



First Record of the Non-native Pond Loach *Misgurnus anguillicaudatus* (Cantor, 1842) (Teleostei: Cobitidae) from the Lower Amu Darya River in Uzbekistan

*Bakhtiyor Sheraliev*¹

¹Department of Zoology and General Biology, Faculty of Life Sciences, Fergana State University, 150100 Fergana, Uzbekistan;
E-mail: bakhtiyorsheraliev@gmail.com

Abstract: This study reports the first record of the non-native pond loach, *Misgurnus anguillicaudatus* (Cantor, 1842) (Oriental Weatherfish), from the lower reaches of the Amu Darya River in northwestern Uzbekistan. The species' identity was confirmed through an integrated approach using morphological data and DNA barcoding of the mitochondrial COI gene. The presence of a reproducing population, including both mature adults and juveniles, suggests the species is well-established. The likely invasion pathway is an introduction from the adjacent Karakum Canal in Turkmenistan, where the species is already established, followed by downstream dispersal. This discovery, representing only the second Cobitidae species known from Uzbekistan, underscores the dynamic nature of biological invasions in the Aral Sea basin and highlights the critical need for continued monitoring of the regional ichthyofauna.

Key words: Aral Sea basin, cytochrome oxidase I, invasive species, loaches

Academic Editor: *Apostolos Apostolou*

Introduction

Biological invasions are an increasingly widespread phenomenon, contributing to the loss of regional biodiversity and the homogenization of global fauna and flora (Walsh et al. 2016). Freshwater ecosystems are particularly vulnerable, with a recent global database documenting 1,538 established non-native fish species across 193 countries (Haubrock et al. 2025). The primary pathways for these introductions include escape from confinement (e.g., aquaculture, ornamental trade) and release in nature (e.g., fishery stocking) (Haubrock et al. 2025). Once established, these species can exert severe ecological impacts through competition, predation, and disease trans-

mission, often leading to significant socio-economic losses (Clavero & García-Berthou 2005, Haubrock et al. 2022). Notably, eight fish species are included among the 100 of the world's worst invasive alien species (Global Invasive Species Database 2023).

Uzbekistan, characterized by predominantly arid landscapes and limited river systems, harbors a relatively low diversity of freshwater fishes, with approximately 70 recorded species (Sheraliev & Peng 2021). However, this fauna exhibits high endemism, with over 25 species restricted to the Aral Sea basin (Mirabdullaev & Mullabaev 2020, Sheraliev & Peng 2021), more than half of which are considered endangered. Nearly one-third of the currently known ichthyofauna consists of introduced or invasive

species (Mirabdullaev & Mullabaev 2020), most of which were introduced after the 1970s for aquaculture and have since colonized lowland water bodies.

The genus *Misgurnus* Lacepède, 1803 (family Cobitidae) comprises small benthic loaches distributed in Europe and East Asia, with 12 currently recognized species (Shedko & Vasil'eva 2022). Among them, only *M. fossilis* (Linnaeus, 1758), originally described from Europe, is the genus's only species native to the region (Kottelat & Freyhof 2007). *Misgurnus anguillicaudatus* (Cantor, 1842) is indigenous to 12 Asian countries and has been introduced into at least 11 countries across Asia, Europe, North America, and Oceania (Keller & Lake 2007, Clavero et al. 2023, Vasil'eva et al. 2024, Cano-Barbacid et al. 2025, Froese & Pauly 2025). *Misgurnus anguillicaudatus* has previously been recorded in Central Asia from the Karakum Canal in Turkmenistan and the Chilik and Usek rivers in the Ili River basin of southeastern Kazakhstan (Rustamov & Shakirova 2013, Vasil'eva et al. 2024). Here, we report the first documented occurrence of *M. anguillicaudatus* in the lower reaches of the Amu Darya River in Uzbekistan, supported by both morphometric and molecular evidence.

Materials and Methods

Live specimens of *Misgurnus anguillicaudatus* were collected in September 2022 (n=3) and September 2023 (n=5) from rice paddies situated adjacent to

the main channel of the lower reaches of the Amu Darya River (41°27'34.4"N, 60°58'31.3"E) (Fig. 1). The specimens were sampled using small hand nets. The pectoral fin was dissected from the right side of each specimen and stored in 96% ethanol at -20°C for molecular research, and the voucher specimens were fixed in 10% formalin for morphometric studies. Counts and measurements were performed following the procedures of Kottelat & Freyhof (2007). Morphometric data are expressed as ratios in the text and as percentages of standard length and head length in the table. Four specimens were deposited in the collection of the Faculty of Life Sciences, Fergana State University (FSU), and four in the private Bakhtiyor Sheraliev Fish Collection (BSFC), both in Fergana, Uzbekistan, with the accession numbers FSU 25092022 and BSFC 0071, respectively.

DNA extraction and PCR. Genomic DNA was extracted using the Qiagen DNeasy Blood and Tissue kit following the manufacturer's protocol. The standard vertebrate DNA barcode region of the COI (cytochrome c oxidase subunit 1) was amplified using the FishF1 (5'-TCA ACC AAC CAC AAA GAC ATT GGC AC-3') and FishR1 (5'-TAG ACT TCT GGG TGG CCA AAG AAT CA-3') primers designed by Ward et al. (2005). The PCR assay was performed in a reaction volume of 25 µL containing 10 ng template DNA, 1 µL of each primer, 12.5 µL 2× Taq Master Mix (Novoprotein, Guangdong, China), and ddH₂O. Thermal cycling



Fig. 1. Map showing the collection locality of *Misgurnus anguillicaudatus* (orange circle) in the lower reaches of the Amu Darya River, Uzbekistan.

Table 1. List of mitochondrial COI sequences retrieved from GenBank with information on drainage and country of origin.

Species	Location	Accession number	Reference
<i>Misgurnus anguillicaudatus</i>	USA: New York	MT667249	Schroeter et al. (2020)
<i>Misgurnus anguillicaudatus</i>	China: Wuhan	KP112319	Shen et al. (2016)
<i>Misgurnus anguillicaudatus</i>	China: Yunnan	KM610760	Chen et al. (2015)
<i>Misgurnus anguillicaudatus</i>	China: Zhejiang	MN127924	Zhang et al. (2021)
<i>Misgurnus anguillicaudatus</i>	Uzbekistan: Amu Darya	OR143297	This study
<i>Misgurnus bipartitus</i>	China: Qinghai-Tibet Plateau	MT413322	Feng (unpublished)
<i>Misgurnus bipartitus</i>	China	KF562047	Huang et al. (2015)
<i>Misgurnus dabryanus</i>	China: Wuhan	KP112350	Shen et al. (2016)
<i>Misgurnus dabryanus</i>	Japan	AP012124	Miya et al. (2015)
<i>Misgurnus dabryanus</i>	China: Hunan	MN127938	Zhang et al. (2021)
<i>Misgurnus fossilis</i>	Austria: Zwerndorf an der March	ON097858	Zangl et al. (2022)
<i>Misgurnus fossilis</i>	Germany: Gorleben	KM286763	Knebelsberger et al. (2015)
<i>Misgurnus mohoity</i>	China	KX505175	Yi et al. (2016)
<i>Misgurnus mohoity</i>	China	KF386025	Yu et al. (2015)
<i>Misgurnus mohoity</i>	China: Heilongjiang	MN127946	Zhang et al. (2021)
Outgroups			
<i>Barbatula barbatula</i>	France	KP715096	Murienne et al. (2016)
<i>Pangio kuhlii</i>	Japan	AP011346	Miya et al. (2015)
<i>Triplophysa ferganaensis</i>	Uzbekistan	MW649603	Sheraliev & Peng (2021)

consisted of an initial step at 94°C for 3 min; 35 cycles at 94°C for 30 s, 54°C for 50 s, and 72°C for 1 min 10 s; and a final extension step at 72°C for 7 min. PCR products were sent to TsingKe Biological Technology Co., Ltd. (Chongqing, China) for sequencing.

Molecular data analysis. A total of 17 sequences were downloaded from NCBI GenBank (Table 1) and combined with the newly generated COI sequence of *M. anguillicaudatus* from the lower reaches of the Amu Darya. *Barbatula barbatula*, *Pangio kuhlii* and *Triplophysa ferganaensis* served as outgroups to root the phylogenetic tree. The COI gene sequences were aligned using the Clustal_W algorithm in MEGA X (Kumar et al. 2018), with manual checks for inconsistencies. The distances between different groups were determined using MEGA X, with 1000 bootstrap replicates calculated using the best selected K2P model. For phylogenetic reconstruction, the datasets were analyzed using both the Neighbor-Joining (NJ) and Maximum Likelihood (ML) methods in MEGA X (Kumar et al. 2018). The best-fit substitution model was determined to be the Generalized Time Reversible model

with Gamma distributed rate variation and a proportion of invariable sites (GTR+G+I). Nodal support was assessed using 1,000 bootstrap replicates for both NJ and ML analyses.

Results

Morphological identification

Photographs of *M. anguillicaudatus* from the Amu Darya River are presented in Figure 2, with morphometric data in Table 2. Specimens of *M. anguillicaudatus* from the Amu Darya River were identified based on the diagnostic characters of *M. anguillicaudatus* provided by Kottelat & Freyhof (2007), Guo et al. (2021) and Shedko & Vasil'eva (2022).

Body elongated, cylindrical from behind operculum to dorsal-fin origin, then compressed toward caudal-fin base; maximum body depth 7.3–8.0 in SL, dorsal-fin origin closer to caudal-fin base than to snout tip; pelvic-fin base level with first branched dorsal-fin ray; pelvic fin with 5 branched rays, short, not reaching anus, length $\sim\frac{1}{2}$ pelvic-anal distance; pectoral fin with 9 branched rays, slightly pointed, length 2.3–3.3 in pectoral-pelvic distance, 6.0–8.0



Fig. 2. *Misgurnus anguillicaudatus*, 52.6 mm SL and 43.6 mm SL; BSFC 0071; Lower reaches of the Amu Darya, Uzbekistan.

Table 2. Comparison of morphometric measurements of *Misgurnus anguillicaudatus* with the literary data on the same species.

Morphometric characteristics	Amu Darya (n=3)		Sichuan (n=20)*
	min-max	mean±SD	min-max
Total length (TL) (mm)	36.1–62.8	50.4	109.9–155.0
Standard length (SL) (mm)	30.6–52.6	42.6	88.0–133.0
In % of SL			
Lateral head length (HL)	20.0–22.5	20.9±1.4	15.9–17.9
Body depth at dorsal fin origin	12.5–13.6	13.1±0.6	11.2–14.3
Body width at dorsal fin origin	9.8–11.7	10.8±1.0	8.6–10.7
Predorsal length	57.9–58.6	58.3±0.3	57.9–60.7
Postdorsal length	28.3–29.8	28.9±0.8	-
Prepelvic length	58.2–60.8	59.2±1.4	-
Preanal length	76.4–77.0	76.7±0.3	-
Dorsal-fin depth	12.4–14.3	13.3±0.9	10.5–15.3
Dorsal fin base length	10.8–14.5	12.4±1.9	8.4–11.2
Anal-fin depth	10.8–13.6	12.2±1.4	8.3–14.6
Anal fin base length	8.5–11.1	9.6±1.4	-
Pectoral-fin length	12.5–16.6	14.1±2.2	10.8–15.6
Pelvic-fin length	8.0–9.4	8.8±0.7	7.5–10.2
Caudal-peduncle length (CPL)	13.6–15.2	14.6±0.8	15.2–18.8
Caudal-peduncle depth (CPD)	9.9–11.0	10.3±0.5	10.5–13.5
Pectoral-pelvic distance	38.1–41.4	40.2±1.8	39.6–43.4
Pelvic-anal distance	16.2–17.7	16.8±0.8	16.3–19.6
Vent-anal fin origin distance	2.1–2.9	2.5±0.4	2.3–4.9
In % of HL			
Head depth at nape	54.1–64.4	59.7±5.2	56.0–60.0
Head depth at eye	49.2–55.5	51.8±3.3	45.0–48.1
Head maximum width	45.3–61.8	56.0±9.2	54.5–56.5
Snout length	40.2–41.2	40.7±0.5	39.1–40.6
Eye diameter	12.7–14.4	13.4±0.9	12.0–15.0
Interorbital width	17.2–19.6	18.6±1.3	17.4–24.0
Postorbital head length	41.1–43.5	41.9±1.4	-

Note. * - data from Guo et al. (2021).

in SL. Dorsal fin with 7½ branched rays, distal margin rounded, depth 7.0–8.1 in SL; anal fin with 5½ branched rays, depth 7.3–9.2 in SL. Dorsal and ventral flanges of caudal fin well-developed along caudal peduncle, ventral flange extends to or past distal end of depressed anal-fin rays; dorsal flange shorter, not reaching distal dorsal-fin rays; caudal peduncle relatively short (length 6.6–7.3 in SL) and deep (depth 9.1–10.1 in SL and 1.4–1.5 in CPL). Caudal fin with 14 branched rays, posterior edge rounded, and 1.2–1.3 times CPL. Body covered with minute scales; lateral line with more than 130 scales. Head short, 4.4–5.0 in SL; mandibular barbel reaching past posterior eye margin; lower lip with four long, barbel-like mental lobes.

Colouration of ethanol-fixed specimen: background body colouration light beige; belly more yellowish; back, head, and sides covered with numerous small dark brown speckles, irregularly scattered but tending to form faint mottling; large leopard-like blotches absent. Indistinct middorsal stripe present from snout almost to dorsal-fin origin; paired stripe along dorsal-fin base not evident; dorsal flange of caudal fin marked with irregular series of spots extending to caudal-fin origin. Midlateral series of small, irregular dark dots forming a discontinuous line from posterior margin of head to

caudal-fin origin; bifurcation above pectoral fin not discernible. Lower lateral row of spots from anal-fin origin to caudal-fin origin weakly developed. Head dorsally speckled with irregular dark dots; faint dark line from snout tip to eye present but poorly defined. Caudal fin with a small and indistinct basal spot (oblong spot poorly developed); scattered dark dots present along rays. Dorsal-fin rays with faint irregular scattered dots, less organized into lines; pectoral-fin rays unpigmented on outer rays; barbels weakly pigmented. Lower part of head, lower sides between head and anal fin, belly, pelvic and anal fins pale, largely unpigmented.

Molecular identification

Phylogenetic analysis of the COI barcode gene confirmed that specimens of *M. anguillicaudatus* from the Amu Darya River form a highly supported clade with conspecific sequences from China and the USA (Fig. 3). The average Kimura 2-Parameter (K2P) genetic distance between the Amu Darya population and populations from China and the USA was 1.8% (Table 3). The analysis identified *M. bipartitus* from China as the sister species to *M. anguillicaudatus*, a relationship that also received high phylogenetic support, with an interspecific K2P distance of 10.1%.

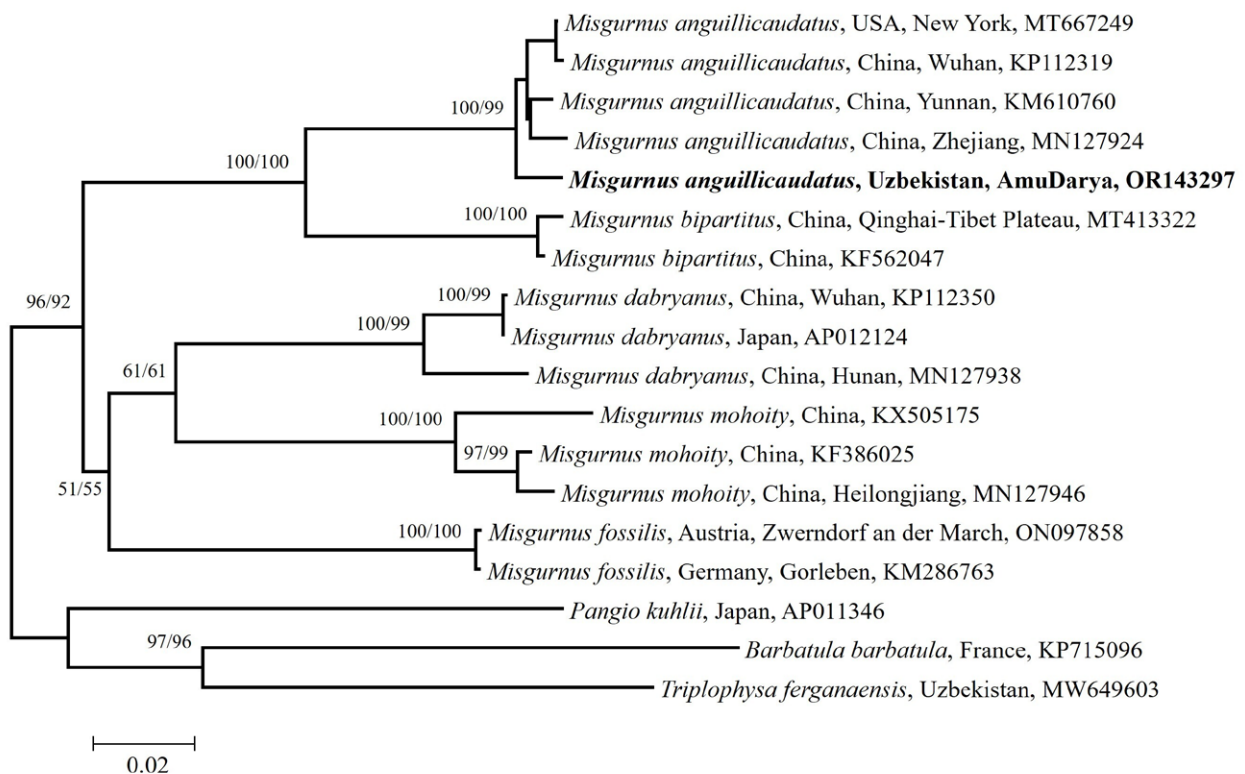


Fig. 3. Phylogenetic tree from the maximum likelihood analysis of the mitochondrial COI barcode region. Numbers at the nodes indicate bootstrap support values (>50%) from 1000 pseudoreplicates for the NJ and ML analyses, respectively.

Table 3. Pairwise K2P genetic distances between *Misgurnus anguillicaudatus* from the Amu Darya River and comparative *Misgurnus* sequences based on the mitochondrial COI gene.

	Species name	1	2	3	4	5	6	7	8	9	10	11	12	13	14
1	<i>Misgurnus anguillicaudatus</i> Amu Darya														
2	<i>Misgurnus anguillicaudatus</i> KM610760	0.013													
3	<i>Misgurnus anguillicaudatus</i> MN127924	0.019	0.011												
4	<i>Misgurnus anguillicaudatus</i> KP112319	0.020	0.013	0.015											
5	<i>Misgurnus anguillicaudatus</i> MT667249	0.021	0.011	0.013	0.001										
6	<i>Misgurnus bipartitus</i> MT413322	0.101	0.100	0.102	0.098	0.095									
7	<i>Misgurnus bipartitus</i> KF562047	0.101	0.100	0.100	0.096	0.092	0.006								
8	<i>Misgurnus dabryanus</i> MN127938	0.173	0.176	0.173	0.178	0.180	0.179	0.172							
9	<i>Misgurnus dabryanus</i> KP112350	0.179	0.181	0.181	0.179	0.181	0.176	0.170	0.036						
10	<i>Misgurnus dabryanus</i> AP012124	0.179	0.181	0.180	0.179	0.177	0.175	0.166	0.036	0.000					
11	<i>Misgurnus fossilis</i> ON097858	0.171	0.179	0.176	0.167	0.165	0.176	0.170	0.174	0.165	0.165				
12	<i>Misgurnus fossilis</i> KM286763	0.173	0.176	0.176	0.164	0.162	0.176	0.170	0.176	0.166	0.166	0.002			
13	<i>Misgurnus mohoity</i> KF386025	0.182	0.193	0.193	0.193	0.190	0.171	0.162	0.150	0.127	0.124	0.146	0.146		
14	<i>Misgurnus mohoity</i> MN127946	0.184	0.189	0.186	0.196	0.197	0.183	0.181	0.147	0.136	0.135	0.150	0.150	0.010	
15	<i>Misgurnus mohoity</i> KX505175	0.202	0.200	0.191	0.197	0.200	0.188	0.184	0.153	0.145	0.145	0.147	0.144	0.047	0.041

Discussion

Morphological and molecular analyses confirmed the presence of *Misgurnus anguillicaudatus* in the lower reaches of the Amu Darya River in northwestern Uzbekistan. The occurrence of both large, sexually mature individuals and small juveniles in rice-growing irrigation waters along the river in 2022 and 2023 indicates that the species is well-established and reproducing in the region. These findings suggest that its presence is not the result of vagrancy, as the existence of multiple age classes is a clear sign of an established population (Blackburn et al. 2011).

Following its intentional introduction into the Karakum Canal system in Turkmenistan (Rustamov & Shakirova 2013), *Misgurnus anguillicaudatus* likely gained access to the Amu Darya via the canal's connection to the river in southern Uzbekistan, subsequently dispersing downstream to the lower reaches where it was recorded.

Overall, the morphological and meristic characteristics of the Amu Darya specimens are consistent with those reported for *M. anguillicaudatus* from water bodies in Europe, China, and Kazakhstan (Kottelat & Freyhof 2007, Guo et al. 2021, Vasil'eva et al. 2024). However, the dark blotch at the base of the caudal fin the base of the caudal appeared smaller and fainter in the Amu Darya specimens than in those from the Chilik River in Kazakhstan (Vasil'eva et al. 2024).

Molecular analyses revealed that the Amu Darya *M. anguillicaudatus* clusters within the same clade as specimens from other regions (Fig. 3), although the intraspecific genetic divergence ranged from 1.3% to 2.1% (mean 1.8%). This is somewhat higher than the typical intraspecific divergence observed in many other fish taxa (Ward et al. 2005, Sheraliev & Peng 2021). In contrast, interspecific divergence within the genus *Misgurnus* was substantially higher (9.8–19.4%). Recent studies have also shown that intraspecific divergence within *Misgurnus* species based on the COI gene can exceed 2% (Tang et al. 2023, Shi et al. 2025).

Misgurnus anguillicaudatus is only the second species of the family Cobitidae recorded from Uzbekistan, joining the native Aral spined loach, *Sabanejewia aralensis* (Kessler, 1877). Given the established status of *M. anguillicaudatus* in the lower Amu Darya, total eradication is likely unfeasible, particularly as the species can survive desiccation and adverse conditions by burrowing into sediment (Cano-Barbacil et al. 2025). Therefore, management efforts should prioritize preventing its secondary spread to uninvaded aquatic systems. Key measures must in-

clude stricter biosecurity protocols in aquaculture to prevent accidental translocations and monitoring of irrigation networks that facilitate dispersal. Furthermore, future climate change scenarios may exacerbate the risk of invasion (Bellard et al. 2013, Gallardo et al. 2017). *Misgurnus anguillicaudatus* possesses high environmental plasticity, including tolerance to broad temperature ranges (2–38°C) and hypoxia (Urquhart & Koetsier 2013). In the arid context of Central Asia, projected temperature increases and water scarcity could favor this tolerant species over sensitive native ichthyofauna, potentially accelerating its range expansion and competitive dominance.

Acknowledgements: I am grateful to Norbek Bekchanov (Khorezm Mamun Academy, Khiva, Uzbekistan) for collecting the fish samples and sending them to me. I also thank Dr. Amaël Borzée (Nanjing Forestry University, China) for his assistance with COI sequencing.

References

- Bellard C., Thuiller W., Leroy B., Genovesi P., Bakkenes M. & Courchamp F. 2013. Will climate change promote future invasions? *Global Change Biology* 19: 3740–3748. <https://doi.org/10.1111/gcb.12344>
- Blackburn T. M., Pyšek P., Bacher S., Carlton J. T., Duncan R. P., Jarošík V., Wilson J. R. U. & Richardson D. M. 2011. A proposed unified framework for biological invasions. *Trends in Ecology & Evolution* 26 (7): 333–339. <https://doi.org/10.1016/j.tree.2011.03.023>
- Cano-Barbacil C., Haubrock P. J. & Radinger J. 2025. Asian loaches: An emerging threat as global invaders. *Freshwater Biology* 70 (4): e70026. <https://doi.org/10.1111/fwb.70026>
- Chen W., Ma X., Shen Y., Mao Y. & He S. 2015. The fish diversity in the upper reaches of the Salween River, Nujiang River, revealed by DNA barcoding. *Scientific Reports* 5: e17437. <https://doi.org/10.1038/srep17437>
- Clavero M. & García-Berthou E. 2005. Invasive species are a leading cause of animal extinctions. *Trends in Ecology & Evolution* 20 (3): 110–110. <https://doi.org/10.1016/j.tree.2005.01.003>
- Clavero M., Suh J., Franch N., Aparicio E., Buchaca T., Caner J., Garcia-Rodriguez S., Llimona F., Pou-Rovira Q., Rocaspana R. & Ventura M. 2023. Invaders they are a-changing: A recent, unexpected surge of invasive loaches in Catalonia. *Freshwater Biology* 68 (4): 621–631. <https://doi.org/10.1111/fwb.14051>
- Froese R. & Pauly D. 2025. FishBase. World Wide Web electronic publication. www.fishbase.org, version (04/2025).
- Gallardo B., Aldridge D. C., González-Moreno P., Pergl J., Pizarro M., Pyšek P., Thuiller W., Yesson C. & Vilà M. 2017. Protected areas offer refuge from invasive species spreading under climate change. *Global Change Biology* 23: 5331–5343. <https://doi.org/10.1111/gcb.13004>
- Global Invasive Species Database 2023. 100 of the World's Worst Invasive Alien Species. https://www.iucngisd.org/gisd/100_worst.php (accessed on 15 August 2023)

- Guo Y., Sun Z., He X., Shi W. & Chen Y. 2021. Colored Atlas of Fishes of Sichuan. Volume II. Sichuan: Sciencepress. pp. 476-973.
- Haubrock P. J., Bernery C., Cuthbert R. N., Liu C., Kourantidou M., Leroy B., Turbelin A. J., Kramer A. M., Verbrugge L. N. H., Diagne C., Courchamp F. & Gozlan R. E. 2022. Knowledge gaps in economic costs of invasive alien fish worldwide. *Science of The Total Environment* 803: e149875. <https://doi.org/10.1016/j.scitotenv.2021.149875>
- Haubrock P. J., Novello M., Abreo N. A., Błońska D., Franco A. C. S., Soto I., Castaldelli G., Katsanevakis S., Kouba A., Balzani P., Kurtul I., Tarkan A. S., Britton J. R. & Briski E. 2025. GFID: A Global Fish Invasion Database. *Ecological Research* 40: e70016. <https://doi.org/10.1111/1440-1703.70016>
- Huang S., Tian X., Wang W., Song W., Zhang X., Bai X. & Cao X. 2015. The complete mitochondrial genome of natural *Misgurnus bipartitus* (Cypriniformes: Cobitidae). *Mitochondrial DNA* 26 (5): 680-681. <https://doi.org/10.3109/19401736.2013.840605>
- Keller R. P. & Lake P. S. 2007. Potential impacts of a recent and rapidly spreading coloniser of Australian freshwaters: Oriental weather loach (*Misgurnus anguillicaudatus*). *Ecology of Freshwater Fish* 16 (2): 124-132. <https://doi.org/10.1111/j.1600-0633.2006.00204.x>
- Kneibelsberger T., Dunz A. R., Neumann D. & Geiger M. F. 2015. Molecular diversity of Germany's freshwater fishes and lampreys assessed by DNA barcoding. *Molecular Ecology Resources* 15 (3): 562-572. <https://doi.org/10.1111/1755-0998.12322>
- Kottelat M. & Freyhof J. 2007. Handbook of European freshwater fishes. Berlin: Kottelat, Cornol & Freyhof. 646 pp.
- Kumar S., Stecher G., Li M., Knyaz C. & Tamura K. 2018. MEGA X: Molecular Evolutionary Genetics Analysis across computing platforms. *Molecular Biology and Evolution* 35: 1547-1549. <https://doi.org/10.1093/molbev/msy096>
- Mirabdullaev I. M. & Mullabaev N. R. 2020. Ichthyofauna of Uzbekistan: modern state and taxonomy. *Uzbek Biology Journal* 5: 43-49. (In Russian with English abstract).
- Miya M., Sato Y., Fukunaga T., Sado T., Poulsen J. Y., Sato K., Minamoto T., Yamamoto S., Yamanaka H., Araki H., Kondoh M. & Iwasaki W. 2015. MiFish, a set of universal PCR primers for metabarcoding environmental DNA from fishes: detection of more than 230 subtropical marine species. *Royal Society Open Science* 2 (7): 150088. <https://doi.org/10.1098/rsos.150088>
- Murienne J., Jeziorski C., Holota H., Coissac E., Blanchet S. & Grenouillet G. 2016. PCR-free shotgun sequencing of the stone loach mitochondrial genome (*Barbatula barbatula*). *Mitochondrial DNA Part A* 27 (6): 4211-4212. <https://doi.org/10.3109/19401736.2015.1022744>
- Rustamov A. K. & Shakirova M. F. 2013. Note of modern ichthyofauna of Turkmenistan. In: Sopiev O. S. & Kherromov S. R. (Eds.): Study of biodiversity of Turkmenistan (vertebrates). Moscow-Ashgabat: Ilim, pp. 78-89.
- Schroeter J. C., Maloy A. P., Rees C. B. & Bartron M. L. 2020. Fish mitochondrial genome sequencing: expanding genetic resources to support species detection and biodiversity monitoring using environmental DNA. *Conservation Genetics Resources* 12: 433-446. <https://doi.org/10.1007/s12686-019-01111-0>
- Shedko S. V. & Vasil'eva E. D. 2022. A new species of the pond loaches *Misgurnus* (Cobitidae) from the south of Sakhalin Island. *Journal of Ichthyology* 62 (3): 356-372. <https://doi.org/10.1134/S0032945222030158>
- Shen Y., Kang J., Chen W. & He S. 2016. DNA barcoding for the identification of common economic aquatic products in Central China and its application for the supervision of the market trade. *Food Control* 61: 79-91. <https://doi.org/10.1016/j.foodcont.2015.08.038>
- Sheraliev B. & Peng Z. 2021. Molecular diversity of Uzbekistan's fishes assessed with DNA barcoding. *Scientific Reports* 11 (1): 16894. <https://doi.org/10.1038/s41598-021-96487-1>
- Shi X., Kou C., He C., Deng H., Yang H., Li X., Liu M., Liu Y., Li J. & Chen W. 2025. DNA barcode reference library and undetected diversity of fish species in the Yuanjiang River, China. *Fishes* 10 (8): 418. <https://doi.org/10.3390/fishes10080418>
- Tang Q., Deng L., Luo Q., Duan Q., Wang X. & Zhang R. 2023. DNA barcoding of fish species diversity in Guizhou, China. *Diversity* 15 (2): 203. <https://doi.org/10.3390/d15020203>
- Urquhart A. N. & Koetsier P. 2013. Low-Temperature Tolerance and Critical Thermal Minimum of the Invasive Oriental Weatherfish *Misgurnus anguillicaudatus* in Idaho, USA. *Transactions of the American Fisheries Society* 143 (1): 68-76. <https://doi.org/10.1080/00028487.2013.829124>
- Vasil'eva E. D., Kegenova G. B., Sharakhmetov S. E. & Mamilov N. Sh. 2024. *Misgurnus anguillicaudatus* (Cobitidae): a new non-native species naturalized in water bodies of the Balkhash-Ili Basin, Kazakhstan. *Journal of Ichthyology* 64 (1): 90-98. <https://doi.org/10.1134/S0032945224010107>
- Walsh J. R., Carpenter S. R. & Vander Zanden M. J. 2016. Invasive species triggers a massive loss of ecosystem services through a trophic cascade. *Proceedings of the National Academy of Sciences* 113 (15): 4081-4085. <https://doi.org/10.1073/pnas.1600366113>
- Ward R. D., Zemlak T. S., Innes B. H., Last P. R. & Hebert P. D. N. 2005. DNA barcoding Australia's fish species. *Philosophical Transactions of the Royal Society B* 360 (1462): 1847-1857. <https://doi.org/10.1098/rstb.2005.1716>
- Yi S., Zhong J., Wang S., Huang S. & Wang W. 2016. Mitochondrial DNA reveals evolutionary status and population genetics of two closely related fish (*Misgurnus bipartitus* and *Misgurnus mohoity*) in northeast China. *Biochemical Systematics and Ecology* 68: 192-199. <https://doi.org/10.1016/j.bse.2016.07.018>
- Yu Y. Y., Song W., Wang Y. Z., Wang W. M. & Zhou X. Y. 2015. Complete mitochondrial genome of the Amur weatherfish, *Misgurnus mohoity* (Teleostei: Cypriniformes: Cobitidae). *Mitochondrial DNA* 26 (2): 310-312. <https://doi.org/10.3109/19401736.2013.825789>
- Zangl L., Schäffer S., Daill D., Friedrich T., Gessl W., Mladinić M., Sturmbauer C., Wanzenböck J., Weiss S. J. & Kobl-müller S. 2022. A comprehensive DNA barcode inventory of Austria's fish species. *PLoS ONE* 17 (6): e0268694. <https://doi.org/10.1371/journal.pone.0268694>
- Zhang H., Wang Y. X., Yang H. L., Tan H. M. & Chen Y. X. 2021. Taxonomic revision of Chinese species of the genera *Misgurnus* and *Paramisgurnus* (Cypriniformes: Cobitidae). *Acta Hydrobiologica Sinica* 45 (2): 414-427. <https://doi.org/10.7541/2021.2019.166>

Received: 24.08.2025

Accepted: 11.01.2026