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ORIGINAL ARTICLE

Morphology and molecular phylogeny of *Glyptosternon oschanini* (Siluriformes, Sisoridae) from Khojaipak River in Uzbekistan

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Abstract
This study first examined the external morphology and molecular-genetic characteristics of the Turkestan catfish *Glyptosternon oschanini* from the Khojaipak River (Surkhandarya basin, Uzbekistan) using combined morphometric and DNA barcoding approaches. Specimens (n=14) were collected in the upper reaches of the Khojaipak River in 2023-2024 and examined for meristic and plastic characters following standard ichthyological methods. The fish is characterized by the following meristic features: dorsal fin rays I 6, anal fin rays III 5, pectoral fin rays I 10, pelvic fin rays I 5, 10 gill rakers on the first gill arch, and 33 vertebrae. The body is naked and low; the head is flat with small eyes; the mouth is lower; and four pairs of barbels are present on the snout. Most plastic (morphometric) features showed low variability, with coefficients of variation ranging from 0.82% to 10.68% relative to standard length and from 3.78% to 12.70% relative to head length; the eye diameter was the most variable character in both cases. For the molecular component, the mitochondrial cytochrome oxidase I (COI) gene was amplified, sequenced, and compared with 21 GenBank sequences of *Glyptosternon* species, using *G. andersoni* as an outgroup. Maximum Likelihood and Bayesian Inference resolved three well-supported clades: a *G. reticulatum/G. maculatum* clade (bootstrap 98%), a *G. oschanini* clade including the Uzbek samples (bootstrap 94%), and a clade composed exclusively of *Glyptosternon* sp. accessions (bootstrap 94%). The Uzbek *G. oschanini* sample showed the smallest genetic distance to other *G. oschanini* sequences (0.0143-0.0195) and to the *Glyptosternon* sp. group (0.00477), but was clearly divergent from *G. reticulatum* (0.0822-0.0887) and from the outgroup *G. andersoni* (0.1439). These results confirm *G. oschanini* as a species distinct from *G. reticulatum* and indicate a close phylogenetic relationship with the unidentified *Glyptosternon* sp. lineage, whose taxonomic status requires further revision. The study demonstrates that the COI gene is an effective molecular marker for species-level discrimination within the genus *Glyptosternon* and provides new morphological and genetic baseline data for *G. oschanini* populations in Uzbekistan.

Keywords: Turkestan catfish, Morphometrics, DNA barcoding, COI gene, Phylogenetic analysis, Surkhandarya basin

INTRODUCTION

The family Sisoridae includes 16 genera and 144 species (Ng, 2003; Ng & Kottelat 2000), and among them, the genus *Glyptosternon* McClelland, 1842 is widespread in Central and South Asia along the Himalayas, and it is found in the Indus basin in Afghanistan, Pakistan, and India; the Brahmaputra basin in India and China; and the Irrawaddy basin in Myanmar and China (Berg 1949; Coad 1981; Eschmeyer 1998; Hora 1932; Jayaram 1999). The type species of the genus *Glyptosternon* is *G. reticulatum* McClelland, 1842, described from specimens collected in the Kabul River (Indus River basin, Afghanistan) (McClelland 1842). Previously described species from Central and South Asia – *Exostoma gracile* (Syr Darya basin, Naryn River), *E. labrax* (upper Amu Darya, Vakhsh River, Karategin Range), *E. stoliczkae* (upper Indus River), and *E. oschanini* (Syr Darya basin, right tributary of the Chirchik – the Ugam River) – were previously considered synonyms of *G. reticulatum* (Berg 1949). However, the name *E. oschanini* for the Turkestan catfish inhabiting the Syr Darya basin was later confirmed and accepted as valid (Thoni et al. 2017).

Glyptosternon oschanini is a vulnerable (VU) endemic species of Central Asian Mountain ecosystems with a highly fragmented and geographically restricted distribution (Mirzayev

2019). It primarily inhabits the upper reaches of mountain and foothill rivers characterized by swift currents and stony or gravel substrates. As a benthic species, it is adapted to rheophilic habitats and exhibits predominantly nocturnal activity (Mirzayev 2019). At the global level, the species is assessed as Least Concern on the IUCN Red List (Karimov 2020). The pronounced morphological conservatism commonly observed among rheophilic, torrent-dwelling catfishes can complicate species identification, as external morphological characters alone may be insufficient to distinguish closely related or potentially cryptic taxa. Consequently, reliance on traditional morphological diagnostics may obscure underlying diversity and contribute to persistent taxonomic uncertainties. In addition to these taxonomic challenges, populations of *G. oschanini* in Central Asian river basins are exposed to increasing anthropogenic pressures, including river flow regulation, water pollution, mudflows, recreational activities, and competition with non-native fish species. These factors have contributed to concerns regarding population declines and the long-term persistence of the species in its natural habitats.

Despite its ecological vulnerability and regional conservation significance, the taxonomic status, morphological variability, and phylogenetic relationships of *Glyptosternon* populations inhabiting geographically isolated river basins remain insufficiently understood. This knowledge gap is particularly evident in the southern tributaries of the Amu Darya basin, including the Surkhandarya River system. Molecular approaches, particularly DNA barcoding based on mitochondrial markers, provide valuable tools for resolving taxonomic uncertainties, identifying genetically differentiated populations, and evaluating the evolutionary relationships among geographically isolated populations. Such assessments are essential for determining whether peripheral populations represent distinct taxonomic entities or independently evolving conservation management units.

To address these knowledge gaps, the present study examines the external morphology and molecular phylogenetic relationships of *Glyptosternon* specimens collected from the Khojaipak River in the Surkhandarya River basin, Uzbekistan. By integrating detailed morphometric analyses with mitochondrial DNA barcoding, we aim to clarify the taxonomic identity of the Khojaipak population, evaluate its phylogenetic affinities with other geographically distinct populations, and provide baseline data to support future conservation assessments and management strategies for this vulnerable Central Asian endemic species.

MATERIALS AND METHODS

The specimens were collected in the upper reaches of the Khojaipok River in April–May of 2023-2024 (Fig. 1). The collection and processing of the samples were carried out in accordance with standard methods (Pravdin 1966; Zinoviev & Mandritsa 2003). Measurements were taken point-to-point using digital calipers. Standard measurements follow Pravdin (1966). Body and head length measurements are provided as proportions of standard length (SL), while head measurements are given as proportions of head length (HL). For morphometric analyses, we calculated the limits of variation (Min-Max), mean, standard deviation (SD), and coefficient of variation (CV, %) (Lakin 1990).

The following abbreviations of features are used in the article: D – dorsal fin; A – anal fin; SL – Standard length; LC – head length; AO – snout length; O – eye diameter; PO – postorbital part of the eye; HC – head height; IO – forehead width; B1 – Nasal barbel length; B2 – Outer mandibular barbel length; B3 – Inner mandibular barbel length; H – body depth; AD – antedorsal distance; PD – postdorsal distance; AA – anteanal distance; Lca – length of the caudal peduncle; Hca – height of the caudal peduncle; LD – Dorsal-fin base length; HD – Dorsal-fin height; LA – Anal-fin base length; HA – Anal-fin height; LP – Pectoral-fin length; LV – Pelvic-fin length; PV – distance between the pectoral and pelvic fins; VA – distance between pelvic and anal fins; LAD – Adipose-fin base length; HAD – Adipose-fin height.

DNA extraction and PCR amplification: The fish

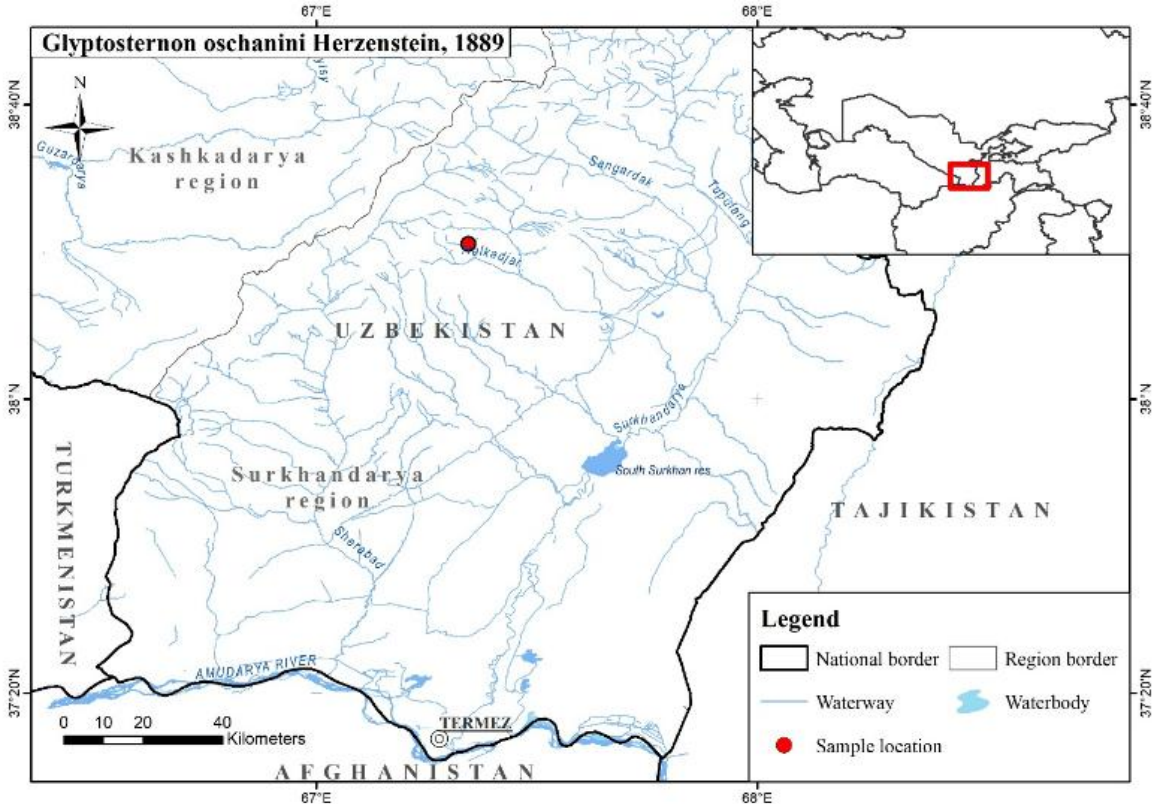


Fig.1. Sampling locality of *Glyptosternon oschanini* in the upper reaches of the Khojaipak River (Surkhandarya Basin, Uzbekistan).

materials used in the study were collected in the upper reaches of the Khojaipak River and are stored in the collection of the Institute of Zoology of the Academy of Sciences, Republic of Uzbekistan. All DNA samples used in this work were obtained from zoological materials (tissues) stored at this Institute. Taxonomic identification of the samples was carried out based on information provided on the labels. Reagents intended for diatom purification were used to isolate DNA. The extraction procedure was carried out under standard laboratory conditions to obtain high-quality DNA suitable for subsequent molecular analysis.

The polymerase chain reaction (PCR) was performed using the primer pair catF (5′-TCT CAA CCA ACC ATAAAAGACATTGG-3′) and catR (5′-TAT ACTTCTGGGTGCCCAAAGAATCA-3′) (Wai et al. 2025). These primers are designed to amplify a fragment of the mitochondrial cytochrome oxidase I (COI) gene (Hebert et al. 2003). During the study, this primer pair was applied to different randomly selected samples. The primers were added to the reaction mixture in a total volume of 20 μl. The PCR protocol included the following steps: initial denaturation at 94°C for 3 minutes; 40 cycles, each consisting of denaturation at 94°C for 30 seconds, annealing at 48.5°C for 30 seconds, elongation at 72°C for 1 minute; final elongation at 72°C for 5 minutes.

The presence of amplified DNA was confirmed by electrophoresis on a 1.0% agarose gel at 120 V. Amplification and subsequent DNA purification from the gel were carried out according to the instructions for the reagent kit provided by Silex M (Moscow, Russia). DNA sequencing was performed using the ABI PRISM® BigDye™ Terminator v3.1 Cycle Sequencing Kit. The resulting sequencing reaction products were analyzed on an ABI PRISM 3100-Avant automated genetic analyzer (Moscow, Russia).

Nucleotide sequences and alignment. The sequences of the COI gene of 21 species of the genus *Glyptosternon* were used for phylogenetic analysis, along with the COI sequence of *G. andersoni* (JQ859842) as the outgroup. The resulting sequences were manually edited using the BioEdit v.7.0.5.2

program (Hall 1999). Automatic alignment of all sequences was performed using the MAFFT program (Katoh et al. 2002).

Phylogenetic tree construction. The phylogenetic tree was constructed using the Maximum Likelihood (ML) method in IQ-TREE 2 (Minh et al. 2020). The best nucleotide substitution model was selected using the ModelFinder tool built into IQ-TREE (Kalyaanamoorthy et al. 2017). The confidence level of the phylogenetic tree topology was assessed using bootstrap analysis on 1000 pseudo-repeats (Felsenstein 1985). Additionally, an analysis was performed using Bayesian Inference (BI) in the MrBayes v.3.1.2 program (Huelsenbeck & Ronquist 2001). The MCMC (Markov Chain Monte Carlo) algorithm was run for 4 million generations with a sample every 1000 generations. The first 1000 trees were excluded as burn-in.

The confidence level of the resulting tree was assessed using the Bayesian posterior probabilities (PP) and bootstrap support (BS): PP ≥ 0.95 and BS ≥ 70% – high confidence; PP = 0.90–0.94 and BS = 50–69% – medium confidence; PP < 0.90 and BS < 50% – low confidence (Huelsenbeck & Hillis 1993). The final phylogenetic tree was visualised using the iTOL (Interactive Tree of Life) online platform (Letunic & Bork 2021).

RESULTS

Morphological and morphometric analysis: According to the results, the Turkestan catfish of the Khojaipak River is characterised by the following meristic features: number of rays in dorsal fin I 6, in anal fin – III 5, in pectoral fins – I 10, in pelvic fins – I 5; first gill arch with 10 gill rakers; number of vertebrae 33; body naked and low; its greatest, depth 6.8-7.6 times body length, and smallest 2.7-3.3 times length of caudal peduncle. Atedorsal distance 1.4 times less than postdorsal. Pectoral and pelvic fins set horizontally; head flat; its length 4.5-6.3 times body length; eyes are small, 3.2-4.3 times in width of forehead; mouth lower; length of snout reaches 45.4-56.4% of head length; 4 pairs of barbels on snout; body colour from dark brown to yellowish-brown; belly light. In most sexually mature fish, body completely covered with small, blurry colouring (Table 1).

According to Table 1, most plastic features of the studied fish are least variable. The most variable traits are eye diameter, the length of the inner mandibular barbel, and body height.

Results of molecular genetic studies: The phylogenetic tree constructed on the basis of the mitochondrial COI gene sequences revealed three main and reliably supported clusters within the studied genus *Glyptosternon* (Fig. 2). The first cluster includes *G. maculatum* (NC021597) and several specimens of *G. reticulatum* (KT023083, KT023085, KT023087, PQ386337, and PQ373940). This group is characterised by a high degree of support – the bootstrap value is 98%, which convincingly indicates its phylogenetic stability and close evolutionary relationships between the included taxa.

The second cluster includes *G. oschanini* samples from Uzbekistan (*G. oschanini Uz*, MW649716, KY849923, KY849924, KY849922, and KY849926). This clade also has high statistical support (bootstrap = 94%) and forms a strong monophyletic lineage, indicating low internal genetic differentiation at the nucleotide level among the sampled individuals. The third cluster includes *G.* sp. accessions (MW649718, MW649724, MW649717, MW649722, MW649720, MW649723, MW649721, and MW649719). The clade is characterised by a high level of bootstrap support (94%), indicating the genetic cohesion of these accessions and their potential status as a separate species or subspecies.

High bootstrap support values (98%, 94%, and 94%) for the three clusters confirm the reliability of the phylogenetic reconstruction and the robustness of the tree topology to random sampling errors. *Glyptosternon andersoni* (JQ859842) was used as an outgroup, which provided optimal conditions for tree construction and assessing phylogenetic divergence among intragroup taxa. Genetic distance analysis showed that the species of the genus *Glyptosternon* are divided into three distinct genetic groups. According to the analysis results, the *G. oschanini* (Uz) sample

Table 1. Morphometric characteristics of *Glyptosternon oschanini* from the Khojaipak River, Uzbekistan (n= 14).

Morphometric characteristics	Min	Max	Mean	±SD	Cv, %
SL, mm	90	130	114.71	10.60	9.24
		% Standard length			
LC	21.1	24.4	23.56	1.00	4.24
AO	10.1	12.0	11.11	0.46	4.16
O	1.4	2.3	1.96	0.21	10.68
PO	10.7	12.7	11.38	0.56	4.9
HC	11.6	13.4	12.18	0.52	4.25
IO	6.1	6.6	6.45	0.12	1.8
H	19.9	19.8	17.13	1.4	8.19
AD	37.1	39.9	38.16	0.89	2.34
PD	52.3	56.2	54.4	1.27	2.34
AA	65.0	66.7	65.91	0.54	0.82
Lca	21.9	24.9	23.82	0.96	4.02
Hca	7.1	8.7	8.03	0.49	6.07
LD	9.2	10.6	9.66	0.45	4.67
HD	16,8	18.6	17.99	0.52	2.86
LA	6.1	7.8	6.98	0.44	6.29
HA	15.7	16.6	16.14	0.32	2.00
LP	20.7	25.7	24.29	1.16	4.77
LV	16.5	20.5	18.09	1.04	5.74
PV	27.3	35.9	32.61	2.14	6.56
VA	19.2	24.5	20.39	1.36	6.68
LAD	32.6	33.9	33.31	0.4	1.19
HAD	4.5	5.4	4.91	0.26	5.39
		% Head length			
AO/LC	45.4	56.4	47.25	3.27	6.92
O/LC	5.7	10.2	8.36	1.06	12.7
PO/LC	45.4	58.3	48.38	3.23	6.69
HC/LC	48.8	60.1	51.82	3.68	7.11
IO/LC	26.3	30.3	27.42	1.04	3.78
B1/LC	26.2	34.1	29.45	2.09	7.1
B2/LC	34.4	41.7	38.53	2.19	5.69
B3/LC	13.5	19.8	16.15	1.81	11.22

showed the greatest genetic similarity to the *G. oschanini* KY849923 sample, with a genetic distance of 0.0195 (Fig. 3). In addition, the genetic distances to samples KY849924, KY849926, and KY849922 were slightly higher, at 0.0143. At the same time, the genetic distance between samples of *G. oschanini* (Uz) and *G.* sp. groups was 0.00477, indicating their extremely close phylogenetic relationship.

The analysis showed that the *G. oschanini* (Uz) sample is at a significant phylogenetic distance from the *G. reticulatum* group. In particular, the genetic distance to the *G. reticulatum* samples (KT023085 and KT023083) was 0.0822, and to the PQ373940 sample it was 0.0887. These values indicate a pronounced genetic divergence of the *G. oschanini (Uz)* sample from the reticulatum clade. The highest genetic divergence was recorded for *G. andersonii* (0.1439), indicating its most distant phylogenetic position. In addition, pairwise genetic distances between *G. sp.* (MW649718–MW649723) and several *G. oschanini* specimens are zero, indicating an extremely close genetic relationship and, probably, a monophyletic origin. Such low distance values indicate virtually no or minimal intragroup genetic variability.

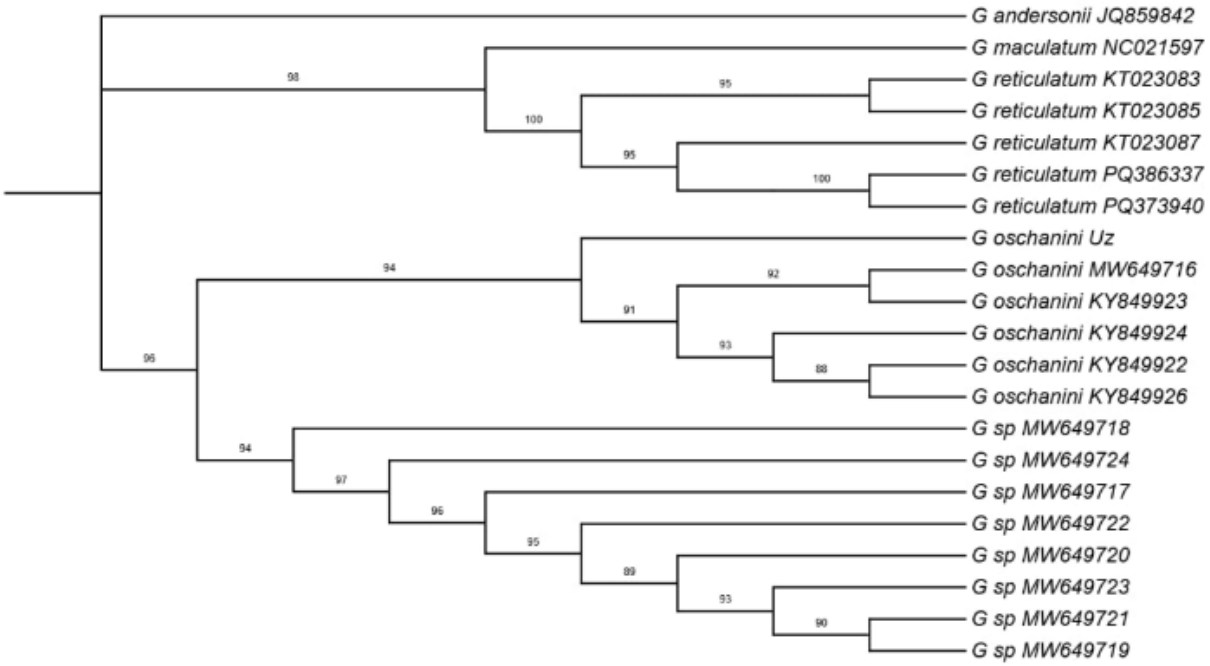


Fig.2. Maximum Likelihood phylogenetic tree of *Glyptosternon* species based on mitochondrial COI sequences. Bootstrap values and Bayesian posterior probabilities are shown at the nodes.

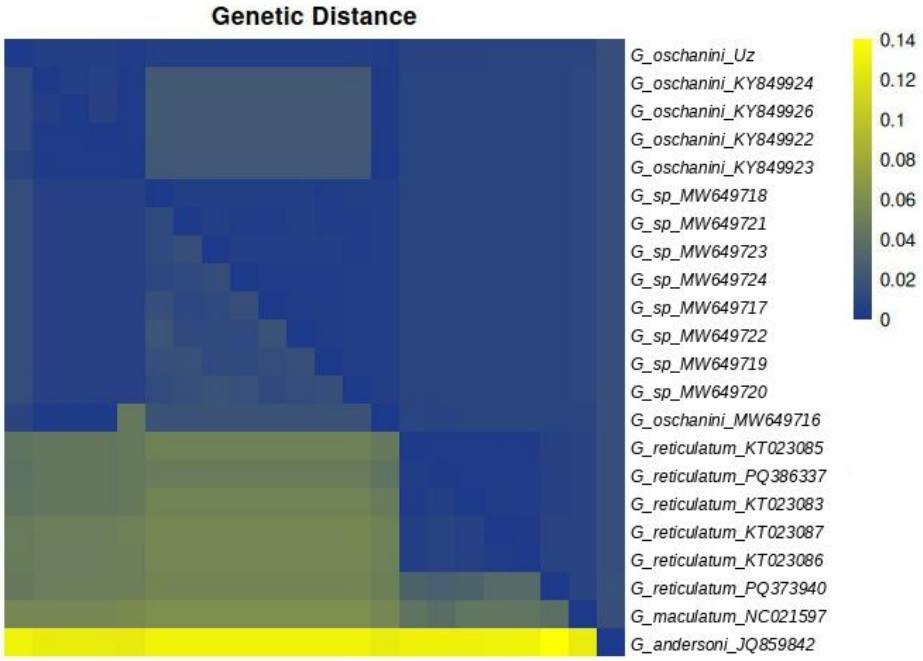


Fig.3. Heat map showing pairwise genetic distances among *Glyptosternon oschanini* and related taxa based on mitochondrial COI sequences. The colour gradient represents genetic divergence values.

The results confirm that *G. oschanini (Uz)* is genetically close to other *G. oschanini* specimens, shows close affinity to the *Glyptosternon* sp. group, but differs significantly from *G. reticulatum* and, especially, from *G. andersonii*. These data provide an important basis for identifying genetic differences between species and clarifying the taxonomic status of the *G.* sp. group.

DISCUSSION

Berg (1949) cites the following meristic features of the Turkestan catfish: D I 6, A II-III 5, P I 11, V I 5. According to Amanov (1985), the Turkestan catfish is characterised by the following meristic features: D I 6, A III 5, P I 10. The body colour is variable – from blackish-grey to yellowish-brown; the belly is light. Phylogenetic analysis identified three distinct, well-supported clades within the genus *Glyptosternon*. The first clade includes *G. maculatum* (NC021597) and several *G. reticulatum* specimens (KT023083, KT023085, KT023087, PQ386337, and PQ373940), with a high bootstrap support value of 98%. This result indicates phylogenetic stability and a close evolutionary relationship of the indicated taxa. This monophyletic grouping reflects the COI gene's high efficiency as a molecular marker with strong discriminatory power for defining species boundaries (Hebert et al. 2003).

The second clade includes *G. oschanini* samples collected in Uzbekistan (MW649716, KY849923, KY849924, KY849922, and KY849926) and is characterised by high bootstrap support (94%). Within this group, internal genetic differentiation is extremely low: the minimum pairwise genetic distance (0.00477) was recorded between samples belonging to the *G. oschanini* (Uz) and *Glyptosternon* sp. clades. This low sequence divergence indicates genetic homogeneity within the population and, probably, membership in a single evolutionary lineage. A third clade consisting exclusively of *Glyptosternon* sp. specimens (MW649718–MW649724) also received high bootstrap support (94%). The absence or low genetic variability among these specimens indicates high genetic integrity and suggests that this lineage may represent a distinct species or subspecies.

The *G. oschanini (Uz)* sample is significantly distant from *G. reticulatum* (0.0822-0.0887) and *G. andersonii* (0.1439), indicating its evolutionary isolation. These genetic divergences correspond to the interspecific boundaries established for other freshwater fish groups (Ward et al. 2005; April et al. 2011). At the same time, the extremely small genetic distance (0.00477) between *G. oschanini* (Uz) and *Glyptosternon* sp. indicates their close relationship. However, their isolated position as an independent monophyletic clade on the phylogenetic tree suggests these forms may have evolved along different paths. The results allow us to draw important taxonomic conclusions. Historically, *G. oschanini* was often considered a synonym of *G. reticulatum*. However, recent molecular studies have confirmed its status as a distinct species (Thoni et al. 2017). Our molecular data also support this interpretation and highlight the need to reconsider the taxonomic status of the *Glyptosternon* sp. lineage.

CONCLUSION

Thus, this research characterized the external morphology of the Turkestan catfish from the Khojaipak River (Surkhandarya basin), established the variability of its morphometric (plastic) characteristics, and conducted a molecular genetic analysis. The morphometric features of the Turkestan catfish are characterised by a low degree of variability. The coefficients of variation of these features relative to body length range from 0.82% to 10.68%. Eye diameter is the most variable feature, while body height is average. The remaining features fall into the low-variability category. The coefficients of variation of the head morphometric features range from 3.78% to 12.70%. Only the eye diameter (*O/LC*) is characterised by the greatest variability, while the remaining features demonstrate a low or moderate level of variability. The COI gene also proves its diagnostic value for species discrimination within the genus *Glyptosternon*. Even in relatively short sequences (~650 base pairs), studies show it reveals genetic divergence ranging from 0.14% to 4.9%, which is sufficient for fish species identification (Hebert et al. 2003; Ward et al. 2005). Thus, this marker represents a reliable molecular tool for DNA barcoding and phylogenetic analysis within the genus *Glyptosternon*.

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مقاله کامل

ریخت‌شناسی و تبارزایی مولکولی گونه *Glyptosternon oschanini* (Siluriformes, Sisoridae) از رودخانه خواجه‌ای‌پاک در ازبکستان

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چکیده: این پژوهش برای نخستین بار، ریخت‌شناسی خارجی و ویژگی‌های ژنتیکی مولکولی گربه‌ماهی ترکستانی، *Glyptosternon oschanini*، را در رودخانه خواجه‌ای‌پاک (حوضه آبریز سرخان‌دریا، ازبکستان) با استفاده از رویکرد تلفیقی ریخت‌سنجی و DNA بارکدینگ مورد بررسی قرار داده است. نمونه‌ها (n=۱۴) طی سال‌های ۲۰۲۳ تا ۲۰۲۴ از بخش‌های بالادست رودخانه خواجه‌ای‌پاک جمع‌آوری شدند و صفات شمارشی و ریختی آنها بر اساس روش‌های استاندارد ماهی‌شناسی مورد ارزیابی قرار گرفت. این ماهی دارای ویژگی‌های شمارشی زیر است: تعداد شعاع‌های باله پشتی I 6، شعاع‌های باله مخرجی III 5، شعاع‌های باله سینه‌ای I 10، شعاع‌های باله شکمی I 5، تعداد ۱۰ خار آبششی بر روی نخستین کمان آبششی و ۳۳ مهره. بدن فاقد فلس و دارای ارتفاع بدنی کم است؛ سر مسطح، چشم‌ها کوچک و دهان در بخش زیرین است. همچنین، چهار جفت سبیلک در ناحیه پوزه وجود دارد. بیشتر صفات ریختی از تغییرپذیری پایینی برخوردار بودند؛ به‌طوری‌که ضرایب تغییرات آنها نسبت به طول استاندارد بدن از ۰/۸۲ تا ۱۰/۶۸ درصد و نسبت به طول سر از ۳/۷۸ تا ۱۲/۷ درصد متغیر بود. در هر دو حالت، قطر چشم متغیرترین صفت ریخت‌سنجی محسوب شد. در بخش مطالعات مولکولی، ژن میتوکندریایی سیتوکروم اکسیداز زیرواحد یک (COI) تکثیر و توالی‌یابی شد و توالی‌های حاصل با ۲۱ توالی مربوط به گونه‌های جنس *Glyptosternon* موجود در پایگاه داده GenBank مقایسه شدند. همچنین، گونه *G. andersoni* به‌عنوان برون‌گروه (Outgroup) در تحلیل‌های تبارزایی در نظر گرفته شد. تحلیل‌های تبارزایی با استفاده از روش بیشینه درست‌نمایی (Maximum Likelihood) و استنباط بیزی (Bayesian Inference)، سه تبار (کلاد) را با پشتیبانی آماری قوی مشخص کردند: تبار نخست شامل گونه‌های *G. reticulatum* و *G. maculatum* با مقدار بوت‌استرپ ۹۸ درصد؛ تبار دوم شامل *G. oschanini*، از جمله نمونه‌های جمع‌آوری‌شده از ازبکستان، با مقدار بوت‌استرپ ۹۴ درصد؛ و تبار سوم متشکل از توالی‌های منتسب به *Glyptosternon* sp. با مقدار بوت‌استرپ ۹۴ درصد بود. نمونه‌های *G. oschanini* از ازبکستان کمترین فاصله ژنتیکی را با سایر توالی‌های این گونه (۰/۰۱۴۳ تا ۰/۰۱۹۵) و نیز با گروه *Glyptosternon* sp. (۰/۰۰۴۷۷) نشان دادند؛ بااین‌حال، اختلاف ژنتیکی آنها با گونه *G. reticulatum* (۰/۰۸۲۲ تا ۰/۰۸۸۷) و برون گروه، یعنی *G. andersoni* (۰/۱۴۳۹)، به‌وضوح بیشتر بود. این نتایج، جایگاه مستقل گونه *G. oschanini* را در مقایسه با*G. reticulatum* تأیید کرده و بیانگر ارتباط تبارزایی نزدیک آن با دودمان شناسایی‌نشده *Glyptosternon* sp. است؛ دودمانی که تعیین وضعیت آرایه‌شناختی آن مستلزم بازنگری‌های بیشتر است. در مجموع، این پژوهش نشان می‌دهد که ژن COI نشانگر مولکولی کارآمدی برای تفکیک گونه‌ها در سطح گونه‌ای در جنس *Glyptosternon* محسوب می‌شود و داده‌های پایه جدیدی در زمینه ویژگی‌های ریخت‌شناختی و ژنتیکی جمعیت‌های *G. oschanini* در ازبکستان ارائه می‌دهد.

کلمات‌کلیدی: گربه‌ماهی ترکستانی، ریخت‌سنجی، DNA بارکدینگ، ژن سیتوکروم اکسیداز زیرواحد یک (COI)، تحلیل تبارزایی، حوضه آبریز سرخان‌دریا