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Hiding in the valley: a new national record of *Ablepharus eremchenkoi*, with rediscovery of *Ablepharus alaicus* in China: phylogeny, morphology and natural history notes

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Abstract

The genus *Ablepharus* Lichtenstein, 1823 contains the common snake-eyed skinks, distributed from southern Europe and northern Africa to eastern Asia. *Ablepharus alaicus* Elpatjevsky, 1901 inhabits Central Asia and, according to historical literature, was once recorded in north-western China. However, there are no voucher records of this species from China. Some populations of a subspecies of *A. alaicus* have been elevated to new species, for example, *A. eremchenkoi* (Panfilov, 1999). However, no detailed studies have been conducted. In August and September 2023, we captured sixteen and fourteen skink specimens from Wuqia County and Qapqal Xibe Autonomous County, respectively, in Xinjiang, northwest China. Morphological and phylogenetic comparisons showed that the skinks collected from these two locations belong to *A. eremchenkoi* and *A. alaicus*, respectively. In this study, we confirmed the first record of *A. eremchenkoi* in China, rediscovered *A. alaicus*, reported voucher records for these two skinks and reviewed the taxonomic history of *Ablepharus* in Xinjiang, northwest China.

Key Words

Ablepharine skink**,** Kyrgyzstan, Kazakhstan, voucher records, Xinjiang

Introduction

The Ablepharine is a widespread skink lineage distributed from Europe to Asia (Vaissi et al. 2023). *Asymblepharus* Eremchenko & Shcherbak, 1986 and *Himalblepharus* Eremchenko, 1987 were established as separate genera from *Ablepharus* Lichtenstein, 1823, based on morphological divergence. In a recent revision of Ablepharine skinks, Mirza et al. (2022) proposed treating *Asymblepharus* and *Himalblepharus* as subjective junior synonyms of *Ablepharus* because both are embedded within *Ablepharus*, which does not have a movable eyelid. This returns species belonging to these two genera to *Ablepharus sensu lato*, including *Asymblepharus alaicus*, which are mainly distributed in Central Asia in Kyrgyzstan, Uzbekistan, Tajikistan, Kazakhstan and China.

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There are three subspecies of *A. alaicus*: *A. a. alaicus* Elpatjevsky, 1901; *A. a. kucenkoi* Nikolsky, 1902; and *A. a. yakovlevae* Eremchenko, 1983. Panfilov (1999) evaluated some populations of *A. a. yakovlevae* as *A. eremchenkoi*, based on variations in reproductive traits. Two subspecies were thought to be distributed in China (Zhao et al. 1999). Of these, *A. a. kucenkoi* was distributed in the Ili Region of Xinjiang; this record was based on two specimens not preserved in China (Eremchenko and Shcherbak 1986). *A. a. alaicus* was thought to be distributed near the south-western Xinjiang border close to Kyrgyzstan and Tajikistan, but no voucher specimens are available to support this distribution. Notably, historical records of *A. alaicus* in China have not been confirmed.

In 2022 and 2023, we observed skinks in Wuqia County, Kizilsu Kirgiz Autonomous Prefecture (KKAP) and Qapqal Xibe Autonomous County, Ili Kazakh Autonomous Prefecture (IKAP), Xinjiang, China, locations in which we had not previously observed them. We subsequently captured skinks from these two locations and conducted morphological and phylogenetic analyses. The results suggest that the skinks from KKAP belonged to *A. eremchenkoi*, a new record for this species in China. The skinks from IKAP were *A. alaicus*, confirming the distribution of *A. alaicus* in Xinjiang, China. In this study, we present the first known records of *A. eremchenkoi* and *A. alaicus* with voucher specimens from within China. In addition, we provide detailed descriptions of the morphology, phylogeny and natural history notes.

Materials and methods

Species delimitation

On 8 and 9 August 2023, we collected sixteen specimens from three locations in Yuqitashi (40.1527°N, 74.6310°E, 3040 m elev.; 40.1495°N, 74.6335°E, 3032 m elev.; 40.13°N, 74.64°E, 3014 m elev.), Wuqia County, KKAP and Xinjiang, China (Fig. 1). On 27 September 2023, we collected fourteen specimens close to Baishifeng (43.43°N, 81.05°E, 2466 m elev.), Qapqal Xibe Autonomous County (IKAP) (Fig. 1). All thirty specimens were transported to Xinjiang Agricultural University.

All specimens were euthanised and muscle or liver samples were dissected from the specimens, preserved in 95% ethanol and stored at –20 °C. All specimens were fixed in 10% buffered formalin and transferred to 75% ethanol for preservation. Liver and muscle tissues used for molecular analysis were preserved in 95% alcohol at –20 °C. All specimens were deposited at the Herpetological Museum, Xinjiang Agricultural University (XJAU), Urumuqi, Xinjiang, China.

Sequence extraction

Total DNA was extracted from tissue samples by using the Foregene Animal Tissue Genomic DNA Extraction Kit per the manufacturer's instructions. We referred to

Figure 1. Map showing the distribution of *A. eremchenkoi* and *A. alaicus* within China. The distribution map of *A. alaicus* was obtained from the IUCN Red List (Accessed on 17 September 2023). Photos by Lei Shi, Lin Leng and Tao Liang.

the primer sequences used by (Mirza et al. 2022). Additionally, we sequenced partial segments of the mitochondrial 16S rRNA (16S), 12S rRNA (12S) and NADH dehydrogenase subunit 2 (ND2) (Tables 1, 2). The PCR reaction volume was 25 µl, containing 1 µl template DNA, 1 µl each of upstream and downstream primers, 12.5 µl 2× Taq PCR Mix and 9.5 µl ddH_2O. The PCR protocol used for amplification was as follows: 95 ℃ for 3 min, (denaturation temperature 95 ℃ for 30 s, annealing time ranged from 40 to 50 s, elongation temperature 72 ℃ for 1 min) × 36 cycles, 72 ℃ for 10 min, hold at 4 ℃ (Mirza et al. 2022). Gel electrophoresis was performed using 0.5% TBE solution and agarose to verify successful amplification of the samples. Subsequently, the successfully amplified PCR stock solution was sent to Sangon Biotechnology for purification and sequencing.

Molecular data and analyses

All sequences were aligned and manually edited using SeqMan in DNASTAR (Burland 1999). Sequences were aligned in Mega 7.0 (Kumar et al. 2016) using ClustalW (Thompson et al. 1994) with default settings. Ultimately, a 12S sequence of approximately 356 bp, a 16S sequence of 389 bp, an ND2 sequence of 509 bp and a spliced sequence of 1323 bp were obtained. We collected reference sequences of the same genus from GenBank, with *Scincella reevesii* as the outgroup and constructed a phylogenetic tree of *Ablepharus* and its species within the genus by using Bayesian Inference (BI) and Maximum Likelihood (ML) to explore the affinities of the sample sequences in *Ablepharus*. The BI and ML analyses were performed using MrBayes and IQ-TREE in PhyloSuite (Zhang et al. 2020) with default parameters, respectively. The resulting phylogenetic tree was visualised using FigTree v.1.4.3 and the effective sample size (ESS) was assessed using Tracer 1.7.2 (Rambaut et al. 2018), with all ESS values for parameters > 200. Finally, the phylogenetic tree was visualised using ITOL v.6 (Letunic and Bork 2021). A posteriori probability (BPP) or ML bootstrap value (BS) > 95% was considered strong support for monophyly.

We used *p*-distance (uncorrected) in MEGE 7.0 (Kumar et al. 2016) to calculate the genetic distances of the three sequences: 12S, 16S and ND2. We divided the sample and reference sequences into groups by using MEGA and *p*-distance to calculate genetic distances amongst the three gene sequences.

Table 1. Localities and GenBank accession numbers for all species used in this study.

Species	Country	ND2	16S	12S	(ID) References
Ablepharus					
A. eremchenkoi	China	OR687189	OR681490	OR677923	(XND20230808001) This study
A. eremchenkoi	China	OR687188	OR681492	OR677924	(XND20230809010) This study
A. eremchenkoi	China	OR687190	OR681491	OR677925	(XND20230808007) This study
A. eremchenkoi	China	OR687191	OR681493	OR677926	(XND20230808023) This study
A.alaicus	China	OR687182	OR681482	OR677917	(XND2023092701) This study
A.alaicus	China	OR687183	OR681483	OR677918	(XND2023092706) This study
A.alaicus	China	OR687184	OR681484	OR677919	(XND2023092711) This study
A.alaicus	China	OR687185	OR681485	OR677920	(XND2023092712) This study
A.alaicus	China	OR687186	OR681486	OR677921	(XND2023092713) This study
A.alaicus	China	OR687187	OR681487	OR677922	(XND2023092714) This study
A. alaicus	Kyrgyzstan	MZ820276	MZ790578	MZ790566	(Mirza et al. 2022)
A. anatolicus	Turkey	MZ848096	–	MZ827906	(Mirza et al. 2022)
A. bivittatus	Iran	–	MZ707375	MZ707427	(Karamiani et al. 2021)
A. budaki	Syria	–	AY561427	MZ827907	(Poulakakis et al. 2005; Mirza et al. 2022)
A. chernovi	Turkey	–	JX847534	–	(Poulakakis et al. 2013)
A. deserti	Kyrgyzstan	MZ820278	MZ790580	MZ790568	(Mirza et al. 2022)
A. deserti	China	–			This study
A. eremchenkoi	Kyrgyzstan	MZ820277	MZ790579	MZ790567	(Mirza et al. 2022)
A. grayanus	–	–	MZ707422	MZ707474	Karamiani et al. 2021
A. himalayanus	China	MN885892	MN885892	MN885892	
A. kitaibelii	Greece	MZ848097	AY561380	MZ827908	(Mirza et al. 2022)
A. ladacensis	China	MW111453	–	MZ790569	(Xu et al. 2021; Mirza et al. 2022)
A. mahabharatus	Nepal	MZ820282	MZ790598	MZ790570	(Mirza et al. 2022)
A. nepalensis	Nepal	MZ820286	MZ790602	MZ790574	(Mirza et al. 2022)
A. pannonicus	Uzbekistan	MZ820287	MZ790584	MZ790575	(Mirza et al. 2022)
A. rueppellii	Israel	MZ848098	KX591472	MZ827909	(Skourtanioti et al. 2016; Mirza et al. 2022)
A. sikimmensis	Nepal	MZ820283	MZ790601	MZ790573	(Mirza et al. 2022)
Protoblepharus					
P. apatani	India	MZ820288	MZ790586	MZ790576	(Mirza et al. 2022)
P. medogensis	China	MW111454	–	–	(Che et al. 2020)
P. nyingchiensis	China	MW183282	–	–	(Che et al. 2020)
Outgroup					
Scincella reevesii	China	NC054206	NC054206	NC054206	(Zhong et al. 2021)

Table 2. Details of the primers used in the study for PCR amplification and sequencing (Mirza et al. 2022).

Gene	Primer name	Primer sequence (5′-3′)
16SrRNA	16Sa	CGCCTGTTTATCAAAAACAT
	16Sb	CCGGTCTGAACTCAGATCACGT
12S rRNA	12Sa	AAACTGGGATTAGATACCCCACTAT
	12Sb	GAGGGTGACGGGCGGTGTGT
ND2	H4980_edite	ATTTTGCGTGTTTGTGTTTGGT
	L4437	AAGCTTTCGGGCCCATACC

Morphological data and analyses

Measurements of seventeen morphological characteristics, selected from published literature, were recorded to the nearest 0.1 mm using digital calipers from Jiang-miao Ran (Zhao et al. 1999; Qi et al. 2022). These characteristics were: snout-vent length (SVL), distance from tip of snout to vent; head length (HL), distance from the tip of the snout to the posterior border of the collar; head width (HW), distance across the widest point of the head; head depth (HD), highest point of the head; axilla-groin distance (AG), distance between posterior edge of fore-limb insertion and anterior edge of hind-limb insertion; fore-limb length (FLL), distance from fore-limb insertion to the longest digit; hind-limb length (HLL), distance from hind-limb insertion to the longest digit; tail length (TL), distance between the cloaca and the tail top; eye diameter (ED); eye-narial distance (END), from anterior margin of eye to posterior margin of nares; internarial distance (IND), distance between the nares, supraocular count (SC); supralabial count; (SL), supralabial count before eyes; ventral count (VC), number of latitudinal scale columns from the midpoint of the fore-limb base to the cloaca; toe IV lamellae count (T4lam), number of enlarged, undivided lamellae beneath Toe IV; mid-body scale-row count (MBSR), number of longitudinal scale rows measured around the mid-body; and neck scale-row count (NSR), number of longitudinal scale rows measured around the neck.

Data availability statement

All data used in this note can be found in the supporting information.

Results

ML and BI phylogenetic trees were constructed, based on three mitochondrial genes (12S, 356 bp; 16S, 457 bp; ND2, 509 bp) from twenty species, with a total length of 1323 bp. The ML and BI analyses resulted in largely identical topologies (Fig. 2).

Ablepharus was monophyletic (BI/ML:1/98) in the phylogenetic tree, forming a sister clade with *Protoblepharus*. The sample sequences of Groups IKAP and KKAP were clustered into a single clade, forming a strong monophyletic group, Group IKAP, BI/ML:1/100; Group KKAP, BI/ML:1/100. Group KKAP clustered with *A. eremchenkoi* with strong support (BI/ML:1/100). The *A. alaicus* clade formed a sister clade with *A. nepalensis*, *A. mahabharatus* and *A. sikimmensis* (BI/ML:0.58/60).

The uncorrected *p*-distance, based on 12S sequences, was up to 20%; based on 16S sequences, it was up to 20%; and, based on ND2 sequences, it was up to 27%. The uncorrected *p*-distance between Group KKAP and *A. eremchenkoi* was 1%/2%/2% in the 12S/16S/ND2 sequences, respectively and was less than 10% for *A. alaicus* 1, from Kyrgyzstan, 12S/16S/ND2: 4%/4%/9%. The uncorrected *p*-distance between Group IKAP and *A. alaicus* 2, from Kazakhstan, was 4% for the ND2 sequences. The results of the genetic distances (Suppl. material 2) were consistent with the results of the phylogenetic analyses (Fig. 2), where the Groups IKAP and KKAP were clustered into a branch with *A. eremchenkoi* and *A. alaicus* and the genetic distances of all four (Groups IKAP, Groups KKAP, *A. eremchenkoi* and *A. alaicus*) were lower than those of other species of the same genus, indicating the closeness of the relationship between them. All newly-collected specimens were largely similar to specimens of the original description of *A. eremchenkoi* and *A. alaicus* (Tables 3–5). Thus, we report the rediscovery of *A. alaicus* and specimens from the KKAP (*A. eremchenkoi*) as a new record in China.

Description of specimens from China

Ablepharus eremchenkoi (Panfilov, 1999)

Chinese names. 叶氏泛蜥 (Yè Shì Fàn Xī).

Description of specimens from China. The sample size comprised 16 specimens, all collected by Lei Shi, Jing An and Tao Liang. The main description of this species is based on the male specimen (XND0808007; Figs 3, 4) whose tail had been naturally regenerated. Data and descriptions of the three female specimens (XND0808001, 002 and 005) are provided in parentheses in the following text (if different). The data available for the four voucher specimens are listed in Table 3.

Morphologies of the remaining specimens were similar to those four adult specimens; these data are in Suppl. material 3.

The recorded characteristics of the specimen were as follows: body was small, nearly uniform in thickness, with SVL 46.5 mm and mass 2.04 g and slender (BW/SVL ratio 0.11) with an elongated trunk (AG/SVL ratio 0.53); imbricate scales were smooth and glossy; snout was slightly pointed; head was small and longer than it was wide (HL 9.6 mm, HW 6.6 mm, HD 4.9 mm); eyes were small; ED external ear opening was small with obviously projecting lobules; END was 3.4 mm; fore-limbs and hind-limbs were relatively short, the fore-limb was shorter than the hind-limb (FLL/HLL ratio 0.79) and the tips of the digits of the fore-limb and hind-limb met when

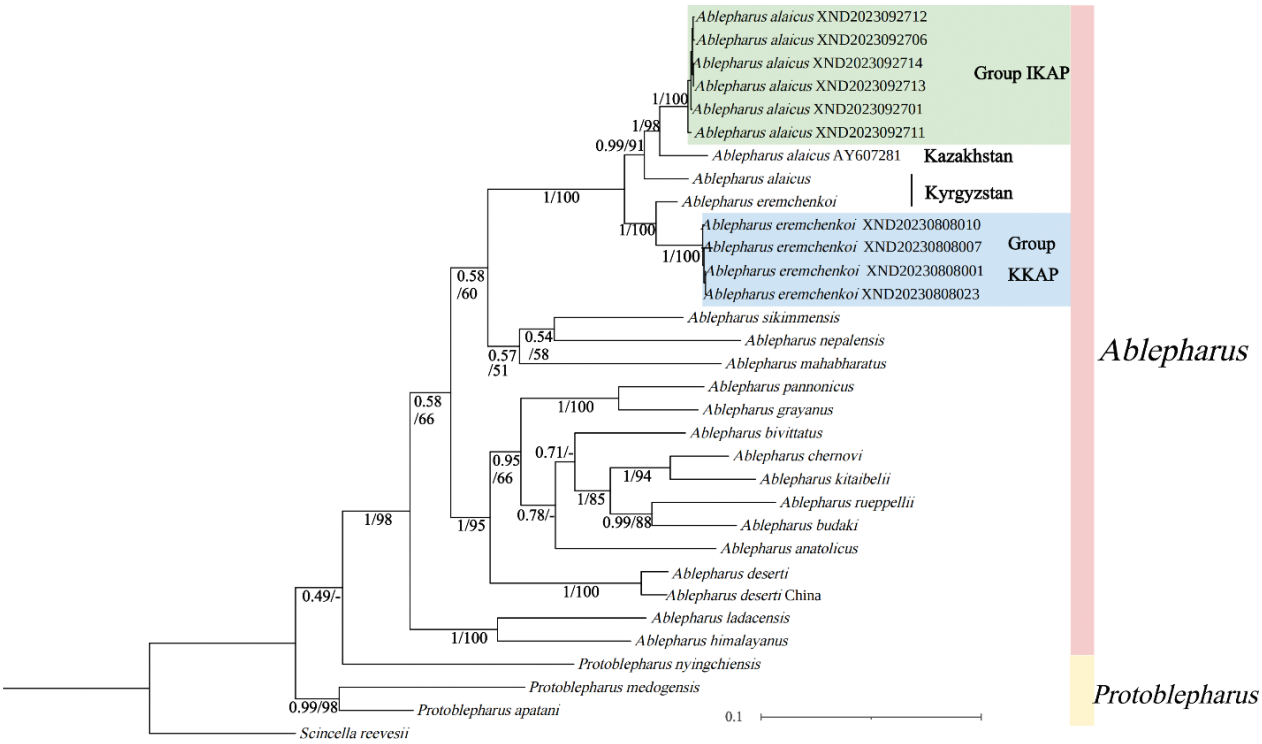

Figure 2. Bayesian phylogenetic trees depicting the relationships amongst *Ablepharus* species using tandem sequences (12S, 16S, ND2). (Note: The values of nodes nearby indicate BI/ML).

Table 3. Measurements (mm) and scale counts of adult *Ablepharus eremchenkoi* from Xinjiang, China. See Materials and Methods for abbreviations. * indicates dropped or regenerated tail.

ID	Sex	BM	SVL	HL	HW	HD	MW	ED	END	IND	AG
XND0808001	Female	3.173	54.2	9.3	6.1	4.2	5.8	1.6	2.1	1.7	29.4
XND0808002	Female	2.348	47.9	9.2	5.1	3. 9	4. 9	1.4	2.8	1.2	29.3
XND0808005	Female	2.381	47.6	8.2	5.5	3.6	5.2	1.3	3.2	1.4	27.9
XND0808007	Male	2.041	46.5	9.6	6.6	4.9	5.9	1.5	3.4	1.5	24.6
	AW	**FLL**	**HLL**	**TL**	**SC**	**VC**	**SL**	**T4lam**	**MBSR**	**NSR**	
XND0808001	9.45	11.59	15.11	40.5	2	46	4	19	26	29	
XND0808002	8.8	12.28	16.01	44.2	2	46	4	19	26	25	
XND0808005	7.96	11.16	15.97	39	2	48	4	16	26	30	
XND0808007	6.23	12.66	15.94	35.3+	2	43	4/5	17	26	26	

Table 4. Descriptive statistics for female reproductive traits of *Ablepharus eremchenkoi*.

ID	Date	Post-oviposition Body Mass (g)	Litter Size	All Litter Mass (g)
XND0808001	20230811	2.13	4	1.04
XND0808002	20230824	1.62	2	0.52
XND0808005	20230825	1.84	2	0.52

the limbs were adpressed against each other along the body axis (except for XND20230808001); the tail was broken, but had regenerated and the regenerated tail was narrower than the body (4.6 mm cf. 6.2 mm) and was shorter than SVL (35.3 mm cf. 46.5 mm) despite tails generally being longer than SVL.

The width of the rostral was greater than its height and it was in contact with the first supralabials, nasals,and fronto-nasal. Nostrils were circular and located at the centre of the nasal cavity. Frontal, fronto-nasal and a pair of prefrontals were connected to a point (seven of sixteen individuals); four of sixteen individuals' prefrontals were widely in contact with each other and frontal and frontal-nasal were separate from each other; three of sixteen individuals' frontal and frontal-nasasl were widely in contact with each other, prefrontals were separate from each other; two of sixteen individuals had three prefrontals, which made frontal and frontal-nasal separate from each other. Prefrontal fan-shaped, a pair of prefrontals were in contact with the postnasal, loreal and first supraocular. A large single frontal, irregularly wedge-shaped, was in broad contact with the third and fourth supraoculars and a pair of frontoparietal posterolaterally. Frontoparietal were widely in contact with parietal and interparietal scales and third and fourth supraoculars. The interparietal rhomboid was posteriorly in contact with parietals. Parietals were anteriorly in contact with frontoparietal, interparietal and fifth supraocular and were laterally touching

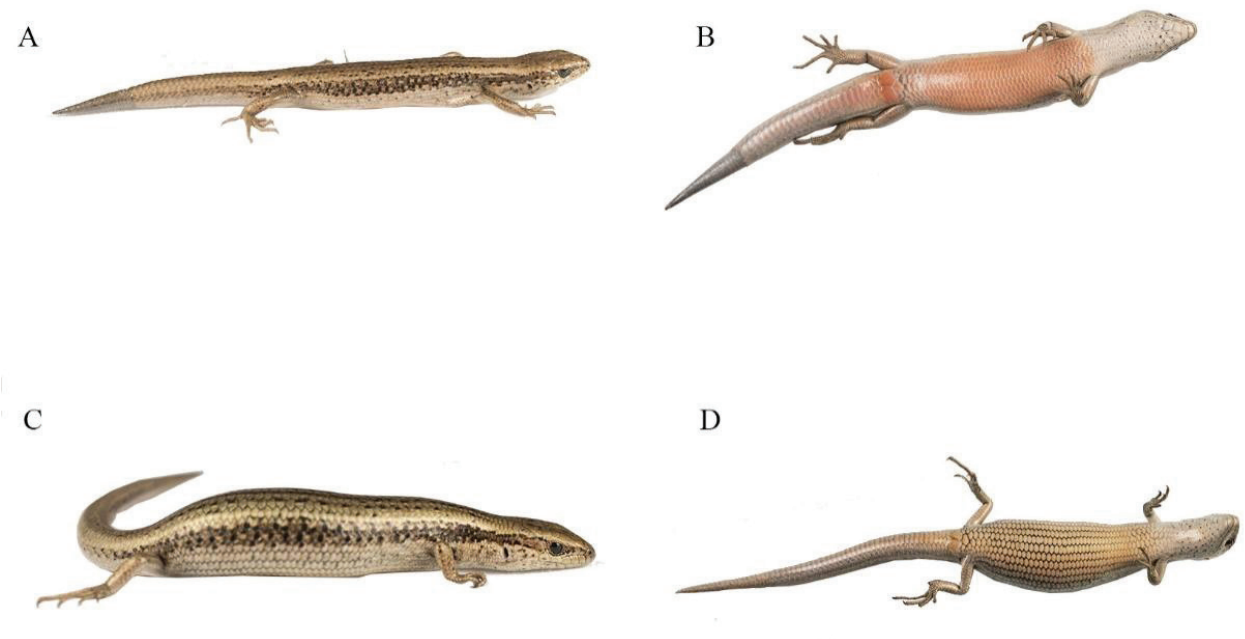

Figure 3. *Ablepharus eremchenkoi* male (**A, B**) and female (**C, D**) in life. Photos by: Tao Liang.

Table 5. Measurements (mm) and scale counts of juveniles of *Ablepharus eremchenkoi*. See Materials and Methods for abbreviations.

ID		BM	SVL	HL	HW	HD	MW	ED	END	IND	AG
XND0808001-1		0.27	22.7	5.7	3.8	2.4	3.5	1.2	1.7	0.97	11.1
XND0808001-2		0.26	22.2	6.1	3.5	2.6	3.2	1.1	1.7	1.04	12.7
XND0808001-3		0.26	23	5.5	3.7	2.5	3.2	1.1	2.1	1.16	13.5
XND0808001-4		0.25	21.7	6.3	3.7	2.4	3.3	1.3	1.9	1.1	11.6
XND0808002-1		0.26	22.5	5.4	4.2	2.7	3.6	0.9	1.3	1.09	12.7
XND0808002-2		0.27	24.1	5.5	3.7	2.5	3.2	1.1	1.5	1.01	12.3
XND0808005-2		0.27	23.5	5.2	3.5	2.4	3.4	1.1	1.9	1.01	11.4
XND0808005-1		0.25	23.4	5.3	3.7	2.2	3.4	1.1	1.9	1.03	11.1
	AW	**FLL**	**HLL**	**TL**	**SC**	**VC**	**SL**	**T4lam**	**MBSR**	**NSR**	
XND0808001-1	2.6	7.5	8.9	25.0	2	45	4	19	29	27	
XND0808001-2	2.8	6.5	8.7	25.8	2	42	4	18	27	28	
XND0808001-3	2.9	7.7	9.8	25.6	2	45	4	19	27	26	
XND0808001-4	3.2	7.9	9.7	26.7	2	43	4	19	29	28	
XND0808002-1	2.8	7.9	10.1	26.3	2	48	4	17	28	27	
XND0808002-2	3.2	7.4	10.2	19.4	2	46	4	19	28	28	
XND0808005-1	3.3	8.1	9.7	26.7	2	40	4	19	28	28	
XND0808005-2	3.4	8.1	9.3	25.3	2	42	4	19	27	28	

the upper posterior temporals. Three supraoculars and the eyes were surrounded by a circle of tiny irregular scales. There were four scales between the nasal cavity and eyes and one individual (XND20230808019) had five scales. For seven supralabials, there was a tiny supraocular between the second and third scales (Figs 3, 4) on the right side (Fig. 4) and seven infralabials. The mental was wider than it was long and was in contact with the first infralabial laterally, postmental posteriorly. Postmental was large and single; four pairs of large chin-shields were present, with the first pair in contact and the second pair narrowly separated by a single medial scale. Dorsal scalation was homogeneous with four columns; longitudinal scale rows were at mid-body 26 (25–29). Twenty-six scales were around the middle of the neck. The number of ventral scales was 43 (46–48). The lengths of the digits (measurements in mm in parentheses) were as follows: left manus IV (2.84) > III (2.69) > II (1.82) > V (1.46) > I (0.98); left pes IV (4.99) > III (3.46) > V (2.31) > II (1.96) > I (1.07). Toe IV lamellae 17.

Colouration in life: Overall, in the one male, the dorsal was coppery brown; dark longitudinal spots were present on the edges of scales and generated three irregular black lines continuing on to the tail. White dots were grouped into six irregular lines along the back of them; the two external dots merged into light lines on the dorsal sides (Fig. 4). The lines on the dorsal sides began at the nasal base until the tail base and they were filled with rare light dots (Fig. 4). The bottom half of the dorsal side was white. The male abdomen was orange-red to the tail, but not the regenerated tail. Females and males were coloured similarly, but the abdomen was paler for females than males;

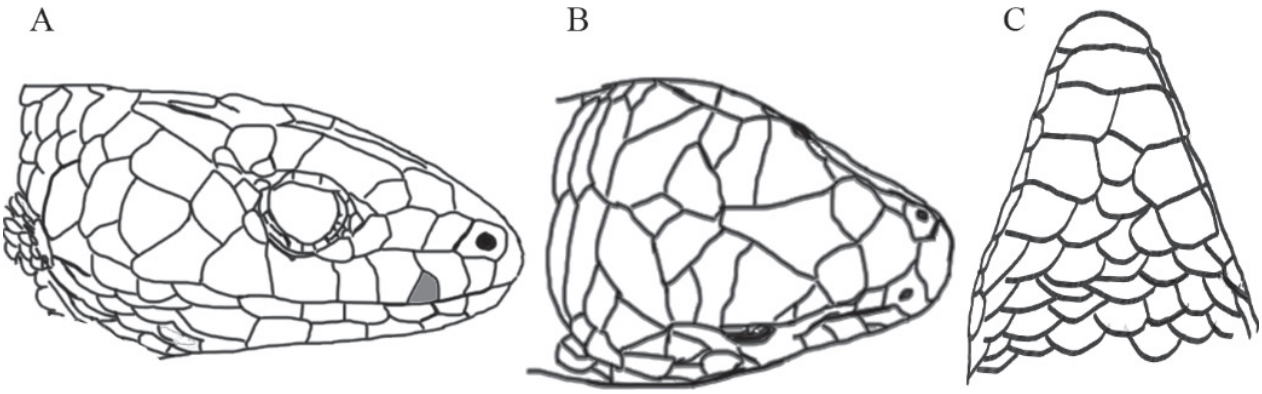

Figure 4. Schematic representation of head scalation of *Ablepharus eremchenkoi*. **A**. Lateral view; **B**. Dorsal view; **C**. Ventral view. The plots were based on the male (XND0808007), the grey scale was the mutational scale between the second and third scales on the right side.

the outline of ventrals was black; and subadults and juveniles had abdomens similar to females, but without the orange-red colour.

Activity, habitats and distribution. All 16 specimens were collected during the day: 16:00–18:00 h and 11:30–13:00 h. According to the residents, these regions receive snow from September to May; thus, the activity times ranged probably from May to August. These individuals were collected at the bottom of a hill, from under rocks and some individuals were collected from riverbeds, 40.20°N, 74.56°E, 3133 m elev., (observations from Ya-hui Huang). This species was observed in Wuqia County, China. Except for Yuqitashi, where we obtained the specimen, this species has been observed in Kalatashi, at 40.0559°N, 74.5941°E and 3004 m elev. and in Jigen Village, at 39.82°N, 74.1069°E and 2709 m elev., identified by images provided by Ya-hui Huang and Jin-Xin Gu, respectively. All individuals were located in a continuous valley (Fig. 1), with altitude ranging from 2709 m to 3133 m (Fig. 1).

Reproduction and diet. Viviparity. Of these individuals, three were gravid females, one female (XND0808001) laid four litters on the morning of 11 August 2023 and two females (XND0808002 and XND0808005) laid two litters on 23 and 24 August (Tables 4, 5) in the laboratory. On average, for these young, weight was 0.26 g, SVL was 22.9 mm and TL was 25.2 mm (Suppl. material 3). Juveniles were coloured and morphologically similar to adults, but had no orange-red colour on their abdomens. The diet of this species remains poorly understood, but they are thought to be carnivorous.

Ablepharus alaicus Elpatjevsky, 1901

Chinese names. 阿赖山泛蜥 (Ā Lài Shān Fàn Xī).

Description of specimens from China. The sample size comprised 14 specimens, all specimens were collected by Peng Ding, Lin Leng and Ke-fan Wu. The main descriptions of this species were based on one specimen (XND2023092704). Additional descriptions were based on the other 13 specimens (in parentheses). All specimen morphological data is in the Suppl. material 3.

The body was small and nearly uniform in thickness, SVL 60.4 mm (26.1–51.1 mm); body mass was 2.93 g (0.29–2.24 g); eyes were small, ED 1.77 mm (1–1.5 mm); END 2.9 mm (1.7–3.3 mm); IND 2.37 mm (1.1–2.3 mm); the head was small, but longer than its width or depth, HL 11.97 mm (6.2–12.5 mm); HW 7.28 mm (3.8–6.9 mm); HD 6.5 mm (2.5–4.7 mm); AG 34.13 mm (14.1–33.1 mm); body was slender (BW/SVL ratio 0.17, 0.12–0.17) with an elongated trunk (AG/SVL ratio 0.56, 0.45–0.64); tail, broken or regenerated tails were excluded, was not as wide (TBW, 5.2 mm, 2.3–5.2 mm) as the trunk, but was longer (64.5 mm, 24.7–55.4 mm) than SVL (TL/SVL ratio 1.06, 0.94–1.17). Limbs were short, FLL 12.53 mm (8.1–12.7 mm) and HLL 16.45 mm (9.5–15.8 mm); the tips of the digits of the fore-limb and hind-limb did not meet each other when the limbs were adpressed against each other along the body axis, but for twelve of fourteen individuals they did meet each other. The lengths of the digits (measurements in parentheses) were as follows: left manus IV (2.68) > III (2.65) > II (1.91) > V (1.6) > I (1); left pes IV (5.07) > III (3.26) > V (2.8) > II (2.15) > I (0.95).

The rostral was single; wider than it was high; and was in contact with the first supralabials, nasals and frontonasals. The nasal rhomboid comprised circular nostrils, located at the centre of the nasal cavity. Fronto-nasal was fan-shaped and connected to the prefrontals. Prefrontals were pentagonal, a pair of prefrontals were connected with a border between them, located between the fronto-nasal and frontal (seven of fourteen individuals); three of the 14 individuals had frontals, fronto-nasals and a pair of prefrontals connected by a point; 3 of the 14 individuals had the frontal and frontal-nasal widely in contact with each other and the prefrontals were separate from each other. The frontal was wedge-shaped, which contacts with the prefrontals, the third and fourth supraoculars and a pair of frontoparietals posterolaterally. Six of the 14 individuals had frontals in contact with fronto-nasals, the prefrontals were not in contact with each

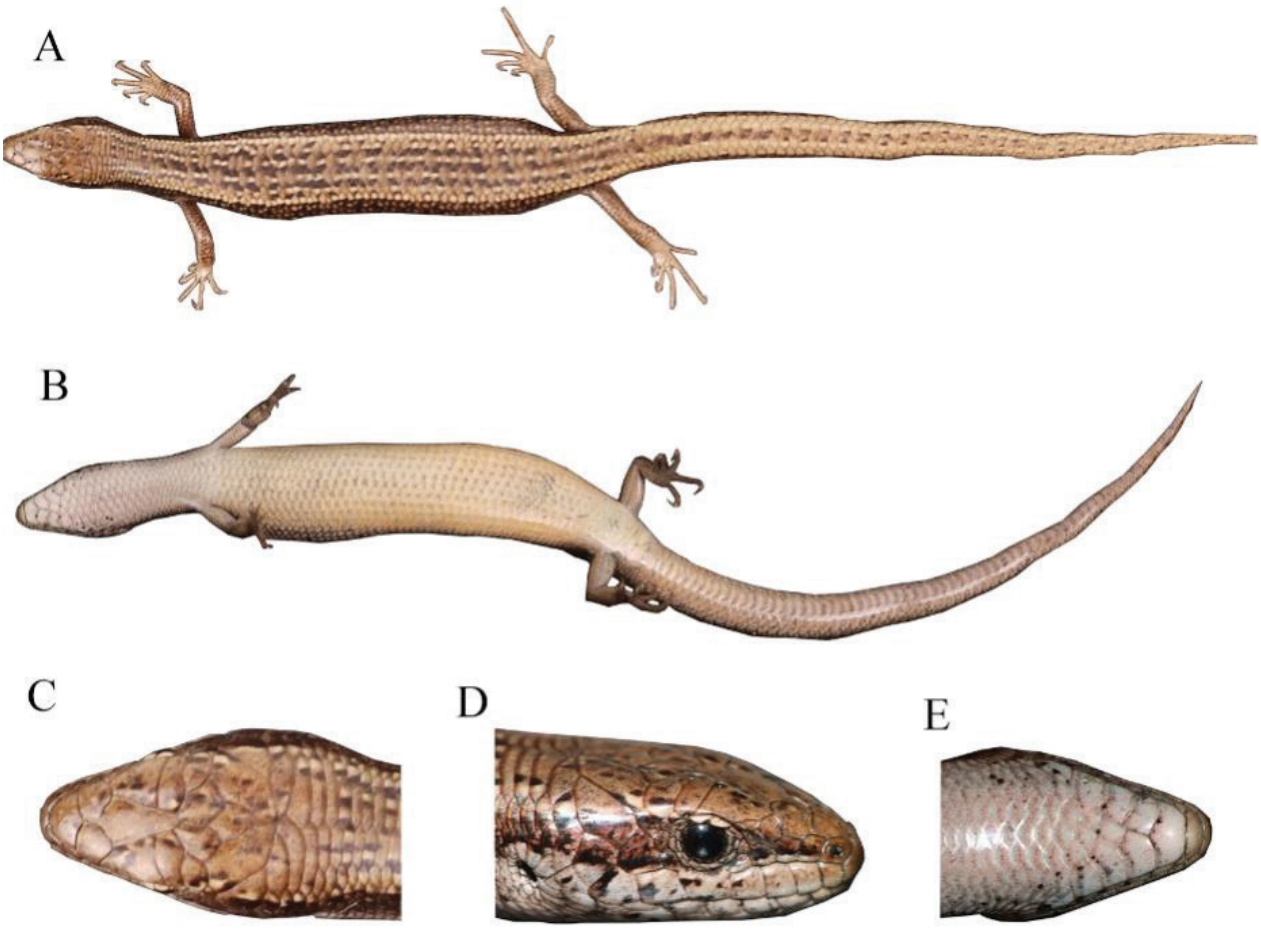

Figure 5. The general aspect and close-up views of *Ablepharus alaicus* (XND2023092704) in life from Qapqal Xibe Autonomous County, Ili Kazakh Autonomous Prefecture, Xinjiang, China. **A.** Dorsolateral view of body; **B.** Ventral view of body; **C.** Dorsal view of head; **D.** Right side view of head; **E.** Ventral view of head. Photos by: Wei-Zhen Gao.

other. The second supraocular region, in contact with the frontal and prefrontal regions, was a single tiny supracular hexagon, between the second supraocular and prefrontal regions. A pair of frontoparietals were in broad contact with each other; besides each frontoparietal was in contact with the frontal, third, fourth supraoculars, the parietal and interparietal. The interparietal rhomboid, in contrast with the frontoparietals, was posteriorly in contact with the parietals. A pair of parietals contact each other; additionally, each parietal was in contact with the interparietal, frontoparietal, fourth supracular and temporals. There were three scales between the nasal cavity and eyes; 10 of the individuals had at least four scales on one side. There were seven supralabials, four loreals between the nasal and eyes and a fourth tiny loreal. The specimen had seven infralabials; three individuals had six infralabials on each side. The temporal 1+2 and the second subtemporal were large and trapezoidal. The mental was wider than long, in contact with the first infralabial laterally and postmental posteriorly. There was a single, large postmental with four pairs of large chin-shields; the first pair was in contact with the second pair narrowly separated by a single medial scale. Dorsal scalation was homogeneous with four columns; there were longitudinal scale rows at mid-body 25 (25–28). There were 28 (25–29) scales around the middle of the neck and 50 (42 –51) ventral scales. There were 17 toe IV lamellae.

Colouration in life. The back was coppery brown, with dark longitudinal spots on the edges of the scales, which generated three black lines continuing on-to the tail; there were white longitudinal spots in the middle of the scales, generating three irregular lines continuing to the back of the tail base. A dark sooty area on each side was sharply defined above, but faded below the belly. The dark sooty area began after the nasal cavity and ended at the middle of the tail (Fig. 5). The abdomen of the females was slightly orange-red during the breeding seasons.

Reproduction, activity, habitats, diet and distribution. Viviparity. All fourteen specimens were collected during the day, from 12:00 to 18:00 h; therefore, this species appears to be diurnal. These individuals were collected at the bottom of a hill at an altitude of 2466 m and the microhabitats were covered with shrubs and gravel. Their diet remains poorly understood, but they are thought to be carnivorous. This species has been observed in Qapqal Xibe Autonomous County, China and probably in adjacent Zhaosu County, which, along with Tianshan, has populations that are connected to those in Kazakhstan (Fig. 1).

Discussion

There have been long-standing questions on the generic taxonomy of Ablepharine skinks (Grismer et al. 2019; Mirza et al. 2022). Nineteen species were included in the genus *Ablepharus* (Uetz et al. 2023). Without molecular data, the genera *Ablepharus*, *Asymblepharus* and *Himalblepharus*, were distinguished using morphological variation which was widely accepted. Our results showed that the latter two genera are embedded within *Ablepharus*, which is consistent with Mirza et al. (2022). The distribution of *A. alaicus* in China was uncertain, although studies and the IUCN have suggested it is distributed in the western Xinjiang border regions (Zhao et al. 1999; Shestopal et al. 2019). Based on the phylogenetic tree of the three sequences (12S, 16S and ND2), our samples, Groups IKAP and KKAP, were close to *A. eremchenkoi* and *A. alaicus*, respectively. Additionally, per the results of the morphological comparison, we identified these two groups as *A. eremchenkoi* and *A. alaicus*.

The distribution of *A. a. kucenkoi* is around north-eastern Tianshan, including south-eastern Kazakhstan, north-eastern Kyrgyzstan and the Ili Valley of Xinjiang (Eremchenko and Shcherbak 1986; Zhao et al. 1999). Group IKAP clustered with *A. alaicus* (AY607281), which was collected from Kazakhstan (BI/ML:1/98, Fig. 2) and with samples from similar altitudes (2466 m vs. 2000 m, respectively). Therefore, the taxon collected from IKAP is likely *A. a. kucenkoi*. However, we found intrapopulation variations in the positions of the prefrontal, fronto-nasal and frontal regions. Six of fourteen (~ 42%) specimens' frontal and fronto-nasal borders were connected. Eight of fourteen (52%) of the specimens were not connected because the prefrontals were connected at the border, but the middle temporal was large and trapezoidal, consistent with *A. a. kucenkoi*. Eremchenko and Shcherbak (1986) demonstrated that approximately 9% of the specimens had prefrontals connected at the border. Such intrapopulation variations in the positions of these scales were also observed in *A. deserti* (Shi et al. 2006). Populations from south-western Xinjiang were assumed to be *A. a. alaicus*; the frontal and fronto-nasal regions of this subspecies were not connected (Zhao et al. 1999). However, based on all voucher specimens in this study, these two scales were connected for most individuals and Group KKAP clustered with *A. eremchenkoi* (BI/ML: 1/100, Fig. 2), which excluded this subspecies. Therefore, whether *A. a. alaicus* is distributed in southern Xinjiang requires further exploration. Notably, we discovered new records of *A. deserti* and substantiated the presence of this species north of the Ili River (Liang et al. 2021). Therefore, at least two skinks are distributed in Ili Valley and further research is necessary to determine whether these two species have a sympatric distribution in China (Kolbintzev et al. 1999).

Xinjiang covers one-sixth of China's territory; however, it remains the least studied area in China for reptiles. For example, the checklist of lizards in China has increased by almost 60 species since 2015 (Cai et al. 2015; Wang et al. 2020; Liang and Meiri 2023), of which only three (two new national records and two newly-described species) are from Xinjiang. The record of *A. eremchenkoi* reported in this study represents the fifth species added to the lizard checklist of Xinjiang. Hence, further research should aim to document the biodiversity of the region.

Conclusion

In summary, we identified the distribution of *A. alaicus* and A. *eremchenkoi* in Xinjiang, northwest China. These records indicate that the number of skink species in Xinjiang ranges from two to three. We also reported the phylogeny, morphology and natural historical notes of these two species.

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Supplementary material 1

Best models for the three sequences

Authors: Tao Liang, Qian-ru Liang, Jiang-miao Ran, Jing An, Ya-hui Huang, Peng Ding, Lei Shi
Data type: docx

Link: https://doi.org/10.3897/herpetozoa.37.e116071.suppl1

Supplementary material 2

Average uncorrected *p*-distances (percentages) between *Ablepharus*

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Data type: xlsx

Link: https://doi.org/10.3897/herpetozoa.37.e116071.suppl2

Supplementary material 3

Morphological traits of all individuals included in this study

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Data type: xlsx

Link: https://doi.org/10.3897/herpetozoa.37.e116071.suppl3