

Dark colouration in *Hemorrhois ravergieri* (Ménétries, 1832) from the western Tian Shan, Uzbekistan

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Melanism, or colouration and pattern tending towards melanism, has been reported only rarely in the snake genus *Hemorrhois* Boie, 1826, although such records are known from a wide area covering North Africa to Central Asia (for review, see Schätti and Agasian, 1985; Tuniyev et al., 1997; Jablonski and Ahmed, 2023; Badis et al., 2024). Within *Hemorrhois*, black colouration is best documented in *Hemorrhois hippocrepis* (Linnaeus, 1758), where such a phenotype is relatively well known and even formed the basis for the description of a distinct island taxon *H. h. nigrescens* (Cattaneo, 1985) from Pantelleria island in Italy (Cattaneo, 1985), an interpretation later rejected by morphology (Corti et al., 2000) and by DNA-based data (Faraone et al., 2020). By contrast, similar records in the remaining *Hemorrhois* species are scattered and mostly anecdotal. Moreover, because dark individuals may be confused with other snake species, as demonstrated by Jablonski and Ahmed (2023), each well-documented case is of particular significance. Here, we report a melanistic specimen from a rarely surveyed area of the western Tian Shan in northeastern Uzbekistan, representing the first documented record of such a phenotype for the region and country.

On 26 July 2023, we found a subadult female (Fig. 1) resembling *H. ravergieri* (Ménétries, 1832) that had been freshly killed by a local shepherd in Ugam-Chatkal National Park, northeastern Uzbekistan (41.9959°N,

70.6385°E; 1478 m elevation). The specimen measured 466 mm in snout–vent length (SVL) and 114 mm in tail length (TL), giving a total length of 580 mm. The head length (HL) was 17.7 mm, head height (HH) 4.8 mm, frontal scale length 5.1 mm, eye diameter 3.6 mm, and rostrum length 3.5 mm. The specimen had 23 dorsal scale rows at midbody and 84 subcaudals, of which the first seven were undivided and the remaining 77 divided. The most remarkable feature of the specimen, however, was its colouration. The specimen was strongly melanistic, with a predominantly black to blackish-brown dorsal ground colour over the entire body. The typical dorsal pattern of the species was not completely absent but persisted as a discontinuous series of irregular cream to yellowish blotches, mainly on the dorsolateral surfaces and less distinctly along the vertebral region. These markings were fragmented and asymmetrical, usually represented by small pale maculae on one or several adjacent scales rather than by well-defined transverse bars. They were most evident on the anterior and middle parts of the body and became less distinct posteriorly. The dorsal surface of the head was almost uniformly dark and lacked a clearly developed pale cephalic pattern, whereas the supralabials, infralabials, and gular region retained contrasting whitish to cream



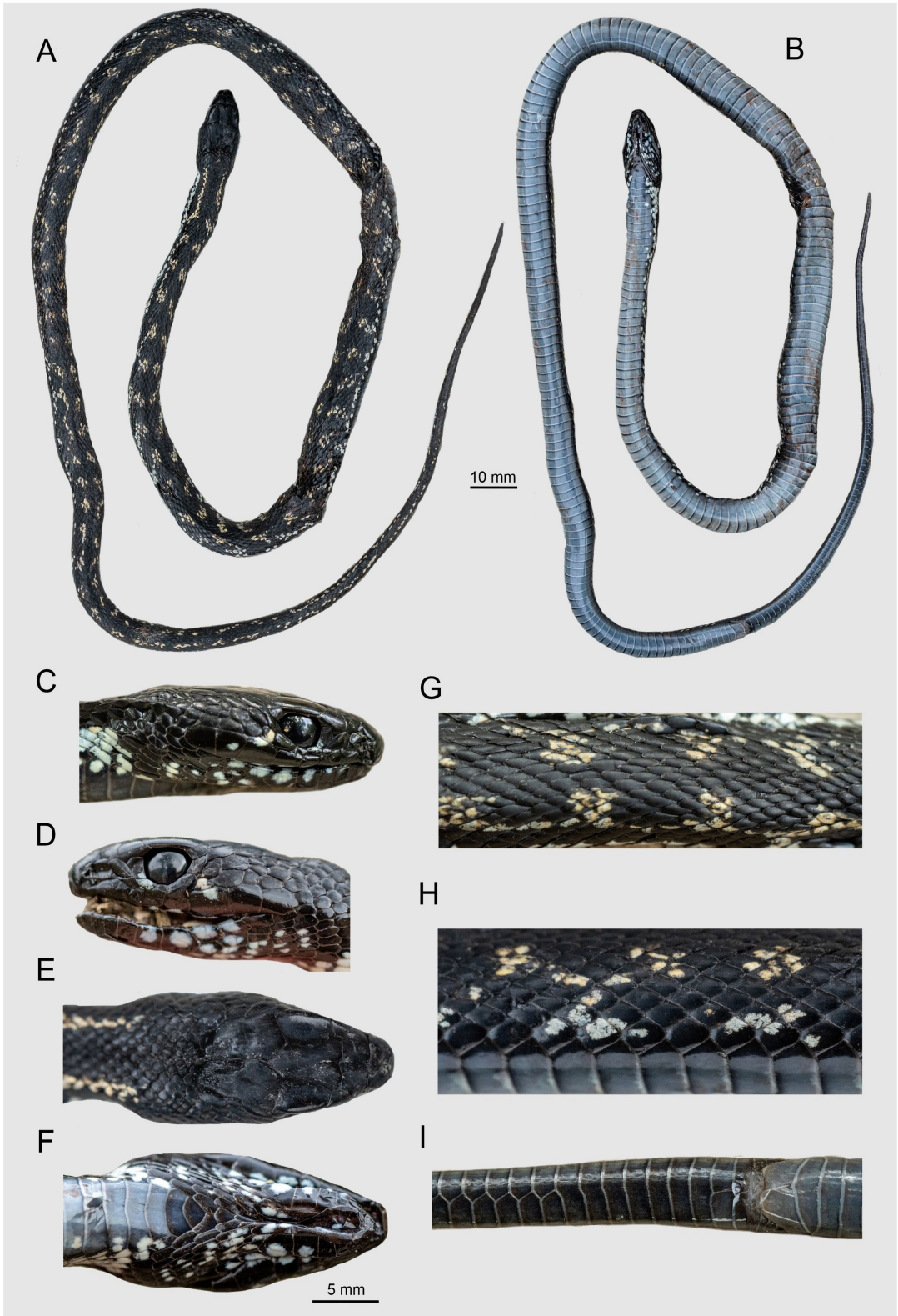
Figure 1. Dark-coloured specimen of *Hemorrhois ravergieri* from Ugam-Chatkal National Park, northeastern Uzbekistan. (A) Dorsal view of the entire body. (B) Ventral view of the entire body. (C, D) Lateral views of the head, showing the predominantly dark cephalic colouration and retained pale labial markings. (E) Dorsal view of the head, illustrating the almost uniformly black dorsal surface. (F) Ventral view of the head, showing contrasting whitish to cream mottling on the infralabial and gular region. (G, H) Details of the dorsal and dorsolateral body pattern, in which the typical pattern persists only as fragmented cream to yellowish blotches on a black to blackish-brown ground colour. (I) Ventral view of the posterior tail region, showing the transition from seven undivided to divided subcaudals. Photos by Daniel Jablonski.

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mottling on a dark background. The ventral side was comparatively uniform, pale grey to slate-grey, with darker pigmentation concentrated along the lateral margins of the ventral scales and becoming more pronounced in the cloacal and subcaudal region. The tail was also darkened, and the subcaudal scales showed only weak pale posterior edging. Thus, melanism in this specimen markedly obscured the normal body pattern, although residual pale pattern elements remained discernible (Fig. 1). The specimen is now stored in the herpetological collection of the Institute of Zoology, Academy of Sciences of the Republic of Uzbekistan under voucher number UZZI RE-19330. Moreover, a similarly dark-coloured subadult individual was reportedly observed by local people at the same locality on 31 July 2025 and was photographically documented, although no detailed data were obtained.

To confirm the expected species assignment of the specimen, we isolated total genomic DNA by a standard procedure including treatment with sodium dodecyl sulphate and proteinase K and subsequent phenol–chloroform extraction (Sambrook et al., 1989) and amplified a fragment of the mitochondrial *cytochrome b* gene (*cyt b*) using the primers L14724 (Hernández et al., 2001) and H16064 (Burbrink et al., 2000). PCR was conducted under the following conditions: an initial denaturation at 95 °C for 5 min, followed by 35 cycles of denaturation at 95 °C for 15 s, annealing at 55 °C for 20 s, and extension at 72 °C for 60 s, with a final extension at 72 °C for 10 min. Sequencing was performed on an ABI 3500 automated capillary sequencer (Applied Biosystems, Austin, TX, USA) with the BigDye™ Terminator v.3.1 Cycle Sequencing Kit (Thermo Fisher Scientific, Vilnius, Lithuania) using the same primers.

A BLAST search of the newly obtained sequence against publicly available DNA sequences showed 95.4% identity to an available sequence of *H. ravergeri* from Armenia (AY486920; ZISP 27733), originally published by Nagy et al. (2004). The haplotype network analysis described below further supported its taxonomic assignment. Unfortunately, the published sequence dataset for Asian *Hemorrhois* is very poor and generally only a few sequences are available for either species, *H. ravergeri* and *H. nummifer* (Reuss, 1834). To visualise relationships among the available *H. ravergeri* sequences, the newly generated 1098-bp sequence (GenBank accession PZ278295) was combined with publicly available sequences and analysed in a haplotype network in Hapsolutely (Vences et al., 2024), using the TCS statistical parsimony

algorithm (Templeton et al., 1992). The final alignment included sequences ranging from 596 to 1105 bp and comprised the following published sequences of *H. ravergeri*: AY486920 (Armenia; Nagy et al., 2004), KY513297 (Iran; Beddek et al., 2018, wrongly identified as *H. nummifer* in the original publication), PV020960 and PV020961 (China; Feng et al., unpublished). One *H. nummifer* sequence, OR234367 (Iraq; Jablonski and Ahmed, 2023), was included for comparison..

The haplotype network based on *cyt b* (common overlap shared by all sequences) recovered three haplotypes within *H. ravergeri* (Fig. 2). Based on the 596-bp shared alignment, the specimen from Uzbekistan shared the same haplotype with the sample from China, whereas the samples from Iran and Armenia each represented distinct haplotypes. The *H. nummifer* sample from Iraq was clearly divergent from all *H. ravergeri* haplotypes and was connected to the network by a long branch of more than 50 mutational steps (Fig. 2). Based on the 596-bp shared alignment, the China–Uzbekistan haplotype differed from the Iranian and Armenian haplotypes by 4.4%, whereas the Iranian and Armenian haplotypes differed by 3.7%.

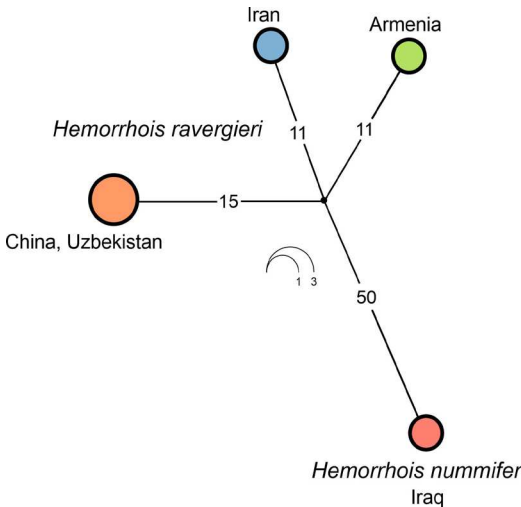


Figure 2. Haplotype network (under the TCS algorithm) based on mitochondrial cytochrome *b* sequences showing the relationships among examined *Hemorrhois ravergeri* haplotypes from China, Uzbekistan, Iran, and Armenia, and their position relative to *H. nummifer* from Iraq. Each circle represents a haplotype, with circle size proportional to the number of individuals. Small black dots represent inferred intermediate, unsampled haplotypes; numbers on the branches indicate the number of mutational steps.

The Iraqi *H. nummifer* sequence differed from the *H. ravergeri* haplotypes by more than 10%.

Our record can be interpreted in the broader context of colour polymorphism already documented in Central Asian *H. ravergeri*. Tuniyev et al. (1997) reported black-headed, typically coloured, uniformly grey, and melanistic individuals of this species in Turkmenistan, including a melanistic specimen from the eastern Kopet Dag. Importantly, that specimen was also not completely patternless, because the dark dorsal colouration still retained lighter elements, especially on the anterior part of the body. In this respect, the Uzbekistan specimen closely resembles the Turkmenistan record (Manysh Village), as melanism strongly obscures but does not eliminate the species-typical pattern. The specimen from Uzbekistan therefore appears to fit the dark extreme of a broader phenotypic continuum already recognised in *H. ravergeri*.

This condition resembles abundism *sensu* Zuffi (2008), as described in *Hierophis viridiflavus* (Lacépède, 1789), where increased dark pigmentation modifies but does not necessarily erase the underlying colour pattern. At the same time, our record extends this possibly mountain-associated polymorphism to the western Tian Shan, i.e. beyond the Kopet Dag and Pamiro-Alai sectors discussed by Tuniyev et al. (1997). Although these authors considered mimicry hypotheses, they ultimately favoured environmental background matching as the primary explanation for colour variation in the *ravergeri*–*nummifer* complex. The montane origin of the present specimen is broadly consistent with such an interpretation, although no further explanation can be provided based on a single record.

The presence of seven anterior undivided subcaudals followed by divided subcaudals is also worth noting as a scalation anomaly because it is rarely observed in *H. ravergeri*. (Schätti and Agasian, 1985; Tuniyev et al., 1997; Bülbül et al., 2019). Although its co-occurrence with aberrant colouration is noteworthy (see Tuniyev et al., 1997), any possible phenotypic association remains speculative and would require additional material for evaluation.

The available mitochondrial data do not indicate that the melanistic specimen represents a genetically unique lineage, as the Uzbekistan sample shares a haplotype with a specimen from China. Nevertheless, the preliminary pattern emerging from the few currently available sequences of Asian *Hemorrhois* is noteworthy. Within *H. ravergeri*, the shared haplotype between Uzbekistan and China, together with distinct haplotypes

in Iran and Armenia, suggests geographically structured mitochondrial variation across its range. Although the present dataset remains far too limited for any phylogeographic inference, it indicates that genetic diversity in Asian representatives of the genus deserves broader investigation based on denser geographic sampling and additional molecular markers.

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