



First Record of *Achalinus juliani* Ziegler *et al.*, 2019 (Serpentes: Xenodermidae) from China

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Dear Editor,

The family Xenodermidae encompasses six recognized genera, among which *Achalinus* Peters, 1869, represents the most species-rich taxon. This genus is extensively distributed across eastern and southeastern Asia, from northern Vietnam through southwestern China, with some populations extending into Japan (Zhao, 2006; Li *et al.*, 2024). Recent advancements in comprehensive fieldwork and molecular techniques have facilitated the revelation of previously underestimated biodiversity within the genus *Achalinus*. Scientific literature has recorded the discovery and description of over 20 new species within the past five years (Li *et al.*, 2024; Xu *et al.*, 2025). Currently, 28 species are recognized within the genus, with a substantial majority (21 species) found in China (Uetz *et al.*, 2025).

Achalinus juliani (Ziegler, Nguyen, Pham, Nguyen, Pham, Van Schingen, Nguyen & Le, 2019) has previously been documented only from its type locality in Cao Bang Province, Vietnam. In this study, we provide the first record of this

species from China, confirmed by both morphological and molecular evidence. A comprehensive morphological examination was conducted on the specimen—an adult female (voucher No. NGAJ01)—during which scalation, color pattern, and body proportions were recorded and measured. Body and tail lengths were measured with a ruler to the nearest 1 mm, while all other morphological measurements were taken using a slide caliper with 0.1 mm precision. For comparative purposes, we compiled morphological data from additional specimens based on published records, adhering to the methodology outlined by Ziegler *et al.* (2019). The abbreviations for the morphological characters used in this study are detailed in Supplementary Table S1.

Genomic DNA was extracted from liver tissue using the Hi-Pure Animal Genomic DNA Kit (Magen, China). The mitochondrial *COI* gene was amplified using the primers Rep COI-F/COI-R (Nagy *et al.*, 2012) and sequenced commercially by Qingke Biotech (Beijing, China).

For phylogenetic analysis, 29 additional *COI* sequences were retrieved from GenBank and incorporated into the dataset (see Supplementary Table S2). Sequence alignment was conducted using MEGA 11 (Kumar *et al.*, 2018). Phylogenetic analyses based on the *COI* gene were carried out using both maximum likelihood (ML) and Bayesian inference (BI) methods. ML analysis was performed with RAxML v8.2.4 (Stamatakis, 2014) under the GTRCAT model with 1 000 bootstrap replicates. BI analysis was conducted using MrBayes 3.2 (Ronquist *et al.*, 2012) with 20 million MCMC generations and sampling every 1 000 generations.

Morphological characters of the specimen NGAJ01: Body slender with a relatively long tail, SVL 386 mm; TaL 110 mm, TaL/TL ratio 0.221; DSR 24-23-23; VEN 190; Subc 77;

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unpaired, cloacal entire; supraocular 1; SL 6; one mental, followed by 5 IL; rostral small, triangular; Intern sut (1.9 mm) longer than Prefr sut (0.99 mm); a single loreal scale. Morphological and related data for this specimen and the three *A. juliani* specimens are provided in Supplementary Table S3. Specimens preserved in ethanol exhibit a reddish-brown color dorsally, with the lower and posterior sides of the head being paler. The ventral surface is greyish cream, with the underside of the tail being slightly darker and the chin region somewhat paler (Figure 1).

The genomic DNA dataset comprises 30 samples with a cumulative sequence length of 630 base pairs. Phylogenetic trees inferred from both BI and ML analyses exhibit largely congruent topologies. All *Achalinus* specimens form a well-supported monophyletic clade (BPP 1.00/UFB 100). The newly collected specimen is robustly nested within the clade containing the Vietnamese holotype of *A. juliani* (Figure 1; BPP 1.00/UFB 99).

This species was described from Vietnam in 2019, and until now, its occurrence outside the type locality has not been documented. The discovery of *A. juliani* in Guangxi represents a 60.5 km northward range extension for this species, bringing the number of *Achalinus* species in China to 22. The female specimen from Guangxi exhibits notable morphological differences compared to the Vietnamese specimens in TaL (110 mm vs. 68 mm) and VEN (190 vs. 179). Despite having an identical number of subcaudal scales, the Guangxi specimens have more ventral scales and

are significantly longer. Furthermore, the individual from Guangxi exhibits differences in certain scale characteristics compared to three specimens from Vietnam, such as IL (5 vs. 6) and DSR (24-23-23 vs. 25-23-23). The observed morphological variation in *A. juliani* could reflect inherent individual differences, geographic divergence, or individual variability, with potential influence from measurement methods (e.g., subjective trait scoring) (Chen *et al.*, 2021). Further taxonomic research, incorporating both morphological and molecular analyses, is crucial for refining the diagnostic characteristics of this species and for a deeper understanding of its geographic and intraspecific variation.

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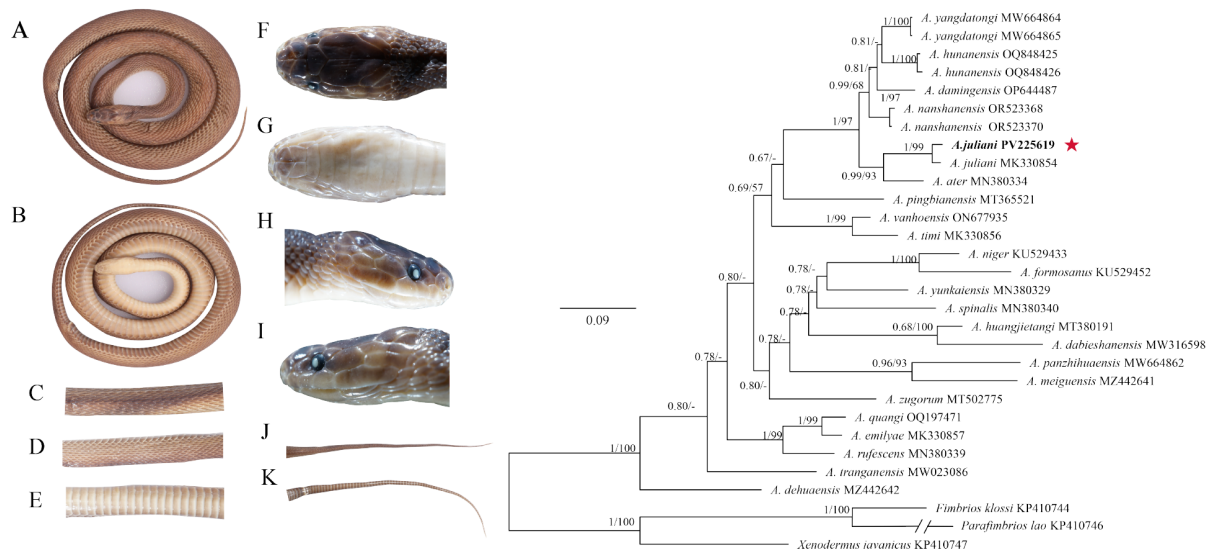


Figure 1 Morphology and phylogenetic position of *Achalinus juliani* (NGAJ01). Preserved specimen: dorsal (A) and ventral (B) views of body; dorsal (C), lateral (D), and ventral (E) views of mid-body; dorsal (F), ventral (G), right (H), and left (I) views of head; dorsal (J) and ventral (K) views of tail. Phylogenetic relationships of *Achalinus* species based on *COI*. Bayesian posterior probabilities (BPP) and ultrafast bootstrap values (UFB) are shown at each node (values <0.5/50 are marked as “-”).

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