

A new moth-preying Alpine pitviper species from
Qinghai-Tibetan Plateau (Viperidae, Crotalinae)

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Supplementary material

Part 1. Supplementary figures

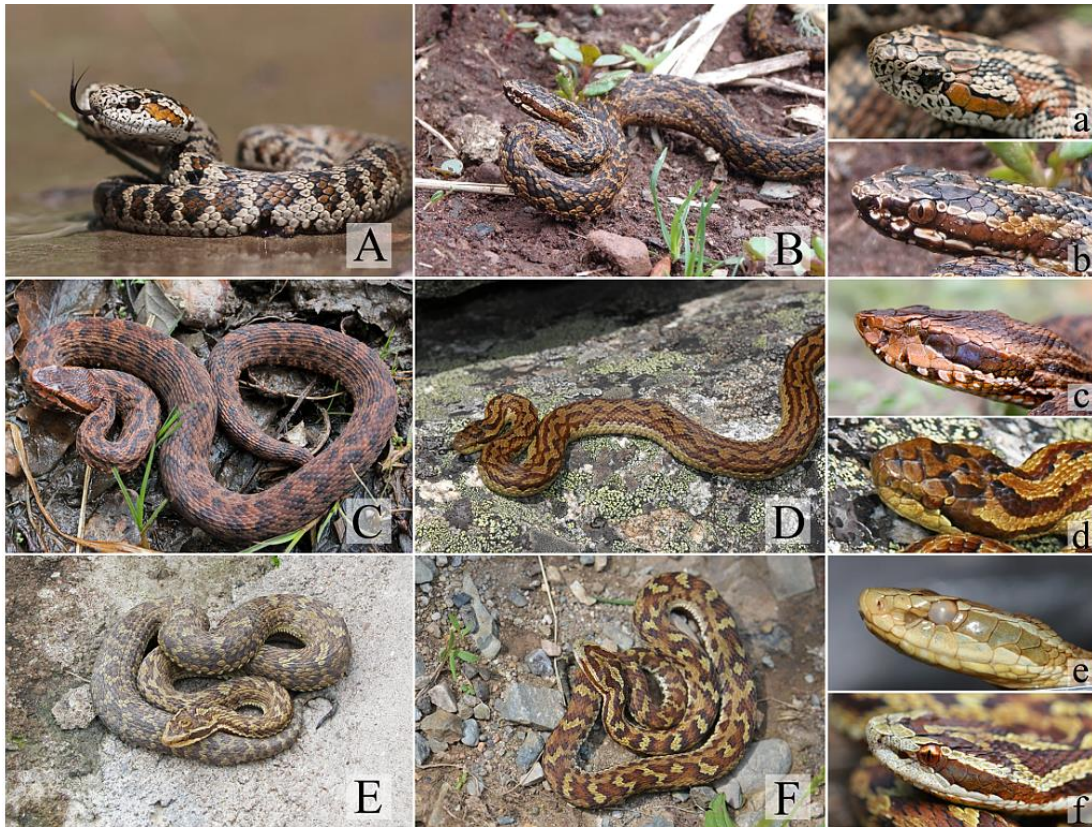


Figure S1. Photographs of the species of *Gloydus strauchi* complex.

(A) *G. rubromaculatus*, sub-adult female, from Jyekundo, Qinghai, by Jiansheng Peng (released); (B) *G. monticola* (DL1), sub-adult, unknown sex, from Lijiang, Yunnan, by Yihao Fang. (C) *G. himalayanus*, from India, by Deepak CK; (D) *G. strauchi*, adult, unknown sex, from type locality, Kangting, Sichuan, by Zhiyuan Tang (note: *G. strauchi* has various body colours e.g. greyish green, yellowish brown or reddish brown); (E) *G. liupanensis*, adult male, from Guyuan, Ningxia, by Chengxiang Sun; (F) *G. qinlingensis* (QLS, topotype), adult male, from Pingheliang, Shaanxi. (a) head of Y2 (*rubromaculatus*, holotype); (b) head feature of the identical specimen with B (*monticola*, DL1); (c) another *G. himalayanus* species' head feature, by Vikas Upadhyay, from Muktesar, India. (d) head feature of the identical specimen with D (*strauchi*); (e) head feature of another alcohol preserved specimen of *G. liupanensis* (LP1); (f) head feature of the identical specimen with F (*qinlingensis*). (C) and (c) are provided by Vivek (Indiansnakes.org).



Figure S2. Diet of *G. rubromaculatus*: (A) debris of moth picked up from the excrements of Y2; (B) vomited by Y3 after caught, identified as a female *Sideridis sp.*; (C) debris of moth from the excrements of Y5; (D) undigested neonate zokors (*Eospalax fontanierii*) discovered in the stomach of NWIPB 630064.

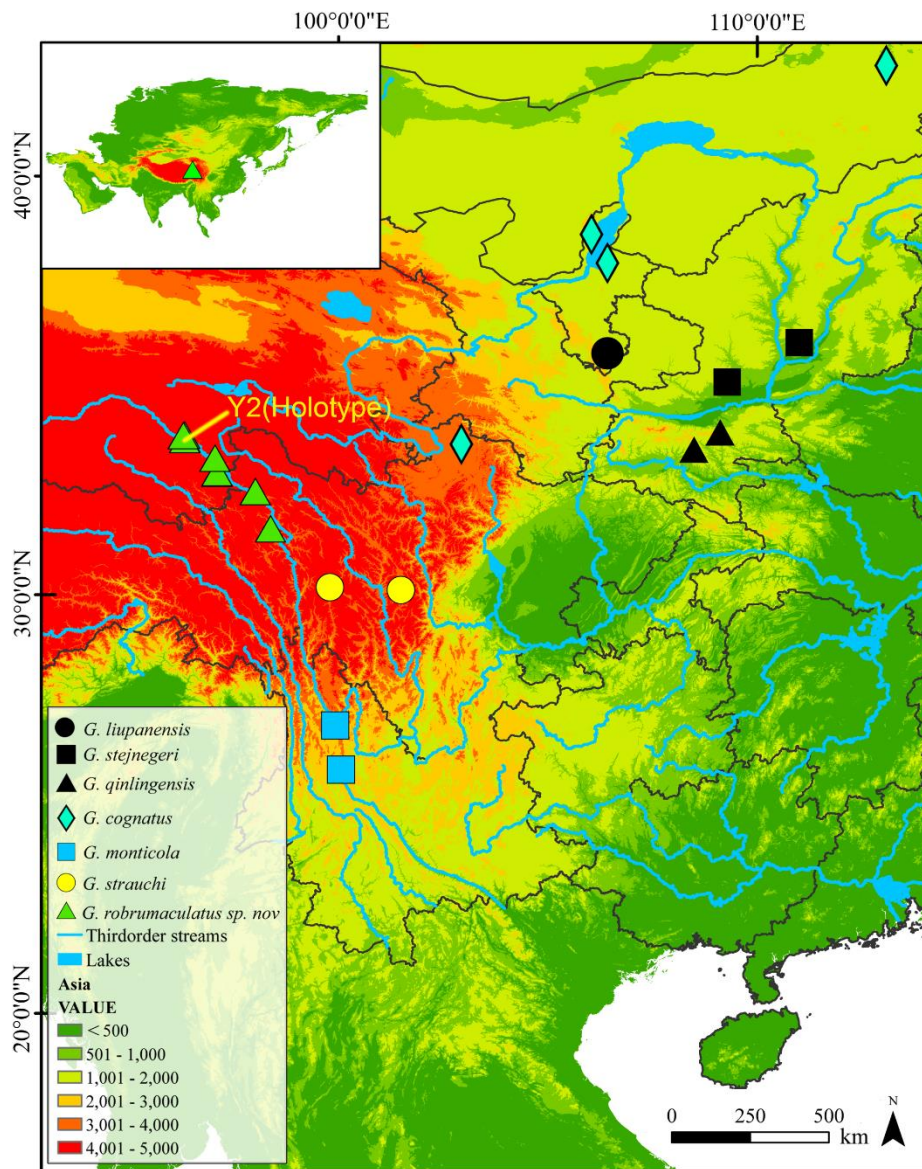


Figure S3. Sampling localities of the *Gloydus strauchi* complex. Green triangles: *G. rubromaculatus*; yellow circles: *G. strauchi*; blue squares: *G. monticola*; light blue diamond: *G. cognatus*; filled triangles: *G. qinlingensis*; filled circle: *G. liupanensis*; filled squares: *G. stejnegeri*. Type locality of the new species is showed as a large green triangle on the Thumbnails view of Asian, on the tope left of the map.

Part 2. Supplementary tables

Table S1. Primers and PCR protocols.

Marker	Annealing temperature	Primer	Primer Sequence	Reference
12S	50	12SFphe 12SRVal	AAAGTATAGCACTGAAAATG CGAGTGCTTTGTGTAAGCTAC	Knight and Mindell (1993)
16S	54	16sF-L 16sR-H	CAACTGTTTAACAAAAACAT CCGGTCTGAACTCAGATCACGT	Palumbi et al. (1991)
ND4	56	ND4 Leu	CACCTATGACTCCCAAAAGCCCATGT ATATTCTATTACTTGGATTTGCACCA	Arévalo et al. (1994)
CytB	48	L14919 H16064	AACCACCGTTGTACATCAACT CTTTGGCTTACAAGAACAATGCTTTA	Burbrink et al. (2000)

Note: Forward (F) and reverse (R) primers are given (in 5'-3' order), some of the nucleotides of each primer sequence are modified for better matching with the family Viperidae.

Table S2. Evolution models selected by Partitionfinder 2.1.1.

Partition names	Best model	# Sites	Use for analysis
ND4_1, cytb_1, 12s	GTR+I+G	1500	Phylogeny (ML, BI)
16s	GTR+I+G	475	Phylogeny (ML, BI)
cytb_2, ND4_2	K81UF+I+G	577	Phylogeny (ML, BI)
ND4_3, cytb_3	TIM+G	577	Phylogeny (ML, BI)
ND4	GTR	666	Corrected p-distance

Table S3. Corrected distance among the species of the genus *Gloydus* (ND4, Tamura-Nei model).

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
1 <i>G. changdaoensis</i> (C5)	-															
2 <i>G. intermedius</i> (SX1)	0.054	-														
3 <i>G. shedaoensis</i> (D2)	0.049	0.011	-													
4 <i>G. h. halys</i> (H9)	0.050	0.041	0.042	-												
5 <i>G. cognatus</i> (I3)	0.042	0.033	0.033	0.033	-											
6 <i>G. stejnegeri</i> (S4)	0.067	0.044	0.049	0.045	0.039	-										
7 <i>G. caraganus</i> (R290)	0.052	0.039	0.047	0.047	0.044	0.059	-									
8 <i>G. rickmersi</i> (R1)	0.066	0.052	0.051	0.054	0.049	0.066	0.052	-								
9 <i>G. qinlingensis</i> (QLS)	0.113	0.110	0.122	0.106	0.104	0.115	0.112	0.113	-							
10 <i>G. liupanensis</i> (GP198)	0.100	0.091	0.103	0.094	0.098	0.101	0.094	0.109	0.072	-						
11 <i>G. strauchi</i> (G3)	0.105	0.098	0.110	0.102	0.097	0.109	0.105	0.116	0.074	0.067	-					
12 <i>G. rubromaculatus</i> sp. n (Y2)	0.112	0.106	0.115	0.100	0.109	0.117	0.111	0.109	0.086	0.099	0.090	-				
13 <i>G. monticola</i> (DL2)	0.120	0.120	0.130	0.122	0.112	0.135	0.132	0.134	0.076	0.086	0.079	0.089	-			
14 <i>G. brevicaudus</i> (B1)	0.156	0.143	0.152	0.135	0.145	0.153	0.142	0.150	0.117	0.121	0.124	0.124	0.122	-		
15 <i>G. ussuriensis</i> (U1)	0.123	0.106	0.116	0.131	0.115	0.131	0.121	0.133	0.119	0.113	0.110	0.110	0.122	0.107	-	
16 <i>G. tsushimaensis</i> (Ts1)	0.126	0.104	0.116	0.125	0.114	0.131	0.119	0.123	0.109	0.104	0.101	0.112	0.110	0.104	0.036	-
17 <i>G. blomhoffii</i> (B524)	0.127	0.114	0.124	0.130	0.122	0.136	0.116	0.129	0.104	0.100	0.099	0.099	0.112	0.101	0.049	0.050

Part 3. Supplementary data blocks

Command block for RAxML

```
raxmlHPC -f a -m GTRGAMMA -p 12345 -x 12345 -# 1000 -s A8.phy -n T16 -o  
SCKT2668,acutus
```

Command block for MrBayes (calculated by partitionfinder 2.1.1)

```
begin mrbayes;  
  outgroup acutus;  
  outgroup SCKT2668;  
  charset Subset1 = 1399-2064\3 1-923 2065-3129\3;  
  charset Subset2 = 924-1398;  
  charset Subset3 = 1400-2064\3 2066-3129\3;  
  charset Subset4 = 2067-3129\3 1401-2064\3;  
  partition PartitionFinder = 4:Subset1, Subset2, Subset3, Subset4;  
  set partition=PartitionFinder;  
  lset applyto=(1) nst=6 rates=invgamma;  
  lset applyto=(2) nst=6 rates=invgamma;  
  lset applyto=(3) nst=6 rates=invgamma;  
  lset applyto=(4) nst=6 rates=gamma;  
  prset applyto=(all) ratepr=variable;  
  unlink statefreq=(all) revmat=(all) shape=(all) pinvar=(all) tratio=(all);  
  mcmc ngen=5000000 printfreq=1000 samplefreq=1000 nchains=4 savebrlens=yes;  
  sumt contype=allcompat burnin=0.25;  
log stop;  
end;
```