylogenetic placement within the *V. griseus* group.

Conclusion

In this study, the molecular-phylogenetic position and interspecific evolutionary relationships of *Varanus griseus caspius* were comprehensively evaluated using three independent methods: phylogenetic analysis based on the Maximum Likelihood (ML) approach, genetic distance analysis based on evolutionary models in IQ-TREE2, and the Disparity Index test conducted in MEGA11. The results of all three methods were mutually supportive and scientifically confirmed the subspecies status of *V. griseus caspius* within the *V. griseus* group.

In the phylogenetic tree, *V. griseus caspius* and *V. griseus* samples clustered together, indicating their close genetic relationship. Genetic distance and Disparity Index analyses also confirmed this result, showing that these taxa have not yet fully diverged evolutionarily. In contrast, comparisons with more distantly related taxa revealed significant differences, indicating the presence of independent evolutionary lineages.

The findings provide a reliable scientific basis for the precise molecular identification of *V. griseus caspius* and for clarifying its phylogenetic position. Future research should include not only mitochondrial markers but also nuclear genetic markers, a broader sample base, and geographic data, allowing for a deeper exploration of the genetic and ecological connections between these taxa.

The results of the molecular-genetic research and bioinformatic analyses led to the first-time submission of the nucleotide sequence of the species *V. griseus caspius* to an international bioinformatics database, where it was successfully registered and assigned an accession number (Accession number: *Varanus griseus caspius* – PX093056).

Acknowledgements

We express our gratitude to the scientific team of the laboratory Molecular Zoology Institute of Zoology of the Academy of Sciences of the Republic of Uzbekistan for their practical assistance in identifying the composition of reptile's species, and to the leadership of the scientific project "Molecular Genetic Classification of Wild Vertebrate Species of Bukhara and Navoi Regions" for conducting the molecular genetic analysis.

References

Abduraupov TV, Khojimatov OK, Bussmann RW (2023) *Varanus griseus caspius* Eichwald, 1831 – VARANIDAE. In: Ethnobiology of Uzbekistan. Ethnobiology. Springer, Cham, 891–895. https://doi.org/10.1007/978-3-031-23031-8_98

Ast JC (2001) Mitochondrial DNA Evidence and Evolution in Varanoidea (Squamata). Cladistics 17(3): 211–226. https://doi.org/10.1111/j.1096-0031.2001.tb00118.x

Bennett D (1995) A Little Book of Monitor Lizards. A Guide to the Monitor Lizards of the World and their Care in Captivity. Viper Press, Aberdeen, 208 pp.

Bondarenko OV (1989) Distribution and population density of the desert monitor in two landscape regions of Uzbekistan. Voprosy gerpetologii. VII Vsesoyuznaya gerpetologicheskaya konferenciya. Avtoreferaty dokladov [Herpetology Issues: Abstracts of the Reports from the VII All-Union Herpetological Conference] (Kiev, 26–29 September 1989). Naukova dumka, Kiev, 85–86. [In Russian]

Böhme W, Ahmed SH, Al-Sheikhly O F, Ararat K, Auer M, Khudur F, Langner C (2023) Desert Monitor Lizards (Squamata: Varanidae: *Varanus*: *Psammosaurus*) from the Middle East: Further Records of Nesterov's Desert Monitor, *Varanus* (P.) *nesterovi* Böhme, Ehrlich, Milto, Orlov et Scholz, 2015, from Iraq, and Adjacent Localities of *Varanus* (P.) *g. griseus* (Daudin, 1803) and *Varanus* (P.) *g. caspius* (Eichwald, 1831), with Comments on Biogeography and Taxonomy. Russian Journal of Herpetology 30(6): 518–528. https://doi.org/10.30906/1026-2296-2023-30-6-518-528

Doughty P, Kealley L, Fitch A, Donnellan SC (2014) A new diminutive species of *Varanus* from the Dampier Peninsula, western Kimberley region, Western Australia. Records of the Western Australian Museum 29(2): 128–140. https://doi.org/10.18195/issn.0312-3162.29(2).2014.128-140

Farris JS (1982) Outgroups and Parsimony. Systematic Biology 31(3): 328–334. https://doi.org/10.1093/sysbio/31.3.328

Felsenstein J (1985) Confidence limits on phylogenies: an approach using the bootstrap. Evolution 39(4): 783–791. https://doi.org/10.1111/j.1558-5646.1985.tb00420.x

Fuller S, Baverstock P, King D (1998) Biogeographic Origins of Goannas (Varanidae): A Molecular Perspective. Molecular Phylogenetics and Evolution 9(2): 294–307. https://doi.org/10.1006/mpev.1997.0476

Hall TA (1999) BioEdit: a user-friendly biological sequence alignment editor and analysis program for Windows 95/98/NT. Nucleic Acids Symposium Series 41: 95–98.

Hebert PDN, Cywinska A, Ball SL, deWaard JR (2003) Biological identifications through DNA barcodes. Proceedings of the Royal Society of London. Series B: Biological Sciences 270: 313–321. https://doi.org/10.1098/rspb.2002.2218

Hekkala E, Shirley MH, Amato G, Austin JD, Charter S, Thorbjarnarson J, Vliet KA, Houck ML, Desalle R, Blum MJ (2011) An ancient icon reveals new mysteries: Mummy DNA resurrects a cryptic species within the Nile crocodile. Molecular Ecology 20(20): 4199–4215. https://doi.org/10.1111/j.1365-294X.2011.05245.x

Huelsenbeck JP, Hillis DM (1993) Success of phylogenetic methods in the four-taxon case. Systematic Biology 42(3): 247–264. https://doi.org/10.1093/sysbio/42.3.247

Kalyaanamoorthy S, Minh BQ, Wong TKF, von Haeseler A, Jermiin LS (2017) ModelFinder: fast model selection for accurate phylogenetic estimates. Nature Methods 14(6): 587–589. https://doi.org/10.1038/nmeth.4285

Katoh K, Misawa K, Kuma K, Miyata T (2002) MAFFT: A novel method for rapid multiple sequence alignment based on fast Fourier transform. Nucleic Acids Research 30(14): 3059–3066. https://doi.org/10.1093/nar/gkf436

Koch A, Ziegler T, Böhme W, Arida E, Auliya M (2013) Pressing problems: distribution, threats, and conservation status of the monitor lizards (Varanidae: *Varanus* spp.) of Southeast Asia and the Indo-Australian Archipelago. Herpetological Conservation and Biology 8(3): 1–62.

Khodzhaev APh, Nuridjanov DA, Abduraupov TV (2019) *Varanus griseus caspius*. In: Red Data Book of the Republic of Uzbekistan. Vol. II. Chinor ENK, Tashkent, 109–117. [In Russian]

Khudirov KO, Mirzobahodurova ShR, Domulloeva ZK (2021) On the ecology of distribution and protection of the desert monitor – *Varanus griseus* (Daudin, 1873) in Tajikistan. In: Fundamental'nye osnovy nauki. Sbornik nauchnyh trudov po materialam XXX Mezhdunarodnoj nauchno-prakticheskoj konferencii [Fundamentals of Science. A Collection of Scientific Papers Based on the Proceedings of the XXX International Scientific and Practical Conference] (Anapa, April 20, 2021). Publishing House of the "Research Center for Economic and Social Processes" in the Southern Federal District, Anapa, 48–54. [In Russian]

Kuchboev AE, Amirov OO, Abramatov MB, Ruziev BH, Egamberdiyev MKH, Karimova RR (2024) Molecular species identification from fecal samples of Caprinae of Uzbekistan. Acta Biologica Sibirica 10: 1433–1443. http://doi.org/10.5281/zenodo.14279887

Kuchboev AE, Amirov OO, Yuldoshkhonov AA (2025) Molecular-genetic characterization of the species *Eryx miliaris* (Squamata: Boidae) distributed in Uzbekistan. Biological Sciences of Kazakhstan 1: 15–20. https://doi.org/10.52301/1684-940X-2025-1-15-20

Letunic I, Bork P (2021) Interactive Tree of Life (iTOL) v5: An online tool for phylogenetic tree display and annotation. Nucleic Acids Research 49(W1): W293–W296. https://doi.org/10.1093/nar/gkab301

Leviton AE, Anderson SC (1970) The amphibians and reptiles of Afghanistan: A checklist and key to their identification. Contributions to Herpetology 1(1): 1–15.

Maddison W P, Donoghue MJ, Maddison DR (1984) Outgroup analysis and parsimony. Systematic Zoology 33(1): 83–103. https://doi.org/10.2307/2413134

Martin T, Guillemin M, Nivet-Mazerolles V, Landsmann C, Dubos J, Eudeline R, Stroud J (2017) The herpetofauna of central Uzbekistan. Amphibian & Reptile Conservation 11(1) [General Section]: 93–107 (e140).

Mertens R (1954) Die Familie der Warane (Varanidae). Abhandlungen der Senckenbergischen Naturforschenden Gesellschaft 487: 1–116.

Minh BQ, Schmidt HA, Chernomor O, Schrempf D, Woodhams MD, von Haeseler A, Lanfear R (2020) IQ-TREE 2: New Models and Efficient Methods for Phylogenetic Inference in the Genomic Era. Molecular Biology and Evolution 37(5): 1530–1534. https:// doi.org/10.1093/molbev/msaa015

Nagy ZT, Sonet G, Glaw F, Vences M (2012) First large-scale DNA barcoding assessment of reptiles in the biodiversity hotspot of Madagascar, based on newly designed COI primers. PLoS ONE 7(3): e34506. https://doi.org/10.1371/journal.pone.0034506

Nuridjanov DA, Chirikova MA, Pestov MV, Zima YuA (2016) New information on the state of the population of the Central Asian Desert monitor *Varanus griseus caspius* (Eichwald, 1831) in Uzbekistan. In: Materialy Respublikanskoj nauchno-prakticheskoj kon-

ferencii "Sovremennye problemy sohraneniya redkih, ischezayushchih i maloizuchennyh zhivotnyh Uzbekistana" [Proceedings of the Republican Scientific and Practical Conference "Modern Problems of Conservation of Rare, Endangered, and Poorly Studied Animals of Uzbekistan"] (Tashkent, 9–10 September 2016). Tashkent, 154–158. [In Russian]

Quvatov AQ, Kuchboev AE, Mirzayev UT, Amirov OO, Atamuratova MSh, Narboev ZU (2023) Morphometric and molecular characteristics of *Cottus jaxartensis*. Egyptian Journal of Aquatic Biology & Fisheries 27(6): 215–223.

Paraskiv A (1956) On the economic importance of desert monitor lizards. Bulletin of Zoology 10(3): 55–62. [In Russian]

Pianka ER, King DR (2004) Varanoid Lizards of the World. Indiana University Press, 608 pp.

Shadloo S, Mahmoodi S, Hosseinzadeh MS, Kazemi SM (2021) Prediction of habitat suitability for the desert monitor (*Varanus griseus caspius*) under the influence of future climate change. Journal of Arid Environments 186: 104416. https://doi.org/10.1016/j.jaridenv.2020.104416

Showler DAA (2018) Checklist of the Amphibians and Reptiles of the Republic of Uzbekistan with a review and summary of species distribution. Freely available PDF, 46 pp.

Sindaco R, Jeremčenko VK (2008) The reptiles of the Western Palearctic. Annotated checklist and distributional atlas of the turtles, crocodiles, amphisbaenians and lizards of Europe, North Africa, Middle East and Central Asia. Monografie della Societas Herpetologica Italica. Edizioni Belvedere, Latina, Italy, 579 pp.

Sobirov HF, Kuchboev AE, Abramatov MB (2025) Morphological and molecular identification of *Nematodirus* species (Nematoda, Molineidae) from domestic ruminants in Uzbekistan. Biosystems Diversity 33(2): 1–7. https://doi.org/10.15421/012524

Stuart BL, Inger RF, Voris HK (2006) High level of cryptic species diversity revealed by sympatric lineages of Southeast Asian Forest frogs. Biology Letters 2(3): 470–474. https://doi.org/10.1098/rsbl.2006.0505

Tamura K, Stecher G, Kumar S (2021) MEGA11: Molecular Evolutionary Genetics Analysis version 11. Molecular Biology and Evolution 38(7): 3022–3027. https://doi.org/10.1093/molbev/msab120

Tsellarius AY, Cherlin VA (1994) The duration of *Varanus griseus* (Reptilia, Sauria) egg incubation and the dates of hatchlings emerging in sandy deserts of Middle Asia. Selevinia 4: 43–46. [In Russian]

Ubaydullayev OK, Amirov OO, Quvatov AQ, Yusupov AP, Narboev ZU, Donayeva ShA, Nomonov JN (2025) Molecular-Genetic Analysis of *Channa argus* (Cantor, 1842) (Teleostei: Channidae) Distributed in the Kashkadarya River, Uzbekistan. Egyptian Journal of Aquatic Biology & Fisheries 29(1): 1171–1180.

Vidal N, Marin J, Sassi J, Battistuzzi FU, Donnellan S, Fitch AJ, Fry BG, Vonk FJ, Rodriguez de la Vega RC, Couloux A, Hedges SB (2012) Molecular evidence for an Asian origin of monitor lizards followed by Tertiary dispersals to Africa and Australasia. Biology Letters 8: 853–855. https://doi.org/10.1098/rsbl.2012.0460

Ziegler T, Schmitz A, Koch A, Böhme W (2007) A review of the subgenus *Euprepiosaurus* of *Varanus* (Squamata: Varanidae): morphological and molecular phylogeny, distribution

and zoogeography, with an identification key for the members of the *V. indicus* and the *V. prasinus* species groups. Zootaxa 1472: 1–28. https://doi.org/10.11646/zootaxa.1472.1.1

Zima YA, Fedorenko VA (2024) The range of the desert monitor *Varanus griseus caspius* in Central Asia. Frontiers of Biogeography 17: e138199. https://doi.org/10.21425/fob.17.138199