A new species of *Pareas* (Squamata, Pareidae) from southern Vietnam

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Abstract

We describe a new species of pareid snake from the Di Linh Plateau in Lam Dong Province of southern Vietnam based on morphological and molecular evidence. *Pareas temporalis* sp. nov. is distinguished from its congeners by having the combination of yellow-brown body colouration; hexagonal-shaped frontal, with lateral sides parallel to the body axis; 16–17 temporals, with 4–5 anterior temporals; loreal and prefrontal not contacting eye; 2–3 preoculars; two suboculars; 2–3 postoculars; 8–9 supralabials; 8–9 infralabials; 15–15–15 dorsal scale rows, all keeled, three vertebral scale rows enlarged; 191 (+1 preventral) ventrals, smooth; 92 subcaudals, all divided; undivided anal scale; two postocular stripes; and a solid dark brown vertebral stripe extending from rear of nuchal collar along the entire length of body and tail. Phylogenetic analyses of mitochondrial DNA data recovered the new species to be nested within the *P. carinatus* complex and to be the sister taxon to *P. nuchalis* from Borneo.

Keywords

Di Linh Plateau, integrative taxonomy, Pareatinae, *Pareas menglaensis*, Southeast Asia

Introduction

The genus *Pareas* is the most species-diverse genus in the subfamily Pareatinae and is distributed throughout tropical and subtropical parts of Asia (Rao and Yang 1992). It differs from other pareid genera by having 15 rows of dorsal scales at midbody, divided subcaudals, suboculars, supralabials not touching the eye, the anterior single inframaxillary, and three pairs of inframaxillaries (Grossmann and Tillack 2003). The monophyly of *Pareas* with respect to other pareid genera has been recovered with statistical support in some studies (e.g., Ding et al. 2020; Vogel et al. 2020), but not in others (e.g., Guo et al. 2011; Pyron et al. 2013; You et al. 2015; Figueroa et al. 2016; Liu and Rao 2021).

After 77 years without any descriptions of new species in the genus (from 1937 to 2014), seven new species have been described since 2015, mostly based on integrative taxonomic approaches incorporating molecular analyses and morphological comparisons (Liu and Rao 2021; Uetz...
et al. 2021; Vogel et al. 2021). These integrative taxonomic approaches have also clarified some taxonomic uncertainties in previously described species. For example, recent studies have shown *P. macularius* Theobald, 1868 to be a species distinct from *P. margaritophorus* (Jan, 1866) (e.g., Hauser 2017; Suntrarachun et al. 2020; Vogel et al. 2020) following their synonymy by Huang (2020). To the contrary, Liu and Rao (2021) considered *P. mengziensis*, a new species very recently described by Wang et al. (2020), to be conspecific with *P. niger* Pope, 1928 based on molecular and morphological data.

During field work in the Di Linh Plateau at the southernmost tip of the Truong Son mountain range in Vietnam, we discovered a single specimen of *Pareas* that differed in morphological and molecular data from all members of the genus. Based on these corroborated lines of evidence, we describe this species as new.

### Methods

Fieldwork was carried out by DTTL and TGT in Doan Ket Commune, Da Huoi District, Lam Dong Province, Vietnam, in July 2020. The specimen was stored in 75% ethanol after preserving liver in 99% ethanol. Specimens and tissue samples were deposited at the Lab of Zoology, University of Science, Ho Chi Minh City (UNS).

### Morphometrics

Measurements of the single Di Linh specimen were taken to the nearest 0.1 mm with dial calipers. Paired meristic characters are given as left/right. Measurements and meristic counts were taken following Wang et al. (2020). Morphological measurements (all in mm) and scale counts included snout-vent length (SVL); tail length (TaL); total length (TL); relative tail length (TaL/TL); number of dorsal scales counted at approximately one head length behind the head, midbody, and one head length before vent; ventral scales; subcaudal scales; supralabials; infralabials; number of keeled dorsal scale rows at midbody; anterior temporals; posterior temporals; preoculars; and postoculars.

Comparative data for other species were taken from relevant publications (Boulenger 1900; Boulenger 1914; Malkmus et al. 2002; Guo and Deng 2009; Stuebing et al. 2014; Vogel 2015; You et al. 2015; Bhosale et al. 2020; Ding et al. 2020; Suntrarachun et al. 2020; Vogel et al. 2020; Wang et al. 2020; Liu and Rao 2021; Vogel et al. 2021).

### Molecular sequencing

Total DNA was extracted from liver preserved in 99% ethanol using aTopPURE genomic DNA extraction kit (ABT Biological solutions company limited, Vietnam). Two mitochondrial gene fragments, cytochrome *b* (*cytb*) and NADH dehydrogenase subunit 4 and its flanking tRNAs (ND4), were amplified by the polymerase chain reaction (PCR) using the primers L14910/H16064 (Burbrink et al. 2000) and ND4/Leu (Arévalo et al. 1994). PCR conditions for *cytb* were denaturation at 94°C for seven minutes, followed by 40 cycles at 94°C for 40 seconds, 46°C for 30 seconds and 72°C for one minute, with a final extension step at 72°C for seven minutes. PCR conditions for ND4 were denaturation at 92°C for three minutes, followed by 35 cycles at 92°C for 45 seconds, 40°C for two minutes and 70°C for 1.5 minutes, with a final extension step at 70°C for five minutes. Sequences were edited using Chromas 2.6.6 (Technelysium Pty. Ltd.) and Geneious Prime 2021.1 (Biomatters Ltd.).

In addition, a 1,071 bp fragment of *cytb* of *P. nuchalis* (FK 2626; Table 1) was provided to the authors after being obtained as bycatch during a phylogenomic analysis by D. L. Rabosky et al. (in prep.). Newly generated sequences were deposited in GenBank under accession numbers MZ603792–MZ603794 (Table 1).

### Phylogenetic analysis

Homologous sequences of all currently recognized species of *Pareas*, two representatives of each of the pareid genera *Aplopeltura*, *Asthendipetas*, and *Xylophis*, and the xenodermatid outgroup *Achalinus rufescens* (following Figueroa et al. 2016, Deepak et al. 2018, Li et al. 2020) were downloaded from GenBank (Table 1). Newly generated and downloaded sequences were aligned using the default parameters in the MAFFT 7.45 alignment algorithm (Katoh and Standley 2013) implemented in Geneious Prime 2021.1.1 (Biomatters Ltd.). Alignments were visually checked to ensure that insertion-deletions did not disrupt translation of coding regions. The dataset was partitioned by tRNA and codon positions of *cytb* and ND4 for a total of seven partitions. The best-fit partitioning scheme and models of sequence evolution were selected using the Akaike Information Criterion (AICc) in Partition Finder 2 (Lanfear et al. 2017). Four partitions were selected with the models TVM+I+G for tRNA, and *cytb* and ND4 first codon positions; TVM+I+G for *cytb* and ND4 second codon positions; TRN+I+G for *cytb* third codon position; and TIM+I+G for ND4 third codon position.

Bayesian inference (BI) was performed on the partitioned dataset using MrBayes 3.2.7a (Ronquist et al. 2012) on the Cyber infrastructure for Phylogenetic Research (CIPRES) Science Gateway version 3.3 (Miller et al. 2010). In each of four independent analyses, four chains were run for 20 million generations using the default priors, trees were sampled every 4,000 generations, and the first 25% of trees were discarded as ‘burn-in’. The resulting trace plots were viewed using Tracer v.1.7 (Rambaut et al. 2018). A 50% majority-rule consensus of the post burn-in trees was constructed to calculate the posterior probabilities of nodes. Maximum likelihood (ML) analysis was performed on the partitioned dataset
Table 1. Samples used in the molecular phylogenetic analyses. Institutional and collector abbreviations of vouchers are defined in the source publications.

| Taxon                  | Voucher          | Locality                     | cytB            | ND4             | Sources                  |
|------------------------|------------------|------------------------------|-----------------|-----------------|--------------------------|

**Achalinus rufescens**
- HS 14023
  - China, Anhui, Qimen
  - China, Taiwan, Yilan
  - China, Guangdong

**Ap. boa**
- LSUHC 7248
  - Malaysia, Sabah, Sepilok
  - Malaysia, Sarawak, Bintulu

**Ap. boa**
- UMMZ 201905
  - Brunei, Belait

**Asthenedopus laevis**
- FMNH 241296
  - Malaysia, Sabah, Lahad Datu

**As. laevis**
- FMNH 273617
  - Malaysia, Sarawak, Bintulu

**Pareas andersonii**
- CAS 235359
  - Myanmar, Chin, Mt. Natmaataung

**P. atayal**
- NMNS 05594
  - China, Taiwan, Yilan, Beiheng

**P. atayal**
- HC 000618
  - China, Taiwan, Yilan

**P. boulengeri**
- None
  - Vietnam, Gia Lai, Kon Chu Rang

**P. boulengeri**
- KIZ 09965
  - China, Hubei, Enshi

**P. boulengeri**
- GP 2923
  - China, Guizhou, Jiangkou

**P. boulengeri**
- GP 207
  - China, Sichuan, Anxian

**P. boulengeri**
- GP 3095 = YBU 13323A
  - China, Hubei, Wufeng

**P. boulengeri**
- GP 4716
  - Yidu, Hubei, China

**P. boulengeri**
- GP 3428
  - China, Anhui, Xiyian

**P. boulengeri**
- GP 4827 = YBU 17155
  - China, Zhejiang, Chunan

**P. boulengeri**
- GP 4886 = YBU 17245
  - China, Zhejiang, Chunan

**P. carinatus**
- DL 2008-S039
  - Malaysia

**P. carinatus**
- GP 1079
  - Malaysia, Kuala Lumpur

**P. carinatus**
- GP 5131 = KIZ 011972
  - Malaysia, Kuala Lumpur

**P. carinatus**
- GP 5129 = KIZ 011970
  - Malaysia, Kuala Lumpur

**P. carinatus**
- CAS 247982
  - Myanmar, Taninthary, Ayeyu

**P. carinatus**
- LUSHC 10604
  - Malaysia, Kedah, Sungai Sedim

**P. chinensis**
- CIB 098269
  - China, Sichuan, Tianquan

**P. chinensis**
- GP 2196
  - China, Sichuan, Junlían

**P. chinensis**
- GP 2383
  - China, Sichuan, Hongya

**P. formosensis**
- GP 2146 = YBU 12015
  - China, Hainan

**P. formosensis**
- GP 2164
  - China, Hainan

**P. formosensis**
- GP 2165
  - China, Hainan

**P. formosensis**
- GP 2170 = YBU 12032
  - China, Hainan

**P. formosensis**
- GP 4581
  - China, Zhejiang, Jingning

**P. formosensis**
- GP 4659 = YBU 17029
  - China, Hainan

**P. formosensis**
- GP 2332 = YBU 12090
  - China, Guizhou, Leishan

**P. formosensis**
- GP 2384 = YBU 12115
  - China, Guizhou, Rongjiang

**P. formosensis**
- GP 3911 = YBU 14508
  - China, Guangxi

**P. formosensis**
- GP 3696
  - China, Jiangxi, Yanshan

**P. formosensis**
- GP 3808
  - China, Jiangxi, Yanshan

**P. formosensis**
- GP 3859 = YBU 14573
  - China, Jiangxi, Yanshan

**P. formosensis**
- NMNH 05637
  - China, Taiwan, Nantou, Xitou

**P. formosensis**
- H26-HAM01
  - China, Guangdong

**P. formosensis**
- ZMMU R-16684
  - Vietnam, Cao Bang, Phia Bac

**P. formosensis**
- ZMMU NAP-08868
  - Vietnam, Quang Nam, Song Thanh

**P. formosensis**
- ZMMU R-13709
  - Vietnam, Lam Dong, Bidaoup - Nui Ba

**P. formosensis**
- ZMMU R-14072
  - Vietnam, Dak Lak, Chu Yang Sin

**P. formosensis**
- ZMMU R-16333
  - Vietnam, Gia Lai, Kon Chu Rang

**P. geminatus**
- ZMMU NAP-09280 = R-16695
  - Laos, Xaisomboun, Long Tien

**P. geminatus**
- ZMMU R-16478
  - Thailand, Chiang Mai, Doi Inthanon

**P. geminatus**
- ZMMU R-16477
  - Thailand, Chiang Mai, Mae Kampang

**P. humptoni**
- AUP-00176
  - Thailand, Chiang Mai, Doi Inthanon

**P. humptoni**
- GP 5127 = YPX 18219
  - Myanmar, Kachin
using raxml GUI 2.0 (Edler et al. 2021). The GTR+I+G model was applied to the four partitions selected by PartitionFinder 2 (Lanfear et al. 2017) in a single analysis. Nodal support values were estimated by the thorough bootstrap with 1,000 pseudoreplicates. Nodes with posterior probabilities $\geq 0.95$ and bootstrap values $\geq 70$ were considered to be supported. Uncorrected pairwise ($p$) distances were calculated using PAUP* version 4.0a165 (Swofford 2003).
Results

Phylogenetic analysis

The dataset contained 1,971 aligned characters and 100 taxa. In the BI analysis, the standard deviation of split frequencies was 0.003490 among the four runs, and the Estimated Sample Sizes (ESS) of parameters were ≥ 2,248. The Di Linh Plateau taxon was deeply nested within the *P. carinatus* complex (sensu Ding et al. 2020; Vogel et al. 2021) and recovered with strong support in both the BI and ML analyses to be the sister taxon of *P. nuchalis*, with a Bayesian posterior probability (PP) of 0.99 (Fig. 1) and a ML bootstrap (BS) value of 74 (Fig. 2). In turn, these two species were sister to a clade containing *P. carinatus* and *P. menglaensis*, with a Bayesian PP of 1.00 (Fig. 1) and a ML BS value of 100 (Fig. 2).

The Di Linh specimen had an uncorrected pairwise divergence in the coding region of cyt b of 19.8% from *P. nuchalis* (*n* = 1), 19.8–20.2% from *P. carinatus* (*n* = 6), and 20.5–21.0% from *P. menglaensis* (*n* = 4). The Di Linh specimen had an uncorrected pairwise divergence in the coding region of ND4 of 17.9% from *P. nuchalis* (*n* = 1), 19.7–19.8% from *P. carinatus* (*n* = 4), and 19.6–19.8% from *P. menglaensis* (*n* = 4).

Taxonomy

*Pareas temporalis* sp. nov.

http://zoobank.org/DD72E44B-2EA4-4C34-AAB6-1799742733AF

Figures 3–5

Suggested Common Names. Di Linh Snail-eating Snake (English), Rắn hổ mây Di Linh (Vietnamese).

Holotype. UNS 09992 (field number LD25711), adult female, Vietnam, Lam Dong Province, Da Huoi District, Doan Ket Commune, 11.340370°N, 107.620561°E, 496 m a.s.l., coll. 25 July 2020 by Duong T.T. Le and Thinh G. Tran.

Diagnosis. *Pareas temporalis* sp. nov. is distinguished from all other *Pareas* by having the combination of yellow-brown body colouration; hexagonal-shaped frontal, with lateral sides parallel to the body axis; 16–17 temporals, with 4–5 anterior temporals; loreal and prefrontal not contacting eye; 2–3 preoculars; two suboculars; 2–3 postoculars; 8–9 supralabials; 8–9 infralabials (Fig. 4); 15–15–15 dorsal scale rows, all keeled (Fig. 3b), three vertebral scale rows enlarged; 191 (+1 preventral) ventrals, smooth; 92 subcaudals, all divided; undivided anal scale; two postocular stripes; and a solid dark brown vertebral stripe extending from rear of nuchal collar along the entire length of body and tail.

Description of the holotype. Adult female (Figs 3a, 5), SVL 426 mm; TaL 152 mm; TL 578 mm; TaL/TL 0.263. Body slender, compressed; head elongate, clearly distinct from neck; snout round in dorsal view; eye slightly enlarged, pupil vertical and slightly elliptical; rostral slightly visible in dorsal view; nasal scale single; two internasals, wider than long, contacting rostral, loreal, nasals, prefrontals; two prefrontals, large, not contacting eye; frontal hexagonal-shaped with lateral sides parallel to the body axis, frontal smaller than parietals; single loreal contacting nasal, internasals, prefrontal, preocular, 2nd and 3rd supralabial (left) or 2nd supralabial (right), below not contacting eye; 1/1 supraocular; 2/2 suboculars; 2/3 preoculars; 2/3 postoculars; 9/8 supralabial scales, 5th, 6th, 7th, 4th, 5th, 6th below (not touching) eye; 9th/8th longest; 16–17 temporals (4+3+4+6/5+3+4+4); 8/9 infralabials, without mental groove; three pairs of chin shields, not equal in size, anterior pair of chin shields longer than broad, slightly longer than two posterior pairs; dorsal scales in 15–15–15 rows, all keeled without apical pits; three enlarged vertebral scale rows; 191 ventrals (+1 preventral), all smooth; 92 subcaudals, all divided; undivided anal scale.

Colouration. In life, top of head light brown with dark brown spots. Sides of head with two postocular stripes; lower stripe extends from the postorbital to the 9th/8th supralabial; upper stripe extends from the upper corner of the eye to the temporal area, then divides into two long stripes, with the upper arms meeting at the nape, while the lower arm extends to the corner of the jaw and sides of the neck before converging to form a black nuchal collar (collar six scales long at mid-dorsals). Ground colour of dorsal brown with dark-brown speckling and numerous irregular black cross-bands on lateral sides of body from neck to vent (64 bands on left and 62 bands on right), and a solid dark-brown vertebral stripe extending from the posterior end of the black nuchal collar along entire length of body and tail. Ventrals light brown with dark brown spots on lateral edges and middle of each scale, spotting weaker on chin shields. Ventral surface of tail dark brown. Colouration in preservative as in life, but with dorsal faded to yellowish brown.

Distribution and natural history. *Pareas temporalis* sp. nov. is currently only known by the holotype specimen from Da Huoi District, Lam Dong Province, southern Vietnam (Fig. 6). The sampling site is located near to the boundary of BinhThuan Province, and so it is likely that the new species is also found in forested areas of that province. The holotype was found at night (2100 hours) on a tree branch 1.5 m above the ground in disturbed mixed broadleaf and bamboo forest, where it occurred in sympatry with *P. margaritophorus* (e.g., UNS 09993). No further information is currently known on the biology of the new species.

Etymology. The specific epithet *temporalis* L. refers to the high number of temporal scales in the new species.
Figure 1. Fifty percent majority-rule consensus phylogram resulting from partitioned Bayesian analysis of 1,971 aligned characters of the mitochondrial cytochrome 6 (cyt6), NADH dehydrogenase subunit 4 (ND4), and flanking tRNA genes of pareid snakes. Trees were rooted with Anchilosis rufescens (not shown). Numbers at nodes are Bayesian posterior probabilities. Sample information is provided in Table 1.
Figure 2. Maximum likelihood phylogeny based on a partitioned dataset containing 1,971 aligned characters of the mitochondrial cytochrome b (cyt b), NADH dehydrogenase subunit 4 (ND4), and flanking tRNA genes of pareid snakes. Trees were rooted with Achalinus rufescens (not shown). Numbers at nodes are bootstrap values based on 1,000 pseudoreplicates. Sample information is provided in Table 1.
Figure 3. Holotype female (UNS 09992) of *Pareas temporalis* sp. nov. in preservative. **a**: whole body in lateral view; **b**: keeled dorsal scales at midbody; **c**: ventral view of head; **d**: dorsal view of head; **e** and **f**: lateral views of head. Scale bars: 5 mm.

Figure 4. Head scalation of holotype female (UNS 09992) of *Pareas temporalis* sp. nov. in ventral, dorsal and lateral views. Illustration by Vo Ngoc Thinh.
Comparisons. *Pareas temporalis* sp. nov. differs from *P. margaritophorus*, *P. macularius*, *P. modestus* Theobald, 1868 and *P. andersonii* (Boulenger, 1888) by having a light brown dorsum with irregular dark bands (vs. uniform grey to black to dark colouration, and with bicolored spots in *P. margaritophorus*, *P. macularius* and *P. andersonii*); prefrontal not contacting the eye (vs. contacting); fully keeled dorsal scale rows at midbody (vs. not fully keeled); three enlarged vertebral scales (vs. not enlarged); and frontal hexagonal with lateral sides parallel to body axis (vs. frontal subhexagonal with lateral sides converging posteriorly) (Ding et al. 2020; Suntrarachun et al. 2020; Vogel et al. 2020; Wang et al. 2020; Vogel et al. 2021).

*Pareas temporalis* sp. nov. differs from *P. boulengeri* (Angel, 1920), *P. monticola* (Cantor, 1839), *P. stanleyi* (Boulenger, 1914), *P. vindumi* (Vogel, 2015), *P. victorianus* (Vogel, Nguyen, Zaw & Poyarkov, 2021) and *P. yunnanensis* Vogt, 1922 by having the prefrontal not contacting the eye (vs. contacting); loreal not contacting the eye (vs. contacting); two suboculars (vs. 0–1 or suboculars fused with postoculars); 2–3 postoculars (vs. 1–2 or postoculars fused with suboculars); fully keeled dorsal scale rows at midbody (vs. not fully keeled); 4–5 anterior temporals (vs. 1–2); and frontal hexagonal with lateral sides parallel to body axis (vs. frontal subhexagonal with lateral sides converging posteriorly) (Boulenger 1914; Guo and Deng 2009; Vogel 2015; Wang et al. 2020; Liu and Rao 2021; Vogel et al. 2021).

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Vogel, 2020, P. atayal You, Poyarkov & Lin, 2015, P. chinensis (Barbour, 1912), P. formosensis (Van Denburgh, 1909), P. hamptoni (Boulenger, 1905), P. iwasa-kii (Maki, 1937), P. komaii (Maki, 1931), P. niger Pope, 1928, P. xuelinensis Liu & Rao, 2021, P. nigriceps Guo & Deng, 2009 and P. kaduri Bhosale, Phansalkar, Sawant, Gowande, Patel & Mirza, 2020 by having the prefrontal not contacting eye (vs. contacting, except in P. nigriceps); two suboculars (vs. one or suboculars fused with postoculars); 2–3 preoculars (vs. one); fully keeled dorsal scale rows at midbody (vs. not fully keeled); 4–5 anterior temporals (vs. 1–3); and frontal hexagonal with lateral sides parallel to body axis (vs. frontal subhexagonal with lateral sides converging posteriorly) (Guo and Deng 2009; You et al. 2015; Bhosale et al. 2020; Ding et al. 2020; Wang et al. 2020; Vogel et al. 2021). Guo et al. (2011) suggested that the P. carinatus complex (as “Pareas I”) may represent a distinct genus from other “Pareas” on the basis of large $p$-distances, their lack of statistical support for the monophyly of Pareas with respect to Aplotelura and Asthenodipsas, and morphological diagnosability in having at least three anterior temporals, the frontal scale hexagonal with the lateral sides parallel to the body axis, and the anterior pair of chin shields broader than long. Our molecular phylogenetic analyses found P. temporalis sp. nov. to be a fourth member of the P. carinatus complex, and consistent with Guo et al.’s (2011) morphological diagnosis of the clade.

The description of Pareas temporalis sp. nov. from southern Vietnam brings the total number of recognized Pareas species to 25, of which seven occur in Vietnam (P. carinatus, P. formosensis, P. hamptoni, P. macularius, P. margaritophorus, P. monticola, and P. temporalis sp. nov.) (Nguyen et al. 2009; Ding et al. 2020). However, with only one specimen collected, information on the precise distribution, natural history, ecology, population status and conservation of the new species is unknown, as with many other Pareas species (see IUCN 2021; Uetz et al. 2021). We suggest that the new species be considered Data Deficient (DD) following IUCN’s Red List categories (IUCN 2021). However, it should be noted that the type locality of P. temporalis sp. nov. consists of disturbed forest on the Di Linh Plateau where no protected areas have been established. Remaining natural forests in the area are under high degree of threat from conversion to agricultural lands and commercial crops. Further surveys for P. temporalis sp. nov., and the possible existence of other endemic lineages on the Di Linh Plateau, are warranted.

**Discussion**

Recent phylogenetic analyses of Pareas have revealed that the genus contains two major clades, the P. carinatus complex/group (Ding et al. 2020; Vogel et al. 2021; referred to “Pareas I” by Guo et al. 2011) consisting of P. carinatus, P. nuchalis, and P. menglaensis, and a second clade consisting of all other congeners (Guo et al. 2011; Ding et al. 2020; Vogel et al. 2020; Wang et al. 2020; Vogel et al. 2021). Guo et al. (2011) suggested that the P. carinatus complex (as “Pareas I”) further differs from P. nuchalis by having prefrontal not contacting eye (vs. contacting); 191 ventrals (vs. 195–220); and 92 subcaudals (vs. 102–120). Pareas temporalis sp. nov. further differs from P. menglaensis by having 191 ventrals (vs. 176–177); 92 subcaudals (vs. 65–79); 2–3 postoculartes (vs. one); 15 dorsal scale rows keeled at midbody (vs. 11); and two black postorbital stripes on lateral side of head (vs. one thin postorbital stripe extending from postocular to neck on lateral side of head) (Boulenger 1900; Malkmus et al. 2002; Guo and Deng 2009; Stuebing et al. 2014; Ding et al. 2020; Wang et al. 2020; Vogel et al. 2021).

![Figure 6. Holotype locality of Pareas temporalis sp. nov. (black star) in Lam Dong Province, Vietnam.](image-url)
An updated key to the P. carinatus complex is provided below:

1 Prefrontal in contact with eye, ≥ 102 subcaudals (Borneo) ................................................................. P. nuchalis
– Prefrontal not in contact with eye, < 102 subcaudals............................................................................. 2
2 All dorsal scale rows keeled at midbody, 4–5 anterior temporals, anterior pair of chin shields longer than broad ...
– Some dorsal scale rows keeled at midbody, three anterior temporals, anterior pair of chin shields broader than long.................................................................................................................. P. temporalis sp. nov.
3 One preocular, a black line from eye to nape, and another from behind eye to angle of mouth ............. P. carinatus
– Two preoculars, a thin postorbital stripe extending from postocular to neck ........................................ P. menglaensis

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Competing interests

The authors have declared that no competing interests exist.

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Barbour T (1912) Some Chinese vertebrates: amphibia and reptilia. Archives du Museum d’Histoire Naturelle De Paris 2: 4–20.

An updated key to the P. carinatus complex is provided below:

1 Prefrontal in contact with eye, ≥ 102 subcaudals (Borneo) ................................................................. P. nuchalis
– Prefrontal not in contact with eye, < 102 subcaudals............................................................................. 2
2 All dorsal scale rows keeled at midbody, 4–5 anterior temporals, anterior pair of chin shields longer than broad ...
– Some dorsal scale rows keeled at midbody, three anterior temporals, anterior pair of chin shields broader than long.................................................................................................................. P. temporalis sp. nov.
3 One preocular, a black line from eye to nape, and another from behind eye to angle of mouth ............. P. carinatus
– Two preoculars, a thin postorbital stripe extending from postocular to neck ........................................ P. menglaensis

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Competing interests

The authors have declared that no competing interests exist.

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