Article

ZOOTAXA

A new genus and species of cryptic Asian green pitviper (Serpentes: Viperidae: Crotalinae) from southwest China

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Abstract

A new genus and species of Asian green pitviper is described from Southwest China based on two female specimens. A new DNA phylogeny recovers the two specimens of the new species as a well-supported clade that is sister group to all sampled representatives of the genera *Viridovipera* and *Cryptelytrops*. The new genus is distinguished from other pitviper genera by a combination of morphological characters, including the absence of a lateral stripe, large body size, and deep red eye in adult females. Morphologically the new species is superficially most similar to species of *Popeia* in body dimension and scalation, but is genetically extremely distinct. The new genus/species is currently known only from south Sichuan, where it was found at about 1000 m above sea level in less disturbed evergreen rainforest.

Key words: southeast Asia, DNA, phylogeny, snakes, taxonomy

Introduction

One of the key tasks in systematics is to identify and describe new taxa, infer their systematic position, and explore their relationships with related taxa. The Asian pitvipers of the genus *Trimeresurus* (*sensu lato*) (see definition in Gumprecht *et al*. 2004), which occur throughout southern and southeastern Asia (Malhotra & Thorpe 2004; Gumprecht *et al*. 2004), comprise about 40 species (David & Ineich 1999; McDiarmid *et al*. 1999; Gumprecht *et al*. 2004; Vogel 2006). In recent years, ongoing studies have revealed high levels of specific diversity (e.g. David *et al*. 2001, 2002; Orlov *et al*. 2004; Vogel *et al*. 2004; Grismer *et al*. 2006, 2008). However, this group is characterized by extraordinary morphological conservativeness, and thus is extremely prone to species misidentification (Malhotra & Thorpe 2000; Giannasi *et al*. 2001; Tillack *et al*. 2003), and determination of systematic relationships among taxa is extremely challenging if based solely on morphological data. Recent molecular phylogenetic studies involving high levels of sampling across most Asian pitvipers have led to radical reorganization of the genus *Trimeresurus* (*sensu lato*) (Gumprecht *et al*. 2004) and uncovered many historically misaligned species (e.g. Herrmann *et al*. 2004; Dawson *et al*. 2008). The potential presence of still unrecognized cryptic species within Asian pitvipers impinges upon our ability to understand the evolution of current patterns of diversity in this group.

In 2003, a female green pit viper was collected in Hejiang County, south Sichuan, China (Fig.1). This specimen was identified initially as *Trimeresurus albolabris* (= *Cryptelytrops albolabris*) by Zhao (2006: 140). However, a subsequent molecular analysis and investigation of morphological characters revealed that this specimen was not closely related to *C. albolabris* (unpublished data). In 2007, another female was collected in the same locality. The collection of two specimens allows us to further study them on the basis of morphological comparison and molecular phylogeny. Here, based on a combination of phylogenetic analysis of mitochondrial DNA sequences and morphological comparison between these two specimens and related species, we explore the relationship of these two unidentified individuals to other Asian pitvipers previously assigned to the genus *Trimeresurus* (*sensu lato*) (Gumprecht *et al*. 2004). We consider them to belong to a cryptic taxon which is here described as a new species and genus.
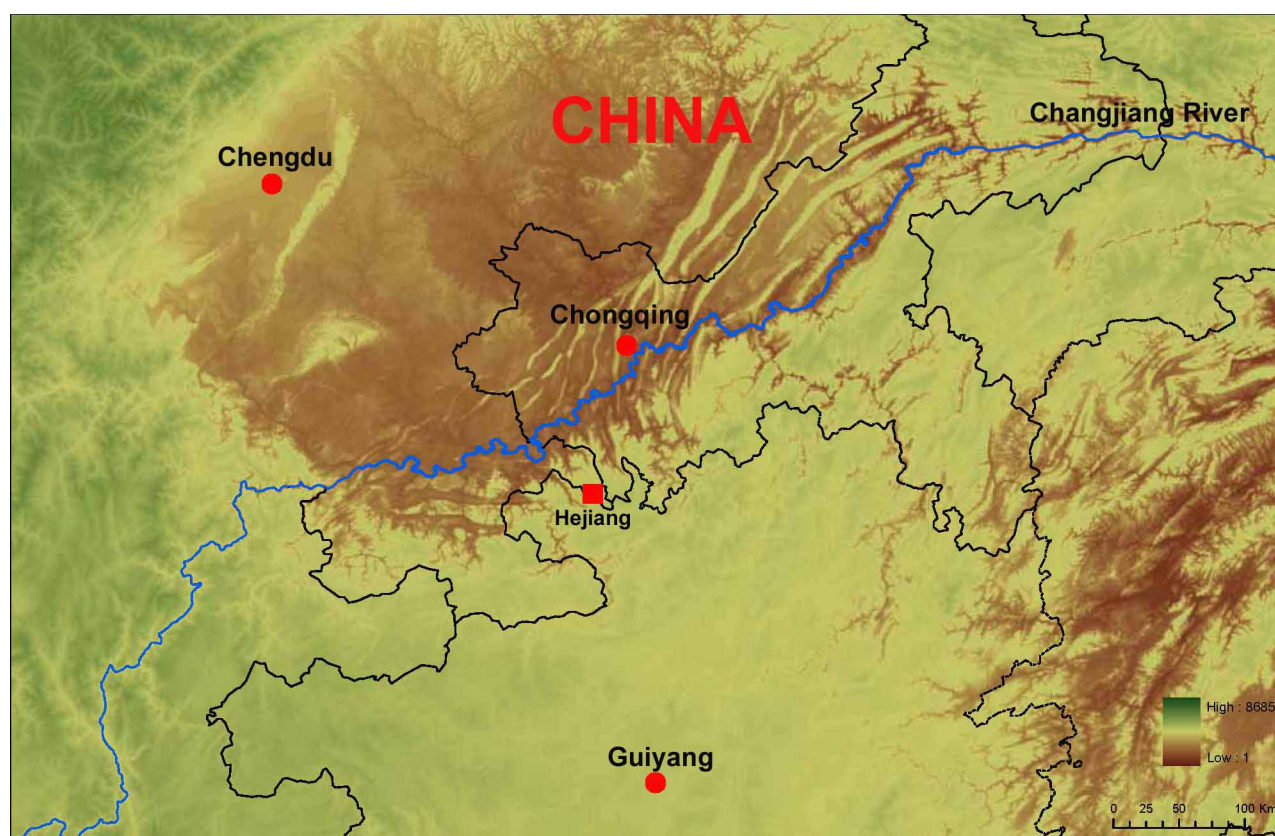
FIGURE 1. The type and only known locality of *Sinovipera sichuanensis* **gen. et sp. nov.**, indicated by a solid square. The black lines show borders between Chinese province-level divisions. Solid circles indicate major cities.

Materials and methods

Molecular methods. The two available specimens, collected in 2003 and 2007, were sequenced and analyzed. Sequences from additional OTUs representing most currently recognized genera and species within the genus *Trimeresurus* (*sensu lato*) (Gumprecht *et al*. 2004; Malhotra & Thorpe 2004) were obtained from GenBank (Table 1). Based on previous molecular studies on Asian pitvipers, several representatives of other Asian pitvipers were included and *Deinagkistrodon acutus* was chosen as outgroup (Malhotra & Thorpe 2004) (Table 1).

Genomic DNA was extracted from 85% ethanol-preserved tissues using standard proteinase *K* and phenol-chloroform protocols (Sambrook & Russell 2002). Four mitochondrial gene fragments were amplified. Cytochrome *b* (cyt *b*) sequences were obtained using primers L14910/ H16064 (Burbrink *et al*. 2000), NADH dehydrogenase subunit 4 (ND4) using ND4/LEU as in Arévalo *et al*. (1994), 12S rRNA as in Knight & Mindell (1993), and 16S rRNA as in Parkinson *et al*. (1997). The PCR products were purified using Spin Column DNA Gel Extraction Kit (Sangon Biotech Co., Shanghai) and the double-stranded product was sequenced using an ABI 3730 Genetic Analyzer (Applied Biosystems) following manufacturer's protocols. Novel sequences generated were deposited in Genbank (Accession Numbers: HQ850445- HQ850450) (Table 1).

DNA sequences were assembled using DNAstar (Seqman). Sequence alignment was carried out using default settings in Mega 4.0 (Kumar *et al*. 2001; Tamura *et al*. 2007). We translated both protein-coding fragments into amino acid sequences using Mega and aligned them with the published sequences to confirm that an open reading frame was maintained and we likely had not amplified pseudogenes (Zhang & Hewitt 1996). Average divergence estimates between genera of interest were calculated from all genes combined, as well as separate genes.

Three different methods were used to infer phylogenetic relationships: Bayesian Inference (BI), Maximum Likelihood (ML), and Maximum Parsimony (MP). The best-fit models of evolution for combined and partitioned data (Posada & Crandall 1998; Posada & Buckley 2004) were inferred in MrModeltest 2.2 (Nylander 2004). BI analysis was performed using MrBayes 3.1.2 (Huelsenbeck & Ronquist 2001; Ronquist & Huelsenbeck 2003),

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TABLE 1. Details of specimens used in this analysis. Abbreviations used as follows: AM: Anita Malhotra (see Malhotra & Thorpe 2004); GP: Authors' catalogue numbers; CAS: California Academy of Sciences, San Francisco; FMNH: Field Museum of Natural History, Chicago; NMNS: National Museum of Natural Science, Taiwan; ROM: Royal Ontario Museum, Toronto; YBU: Yibin University, Sichuan; ZMB: Zoologisches Museum fur Naturkunde der Humboldt-Universitat, Berlin.

Species	Specimen No.	Locality	GenBank Accession No. (cytb, ND4, 12S, 16S)
Cryptelytrops albolabris	AMA104/ROM30854	Vin Phuc, Vietnam	AY352769,AY352837,AY352803, AY352742
C. albolabris	AMA157	Shek Kwu Chan, Hong Kong	AF171884,AY352839, AY352805, AY352744
C. albolabris	AMB22	Nonthaburi, Thailand	AF517189,AF517221, AF517165, AF517178
C. albolabris	AMB183/ROM34544	Gia Lai, Vietnam	AY352770,AY352838, AY352804, AY352743
C. albolabris	AMB117	Ho Chi Minh, Vietnam	AF517190,AF517222, AF517166, AF517179
C. albolabris	AMB6	Cilacap, Java	AF517186,AF517213, AF517158, AF517171
C. albolabris	AMB47	Phetburi, Thailand	AF517187,AF517216, AF517160, AF517173
C. albolabris	AMA165	Loei, Thailand	AF517185,AF517214, AF517169, AF517182
C. albolabris	AMA229	Pha Yao, Thailand	AY059566,AY059583, AY059544, AY059560
C. erythrurus	AMA209	Rangoon, Myanmar	AF171900,AF517217, AF517161, AF517174
C. erythrurus	AMB220	Chittagong, Bangladesh	AY352768,AY352834, AY352800, AY352739
C. purpureomaculatus	AMB418/CAS212246	Ayeyarwade, Myanmar	AY352772,AY352841, AY352807, AY352746
C. purpureomaculatus	AMA83	Satun, Thailand	AF517188,AF517218, AF517162, AF517175
C. purpureomaculatus	AMB139	Perak, Malaysia	AY352771,AY352840, AY352806, AY352745
C. andersoni	AMA77	Andaman Islands, India	AF171922,AY352835, AY352801, AY352740
C. cantori	AMA85	Nicobar Islands, India	AF171889,AY352836, AY352802, AY352741
C. septentrionalis	AMA100	Mahattari, Nepal	AF171909,AY059592, AY059543, AY059559
C. septentrionalis	AMB487	Kathmandu, Nepal	AY352755,AY352818, AY352784, AY352724
C. insularis	AMB7	Timor, Indonesia	AY059568,AY059586, AY059534, AY059550
C. insularis	AMA109	Java, Indonesia	AY352767,AY352833, AY352799, AY352738
C. venustus	AMA241	Nakhon si Thammarat, Thailand	AF171914,AY293930, AY293931, AY352723
C. macrops	AMB27	Bangkok, Thailand	AF517184,AF517219, AF517163, AF517176
C. kanburiensis	AMB522	Kanchanaburi, Thailand	AY289225,AY289231,AY289219, AY352737

TABLE 1. (continued)

Species	Specimen No.	Locality	GenBank Accession No. (cytb, ND4, 12S, 16S)
Viridovipera gumprechti	AMB174/FMNH255579	Nghe An, Vietnam	AY059573,AY059595, AY059547, AY059563
V. gumprechti	AMA164	Loei, Thailand	AY352766,AF157224, AF517168, AF517181
V. gumprechti	AMB15/NMNS3113	Yunnan, China	AY321487,AY352832, AY352798, AY352736
V. stejnegeri	AMA160	Taipei, Taiwan	AF171896,AY059593, AY059539, AY059555
V. stejnegeri	AMA222/NMNS3651	Fujian, China	AF277677,AY059594, AY059541, AY059557
V. vogeli	AMB125/FMNH 258945	Champassak, Laos	AY059581,AF517225, AF517170, AF517183
V. vogeli	AM B97	Nakhon si Ratchasima, Thailand	AY059574 AY059596 AY059546 AY059562
V. medoensis	AMB416/CAS221528	Kachin, Myanmar	AY352765,AY352831, AY352797, AY352735
V. truongsonensis	AMB659	Quang Binh, Vietnam	EU443815,EU443816,EU443817,EU443818
V. yunnanensis	GP37	Sichuan, China	EF597522,EF597527,EU443811,EU443812
Popeia popeiorum	AMB196/FMNH258950	Phongsaly, Laos	AY059571,AY059590, AY059538, AY059554
P. popeiorum	AMA204	Chiang Rai, Thailand	AF171902,AY371843, AY371742, AY371784
P. popeiorum	AMB419/CAS222195	Mon State, Myanmar	AY371806,AY371841, AY371738, AY371777
P. popeiorum	AMB238	Pahang state, Malaysia	AY371814,AY371839, AY371737, AY371774
P. popeiorum	AMB34	Phetburi, Thailand	AY059572,AY059591, AY059542, AY059558
P. popeiorum	AMB361	Bengkulu, Sumatra	AY371801,AY371837, AY371753, AY371769
P. popeiorum	AMB344	Sabah, Malaysia	AY371815,AY371842, AY371736, AY371771
P. popeiorum	AMB246	Selangor, Malaysia	AY059570,AY059589, AY059540, AY059556
P. popeiorum	AMA203	Nakhon si Thammarat, Thailand	AY371796,AY059588, AY059537, AY059553
Himalayophis tibetanus	AMB258/ZMB65641	Helambu, Nepal	AY352749,AY352810, AY352776, AY352715
Parias flavomaculatus	AMB3	Luzon, Philippines	AF171916,AY059584, AY059535, AY059551
P. flavomaculatus	AMB4	Mindanao, Philippines	AY352764,AY352830, AY352796, AY352734
P. mcgregori	AMB289	Batan islands, Philippines	AY371831,AY371858, AY371756, AY371795
P. sumatranus	AMB367	Bengkulu, Sumatra	AY371824,AY371864, AY371765, AY371791

TABLE 1. (continued)

Species	Specimen No.	Locality	GenBank Accession No. (cytb, ND4, 12S, 16S)
P. sumatranus	AMB347	Sabah, Malaysia	AY371823,AY371859, AY371759, AY371788
P. schultzei	AMB210	Palawan, Philippines	AY352756,AY352819, AY352785, AY352725
P. malcolmi	AMB349	Sabah, Malaysia	AY371832,AY371861, AY371757, AY371786
P. hageni	AMB33	Songhkla, Thailand	AY059567,AY059585, AY059536, AY059552
P. hageni	AMB364	Bengkulu, Sumatra	AY371825,AY371863, AY371763, AY371790
Trimeresurus gramineus	AMA220	Tamil Nadu, India	AY352761,AY352827, AY352793, AY352731
T. gramineus	AMB261	Maharashtra, India	AY352762,AY352828, AY352794, AY352732
T. trigonocephalus	AMA58	Balangoda, Sri Lanka	AF171890,AY059597, AY059549, AY059565
T. malabaricus	AMA218	Tamil Nadu, India	AY059569,AY059587, AY059548, AY059564
T. malabaricus	AMB260	Maharashtra, India	AY352763,AY352829, AY352795, AY352733
T. puniceus	AMB213	Indonesia	AF517192,AF517220, AF517164, AF517177
T. puniceus	AMB392	Bengkulu, Sumatra	AY352757,AY352820, AY352786,–
T. borneensis	AMB301	Sabah, Malaysia	AY352754,AY352817, AY352783, AY352722
Sinovipera sichuanensis	GP7/YBU030116	Sichuan, China	HQ850447,HQ850449,HQ850445,HQ850446
S. sichuanensis	GP503/YBU071077	Sichuan, China	HQ850448, HQ850450, –, –
Azemiops feae	AMB499	China	AY352747 AY352808 AY352774 AY352713
Daboia russelii	AMA4	Thailand	AY165090,AY165065,AY352773, AY352712
Deinagkistrodon actus	AMA223	Taitung, China	AF171919,AY352811, AY352777, AY352716
Protobothrops jerdonii	AMB485	China	AY294273,AY294263, AY294277, AY294268
P. kaulbacki	GP112	Xizang, China	DQ666060,DQ666057,DQ666056,DQ666055
Hypnale hypnale	AMA53	Tamil Nadu, India	AY352750,AY352812, AY352778, AY352717
Ovophis monticola	AMB482	China	AY352748,AY352809, AY352775, AY352714
Gloydius blomhoffi	AMB524	Teuri Isl., Hokkaido, Japan	AY352751,AY352814, AY352780, AY352719
Bothrops atrox			AF191587,AF246277, AY223659, AY223672

with three runs and four Markov chains (three heated chains and a single cold chain) using the models selected under the Akaike Information Criterion (AIC), and starting from a random tree. Each run was conducted with a total of 6×10^6 generations and sampled every 1000 generations. Likelihood stationarity, evaluated using Tracer v1.4 (Rambaut & Drummond 2007), was reached by 2 million generations. ML analyses were run using default settings in RAxML (Stamatakis 2006). MP trees were obtained using PAUP* 4.0b10 (Swofford 2003) from equally weighted characters with a heuristic search using 1000 random sequence addition replicates and TBR (tree bisection–reconnection) branch swapping. Bootstrap support values (BS) were calculated from 1000 pseudoreplicates (Felsenstein 1985).

Morphological comparison. A number of characters relating to scalation, color pattern, and body morphometry, were recorded from the two specimens. Measurements of body and tail lengths were taken with a ruler to the nearest 1 cm; the others were taken with a slide caliper to the nearest 0.1 mm. Symmetric mensural head characters were taken only on the right side unless they were unavailable (e.g. damaged); meristic characters were recorded on both sides and means were used. Ventral scale counts were after Dowling (1951). For comparison, the data for other species were taken from published work (David *et al*. 2001, 2002; Orlov *et al*. 2004; Guo *et al*. 2009).

Some abbreviations used in the text are: YBU: Yibin University; SVL: distance between the tip of the snout and the cloaca (snout-vent length); TL: distance between the cloaca and the tip of the tail (tail length); HW: width of the head measured between the outer edges of the supraoculars; HL: length of the head measured between the tip of the snout and the posterior edge of the lower jawbone.


Results

Molecular phylogenetic analysis. The final data set (alignment available from authors on request) consisted of 2,360 base pairs (bp) of sequence data: 420 bp of 12S, 504 bp of 16S, 650 bp of ND4, and 786 bp of cyt *b*. Of these, 1071 bp were variable (45.4%, including outgroups) and 832 bp are parsimony informative characters (35.3%, including outgroups). No insertions, deletions or stop codons were detected in the protein coding genes, indicating pseudogenes likely had not been amplified (Zhang & Hewitt 1996). Table 2 gives average divergence estimates between the unidentified specimens and the major pitviper genera, together with distances between pitviper genera for comparison. For combined genes, the lowest between-group difference is between the unidentified samples and *Viridovipera* (0.112). This is similar to, or exceeds, the average divergence between some other pitviper genera (e.g. *Viridovipera* and *Himalayophis*, *Popeia* and *Himalayophis*).

MrModeltest 2.2 identified the best-fit model as $GTR + I + \Gamma$ for the combined data. Best trees for all of the analyses [BI, ML, MP with one or four partitions (partitioned by genes), excluding or including third codon positions] all included a monophyletic *Viridovipera*+*Cryptelytrops* to the exclusion of the two unidentified samples. The two unidentified samples grouped very strongly together, and generally as the sister group to the *Viridovipera*+*Cryptelytrops* clade. Thus, based on DNA the two unidentified samples can not be assigned with confidence to any currently recognised pitviper genus. All representatives from *Trimeresurus* (*sensu lato*) (Malhotra & Thorpe 2004), currently including the genera *Popeia*, *Himalayophis*, *Viridovipera*, *Cryptelytrops*, *Parias* and *Trimeresurus*, formed a strongly supported clade along with the two unidentified specimens.

TABLE 2. Mean divergence estimates (%, Tamura-Nei distances, with gamma correction) between *Sinovipera* and related genera. Above diagonal: distances calculated from 16s/12s; below diagonal, distances calculated from ND4/cyt.b/all genes.

	Himalayophis	*Cryptelytrops*	*Trimeresurus*	*Parias*	*Popeia*	*Viridovipera*	*Sinovipera*
Himalayophis		3.6/8.6	5.0/11.9	4.7/8.0	3.9/6.3	3.1/7.3	3.7/7.9
Cryptelytrops	19.0/16.4/12.4		5.2/11.8	6.0/8.5	5.1/7.2	3.7/7.3	3.3/7.1
Trimeresurus	20.8/21.1/15.6	22.7/20.9/16.0		6.6/11.4	6.4/11.0	5.4/11.0	4.7/10.8
Parias	17.8/17.7/12.5	20.9/20.9/14.6	21.0/23.0/16.4		5.2/7.2	4.2/7.7	4.8/6.6
Popeia	14.3/14.1/10.0	18.5/17.9/12.6	21.5/21.3/15.8	18.5/16.3/12.2		3.5/7.4	3.6/6.8
Viridovipera	14.4/15.6/10.6	18.9/18.212.5	20.3/21.0/15.4	15.9/17.7/11.9	17.2/15.7/11.3		2.6/6.4
Sinovipera	13.7/13.9/11.9	19.9/20.0/16.5	20.5/23.1/18.8	16.6/17.3/14.4	17.8/16.6/14.3	13.1/13.4/11.2	
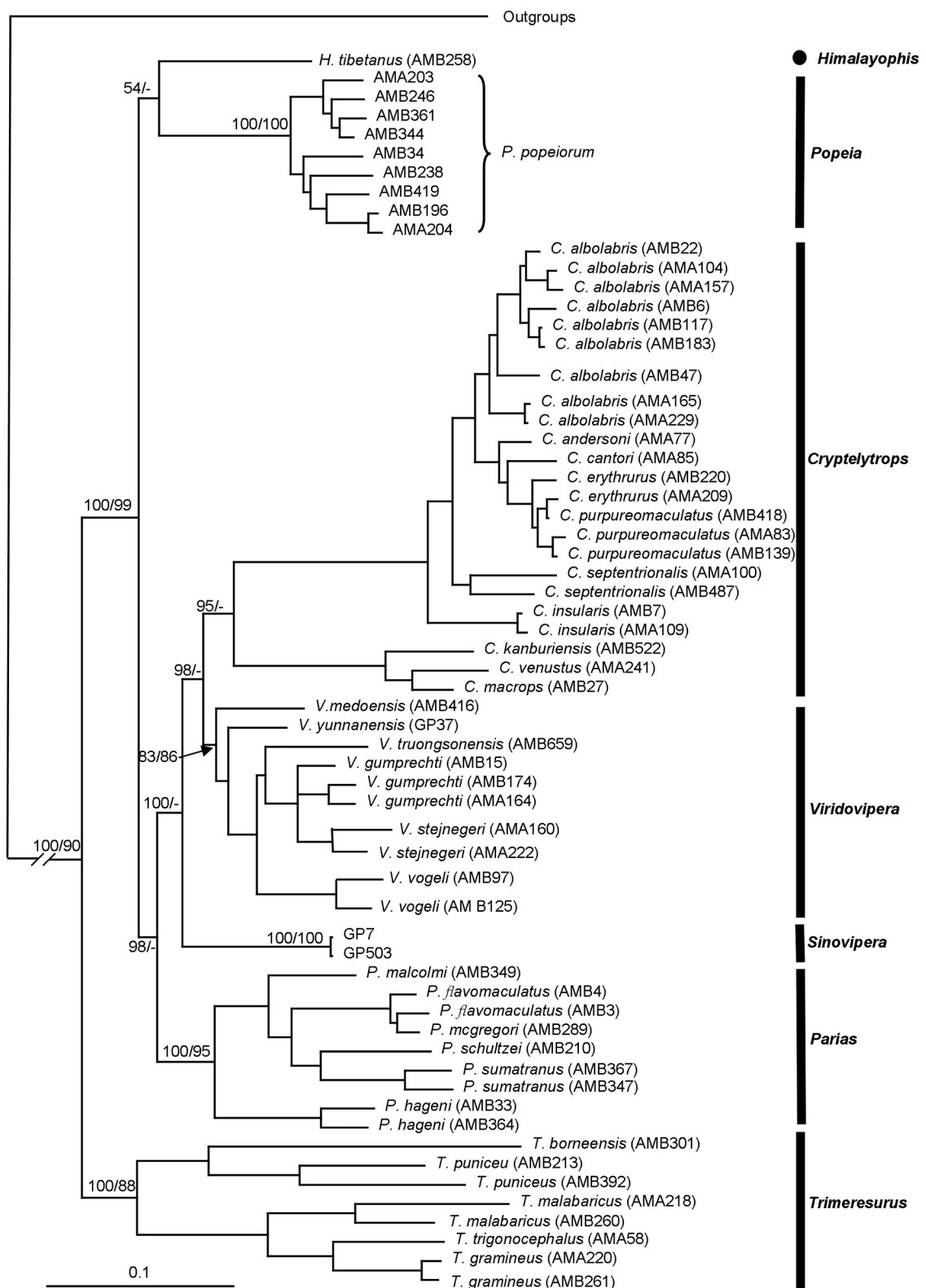
FIGURE 2. The Bayesian 50% majority-rule consensus tree inferred from the combined dataset of 12S rRNA, 16S rRNA, cyt *b* and ND4, including third codon positions. Posterior probabilities (BI) /bootstrap values (MP) for the clades are shown adjacent to the node to which they refer. "-" indicates values < 50.

The monophyly of each of *Viridovipera* and *Cryptelytrops* was not always recovered in all best trees. The best BI tree for the unpartitioned analysis including all positions is shown in Fig. 2. The parsimony analysis produced 30 optimal trees with length = 5757 steps, CI = 0.283, RI = 0.6057, RC =0.171.The monophyly of *Viridovipera+Cryptelytrops* is less robust in best ML trees than Bayesian ones, but the new species is always recovered outside and as sister to this clade.

Morphological study. The two specimens are uniform green in body color without ventrolateral stripes or postocular streaks. The head is covered with tiny scales. A pit is present between nasal and eye. The eye is deep red, and the tail is rusty dorsally. Both are large, more than 1000 mm in total length. The first supralabial is completely separated from the nasal. The anal is single.

Sinovipera gen. nov.
Figs. 3–7

Type species. *Sinovipera sichuanensis* **sp. nov.**

Diagnosis. A genus of Asian pitviper within *Trimeresurus* (*sensu lato*) having the following combination of characters: (1) the first supralabial completely separated from the nasal; (2) a uniform green dorsum without postocular streak and ventrolateral stripes in females; (3) eyes deep red in females; (4) tail prehensile, its end rusty red in upper part; (5) large body size, with the maximum total length exceeding 1000 mm in females.

Distribution. Presently, it is only known from the type locality, although it also likely occurs in western Chongqing, northwestern Guizhou, China.

Etymology. The generic nomen *Sinovipera* is derived from the modern Latin adjective *sinicus* (*a*, *um*), based on the noun *Sina* (*-ae*), "China", and the Latin noun *Vipera* (-ae), meaning "'a viper". We suggest that the common name of this new genus be "Chinese pitviper" in English.

Content. This genus at present contains a single species, *Sinovipera sichuanensis* sp. nov, the description of which is given below.

FIGURE 3. General view of the holotype (YBU071077) of *Sinovipera sichuanensis* **gen. et sp. nov.** in life.
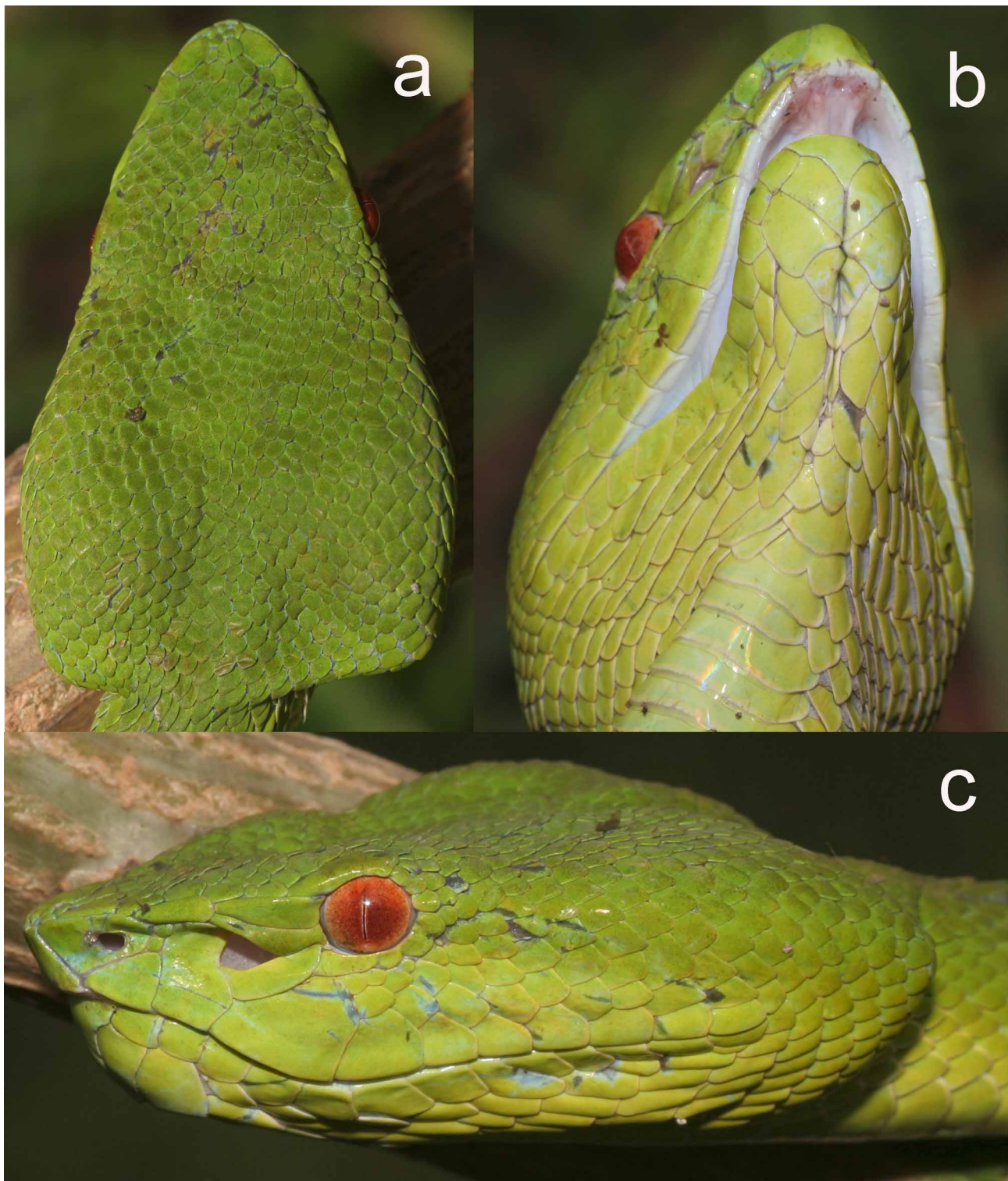
FIGURE 4. Dorsal (a), ventral (b), and lateral (c) views of the head of the holotype (YBU071077) of *Sinovipera sichuanensis* **gen. et sp. nov.**

Sinovipera sichuanensis **sp. nov.**
Figs. 3–7

Trimeresurus stejnegeri (non *Trimeresurus stejnegeri* Schmidt, 1925).—Zhao *et al.* (2002: 233).
Trimeresurus albolabris (non *Trimeresurus albolabris* Gray, 1842).— Zhao (2006: 140).

Holotype. YBU071077, an adult female (Figs. 3–4) from Hejiang County, Sichuan Province, China. It was collected near a small river in the forest by a local farmer at an elevation of 1000 m above sea level in August 2007. The specimen is deposited in Yibin University.

Paratype. YBU030116, an adult female (Figs. 5–6). Collected in July 2003, from the same locality, and by the same farmer, as that of the holotype. The specimen is deposited in Yibin University.

FIGURE 5. Dorsal (left) and ventral (right) views of the paratype (YBU030116) of *Sinovipera sichuanensis* **gen. et sp. nov.** in preservative.

Diagnosis. As for the generic diagnosis.

Description of the holotype. Adult female. Nearly uniformly green, lacking postorbital and ventrolateral stripe. Body elongated, cylindrical, and stout; head distinctly triangular and elongated, distinct from the neck; snout elongated and pointed. SVL 900 mm, TL180 mm, ratio TL / Total length 0.167. HL 44.20 mm, HW 27.84 mm. Third supralabial = 5.06 mm high, 6.58 mm wide. Supraocular has a maximum length of 4.93 mm, maximum width of 2.57 mm. The eye is deep red in life, diameter 4.97 mm. The pupil is vertical. The distance between the rear edge of the nasal to the front edge of the eye is 17.77 mm. The tail is distinctly prehensile, with about 1/3 of the TL is rusty red dorsally (Fig. 3). Rostral rapeziform, invisible from above. Pit present between nostril and eye, surrounded by three scales (Fig. 4).

Ten supralabials on both sides; the first separated from nasal by a distinct suture; the second the highest, forming the anterior border of the pit cavity, and separated from the nasal by two small scales that are vertically arranged; the third is the largest, separated from the eye by an elongated subocular; the fourth supralabial separated from eye by three scales, of which the upper two are in line. Nasals separated by three scales, and internasals do not touch the rostral. There are 14 cephalic scales in a line between the supraoculars. Two elongated scales are present between the eye and nostril. The temporal region and rear head scales are smooth. Body scales feebly keeled except outer four to five rows. Three preoculars, elongated, the middle and lower ones forming the border of the pit cavity. Two postoculars; one subocular, elongated. Supraoculars bordered by nine/eight scales (excluding the postoculars and preoculars). Infralabials 13/13, the first pair separated by the first pair of chin shields, and in contact with two pairs of chin shields. The second and third pair of infralabials touching the second chin shields. Six scales in a line between the first preventral and the posterior chin shields.

Ventrals 172, plus 2 preventrals. Anal entire. Body scales 21-21-15. Scale reduction formula at the rear of the body as given below:

$$21\frac{104(5+6)}{104(4+5)}19\frac{115(4+5)}{113(4+5)}17\frac{125(4+5)}{127(4+5)}15$$
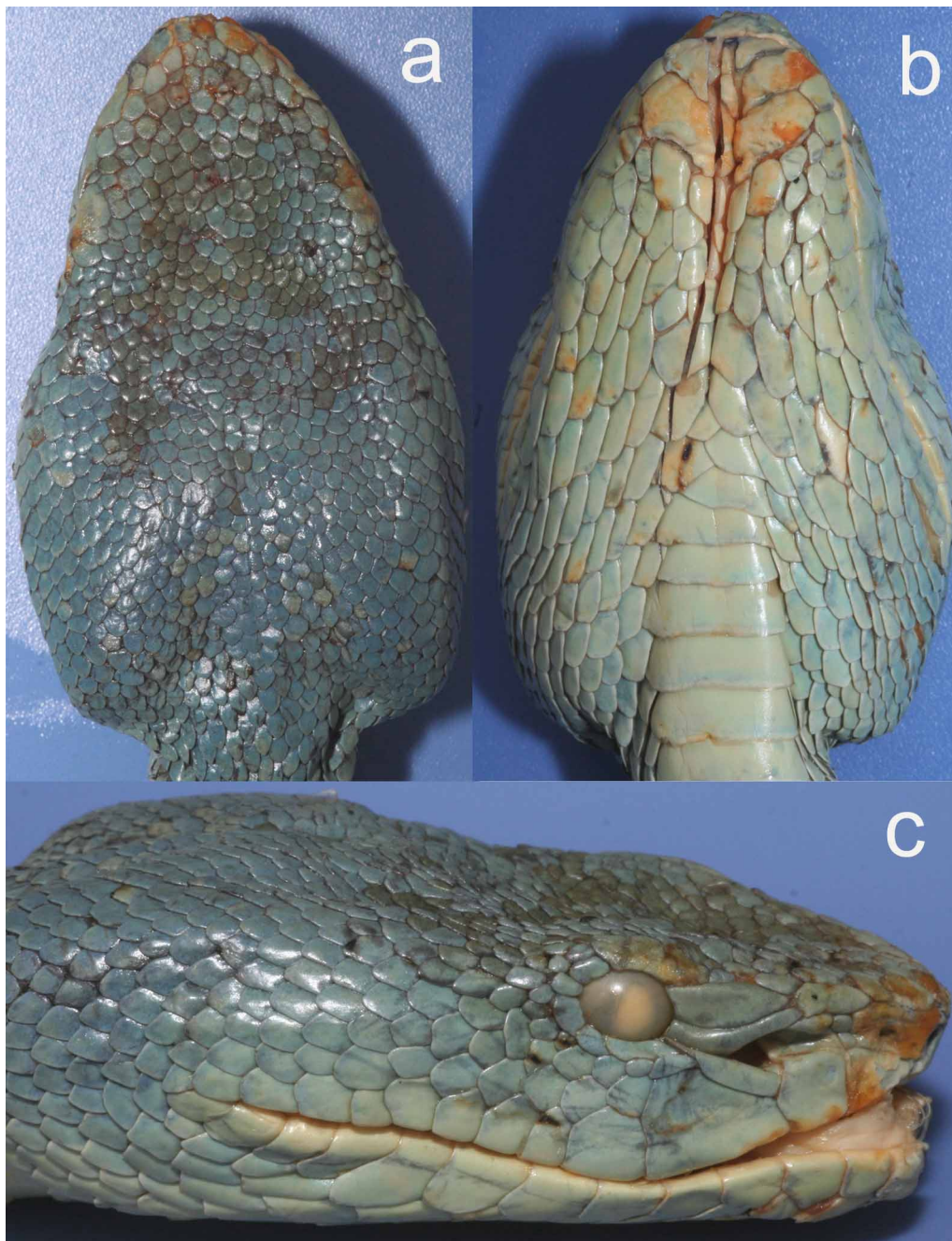
FIGURE 6. Dorsal (a), ventral (b), and lateral (c) views of the head of the paratype of *Sinovipera sichuanensis* **gen. et sp. nov.**

Subcaudals 68 pairs. Scale reduction formula in tail as given below:

$$8\frac{10(3+4)}{11(3+4)}6\frac{33(2+3)}{33(2+3)}4$$

Description of the paratype (Figs 5–6). Adult female with SVL 1010 mm, TL 210 mm, ratio TL / Total length 0.172. HL 48.08 mm, HW 30.98 mm. Supralabials 10 on left and 12 on right. Infralabials 14/13, the first pair fused with first pair of chin shields. Six scales in a line between the preventral and the posterior chin shields.

Ventrals 171 plus 3 preventrals. Body scales 21-21-15. Scale reduction formula at rear of body as below:

$$21\frac{110(5+6)}{108(4+5)}19\frac{115(3+4)}{115(4+5)}17\frac{138(4+5)}{134(4+5)}15$$

Subcaudals 68 pairs. Scale reduction formula of tail as below:

$$8\frac{13(3+4)}{10(3+4)}6\frac{38(2+3)}{40(2+3)}4$$

All other morphological characters, including the body coloration, are consistent with those of the holotype.

Etymology. The specific nomen is based on the Chinese province of Sichuan, which includes the type locality of the new species. We suggest that the common name of this new species be "Sichuan pitviper" or "Sichuan Chinese pitviper" in English.

Distribution. This species is currently known only from the type locality (Figs.1 & 7), where it is sympatric with *Viridovipera stejnegeri*. It is likely that the new species species also occurs in Chongqing and Guizhou. No other data on its feeding and reproduction are available.
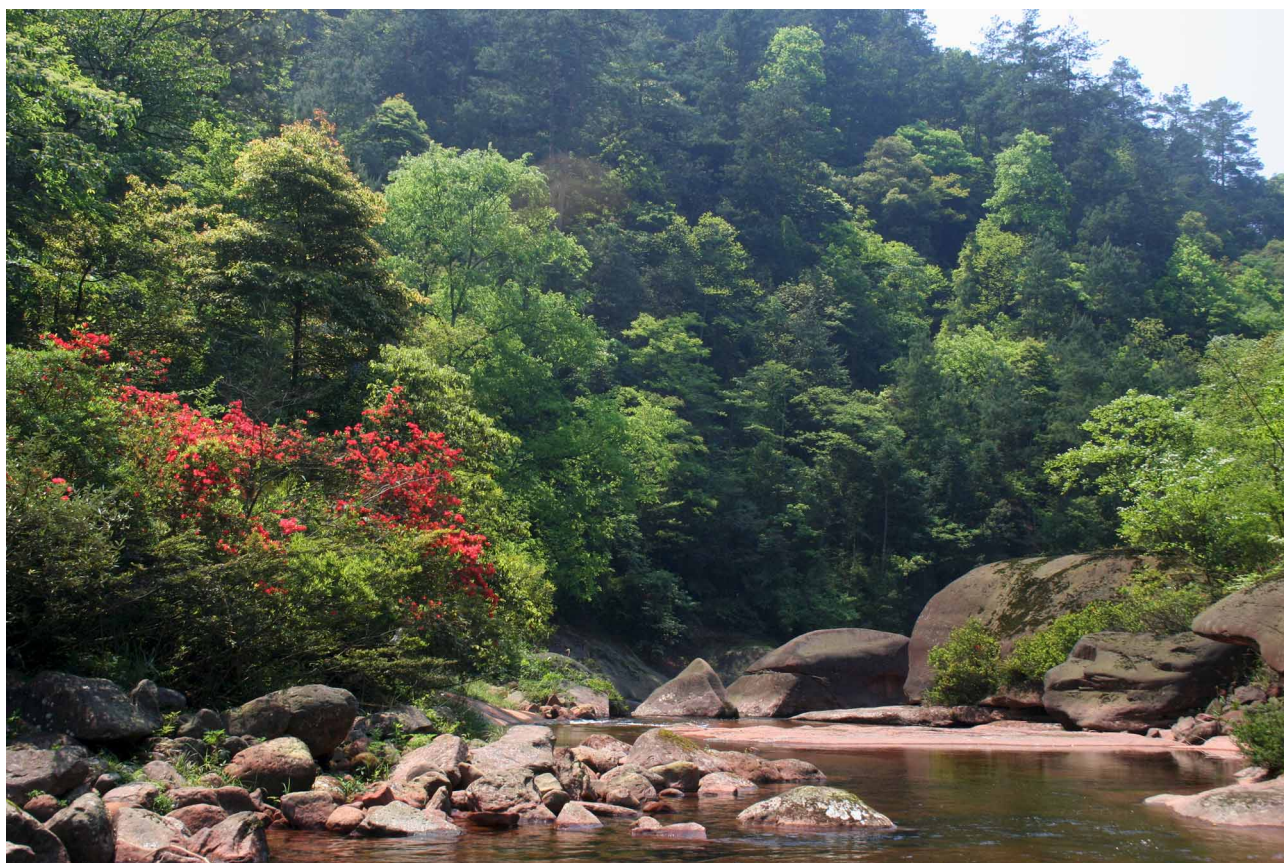
FIGURE 7. The habitat in the vicinity of the type locality of *Sinovipera sichuanensis* **gen. et sp. nov.**.

Discussion

Based on a combination of morphological comparison and mitochondrial DNA phylogeny with extensive samples of Asian pitvipers, Malhotra & Thorpe (2004) proposed a new taxonomy for the genera *Trimeresurus* (*sensu lato*). In their revised taxonomy, Malhotra & Thorpe (2004) erected three new genera including *Viridovipera*, *Popeia* and *Himalayophis*, and resurrected *Parias*, *Crytelytrops* and *Peltopelor*. Based on the studies of Malhotra & Thorpe (2004), morphologically the main differences between these genera are in their hemipenial morphology. The new

taxon is known only from two female specimens, and so we are not able to use hemipenial characters in this instance. Although superficially the new material resembles *Popeia*, it is genetically far removed from members of that genus, and the new specimens undoubtedly represent a new species.

Here, the BI gene tree indicates that the new species forms a strongly supported clade with *Viridovipera* + *Cryptelytrops*. From a molecular phylogenetic perspectivein which named taxa are monophyletic, the new species should represent a new genus, or alternatively one congeneric with both *Viridovipera* and *Cryptelytrops* (requiring synonymy of the former with the latter). However, the marked morphological differences between *Viridovipera* and *Cryptelytrops* (see Malhotra & Thorpe 2004) prevent us from concluding that *Viridovipera* is synonymous with *Cryptelytrops* and thus we have described a new genus. Morphologically, the new genus differs from *Viridovipera* and *Cryptelytrops* by adult females having red eyes and lacking ventrolateral stripes, and in the separation of the first supralabial from the nasal. Our hypothesis and preferred classification can be tested with additional molecular phylogenetic analyses and/or collection of adult males of the new species.

Presently, seven putative species of pitviper belonging to four genera occur in China: *Viridovipera stejnegeri*, *V. gumprechti*, *V. medoensis*, *V. yunnanensis*, *Cryptelytrops albolabris, Himalayophis tibetanus* and *Sinovipera sichuanensis*. The new species differs from all other Chinese species by the absence of ventrolateral stripes and presence of red eye in females (David *et al*. 2001, 2002; Gumprecht *et al*. 2004; Orlov 2004). It is also distinct from other Chinese species in various combinations of morphological characters. For example, it differs from *C. albolabris* in that the first supralabial is fully separated from the nasal, from *V. medoensis* by having more scale rows at midbody (21 vs. 17), more ventrals (171.7 vs. 143.7) and subcaudals (67 vs. 54.6) in females (David *et al*. 2002), has and in reaching a much greater size (maximum female SVL >1000 mm vs. 530 mm in *V. medoensis*, David *et al*. 2002). *Sinovipera sichuanensis* differs from *V. yunnanensis* in having 21 vs. 19 scale rows at midbody and a larger body size in females (maximum SVL > 1000 mm vs. 778 mm in *V. yunnanensis*, Guo *et al*. 2009).

At its type locality, *S. sichuanensis* is sympatric with *V. stejnegeri*. Besides the obvious distinction indicated in molecular phylogenetic trees (Fig.2), *V. sichuanensis* also differs from *V. stejnegeri* in reaching a larger size (maximum SVL > 1000 mm vs. 765 mm in female *V. stejnegeri,* Guo *et al*. 2009), and in lacking ventrolateral stripes (see above). In Hejiang, local farmers can easy identify these two taxa and they give them different names (*S. sichuanensis* is referred to as "Caotou Qing" and *V. stejnegeri* as "Jinxian luotietou", translating as "gold strips pitviper").

Since 2003, we have tried to collect more specimens of the new species, including mobilizing the local snake traders, but only two specimens have been collected. It would be particularly valuable to obtain males, given the importance of the hemipenis in the classification of Asian pitvipers. It is possible that this species is very rare in this locality. Further study of its distribution, population ecology, and natural history is highly desirable.

Acknowledgements

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