



Research article

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A new *Cyrtodactylus* (Squamata: Gekkonidae) from Binh Thuan Province, southern Vietnam

Sabrina OSTROWSKI¹, Minh Duc LE², Hanh Thi NGO³, Cuong The PHAM⁴,
 Trung My PHUNG⁵, Truong Quang NGUYEN⁶ & Thomas ZIEGLER^{7,*}

^{1,7}Cologne Zoo, Riehler Str. 173, D-50735 Cologne, Germany.

^{1,7}Institute of Zoology, University of Cologne, Zùlpicher Str. 47b, D-50674 Cologne, Germany.

^{2,3}Faculty of Environmental Sciences, University of Science, Vietnam National University, Hanoi, 334 Nguyen Trai Road, Hanoi, Vietnam.

^{2,3}Central Institute for Natural Resources and Environmental Studies, Vietnam National University, Hanoi, 19 Le Thanh Tong, Hanoi, Vietnam.

²Department of Herpetology, American Museum of Natural History, Central Park West at 79th Street, New York, New York 10024, USA.

^{4,6}Institute of Ecology and Biological Resources, Vietnam Academy of Science and Technology, 18 Hoang Quoc Viet Road, Hanoi, Vietnam.

⁵Institute of Applied Technology, 6 Tran Van On, Thu Dau Mot City, Binh Duong Province, Vietnam.

⁶Graduate University of Science and Technology, Vietnam Academy of Science and Technology, 18 Hoang Quoc Viet Road, Cau Giay, Hanoi, Vietnam.

* Corresponding author: ziegler@koelnerzoo.de

¹Email: sabrinaostrowski@mail.de

²Email: le.duc.minh@hus.edu.vn

³Email: ngohanhhus@gmail.com

⁴Email: cuongiebr@gmail.com

⁵Email: pmytrung@gmail.com

⁶Email: nqt2@yahoo.com

¹urn:lsid:zoobank.org:author:30862A2D-E20E-4FC2-B81C-A7E5FBF3E1C7

²urn:lsid:zoobank.org:author:785D605E-6A6F-4A67-BD18-7F40F426FC2C

³urn:lsid:zoobank.org:author:6B87B552-B68B-46A7-8678-4E6EAE01428A

⁴urn:lsid:zoobank.org:author:9ECAAF214-1F25-4B1A-8BEA-701B218E22BD

⁵urn:lsid:zoobank.org:author:F05DF764-A42C-4993-B570-04E351E31A7D

⁶urn:lsid:zoobank.org:author:822872A6-1C40-461F-AA0B-6A20EE06ADBA

⁷urn:lsid:zoobank.org:author:5716DB92-5FF8-4776-ACC5-BF6FA8C2E1BB

Abstract. We describe a new species of *Cyrtodactylus* on the basis of two specimens collected from Ta Kou Nature Reserve, Binh Thuan Province, southern Vietnam. *Cyrtodactylus chungii* sp. nov. is distinguished from the remaining Indochinese bent-toed geckos by a combination of the following characters: relatively small body size (SVL up to 68.5 mm); a continuous neckband; 5 or 6 irregular transverse dorsal bands; 11 or 12 bands on original tail; keeled tubercles present on dorsum, posterior limbs and tail; 17 or 18 irregular dorsal tubercle rows; 30 or 31 ventral scale rows; ventrolateral skin

folds indistinct; an angular series of seven precloacal pores in male and six pitted, enlarged precloacal scales in female, each series separated by a diastema of undifferentiated scales from 4–6 enlarged, poreless femoral scales; median subcaudals slightly enlarged; 17–20 subdigital lamellae under the fourth toe. Based on molecular analyses of the fragment of mitochondrial gene cytochrome c oxidase subunit I (COI), the new species is recovered as the sister taxon to *Cyrtodactylus cattienensis* s. str. with a genetic divergence of more than 9%. In phylogenetic analyses, the new species is recovered as a member of the *Cyrtodactylus irregularis* species group.

Keywords. *Cyrtodactylus chungi* sp. nov., molecular phylogeny, taxonomy, Ta Kou Mountain, COI gene.

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Introduction

The gekkonid genus *Cyrtodactylus* Gray, 1827 is by far the most speciose with many new species being described every year (Grismer *et al.* 2018; Murdoch *et al.* 2019). A total of 305 species have been recognized to date (Uetz *et al.* 2020). Vietnam has been a hotspot of new discoveries with 43 recorded species (Nazarov *et al.* 2012; Luu *et al.* 2017; Ostrowski *et al.* 2020; Uetz *et al.* 2020). *Gymnodactylus peguensis* var. *irregularis* was described by Smith (1921a) from an open pine forest at Camly in the Langbian Plateau, Vietnam. Nazarov *et al.* (2008) suggested that this and all other allied species belonged to a species complex (Nazarov *et al.* 2012; Pauwels *et al.* 2018). The *C. irregularis* complex has recently been the subject of numerous morphological and molecular studies. So far, 20 species have been described along with several additional populations whose taxonomic status is unresolved or still unknown (S.N. Nguyen *et al.* 2017; Pauwels *et al.* 2018; Ostrowski *et al.* 2020; Uetz *et al.* 2020). Thus, Neang *et al.* (2020) described *C. phnomchiensis*, the only member of the *C. irregularis* complex, which occurs west of the Mekong River in Kampong Thom Province, Cambodia.

S.N. Nguyen *et al.* (2017) investigated the effectiveness of DNA barcoding based on the COI gene using 164 samples of Vietnamese bent-toed geckos within the *C. irregularis* complex. They discovered eleven unnamed lineages from different localities, including the population analyzed in this study. Based on an integrative taxonomic approach, viz. combining morphological and molecular data, we herein clarify the status of the *Cyrtodactylus* population from Ta Kou, Binh Thuan Province.

Material and methods

Sampling

Field surveys were conducted in Ta Kou Nature Reserve, Ham Thuan Nam District, Binh Thuan Province, southern Vietnam in June 2017 (Fig. 1). Specimens were euthanized in a closed vessel with a piece of cotton wool containing ethyl acetate (Simmons 2002), fixed in 80% ethanol and subsequently stored in 70% ethanol. Specimens were deposited in the collections of the Institute of Ecology and Biological Resources (IEBR), Hanoi, Vietnam.

Molecular data and phylogenetic analyses

All taxa of the *Cyrtodactylus irregularis* species complex were included in our analyses. Available sequences of the species were obtained from GenBank. Two new samples from a population in Ta Kou Mountain, Binh Thuan Province of southern Vietnam (IEBR 4581 and 4582) were included in the analysis. Two species, *C. spelaeus* Nazarov, Poyakov, Orlov, Nguyen, Milto, Martynov, Konstantinov &



Fig. 1. Map of Vietnam showing the type locality of *Cyrtodactylus chungii* sp. nov. in Binh Thuan Province.

Chulisov, 2014 and *C. wayakonei* Nguyen, Kingsada, Rösler, Auer & Ziegler, 2010, were used as an outgroup based on the results from Luu *et al.* (2016).

DNA was extracted using a DNeasy Blood and Tissue kit (Qiagen, Germany) following the manufacturer's instruction. Extracted DNA was amplified by HotStar Taq PCR mastermix (Qiagen, Germany) with 21 µl volume (10 µl of mastermix, 5 µl of water, 2 µl of each primer at 10 pmol/ml and 2 µl of DNA). PCR condition was: 95°C for 15 minutes to active the taq; with 40 cycles at 95°C for 30 s, 45°C for 45 s, 72°C for 60 s; and the final extension at 72°C for 6 minutes. A fragment of the mitochondrial gene, cytochrome c oxidase subunit I (COI), was amplified using the primer pair VF1-d (5'-TTCTCAACCAACCACAARGAYATYGG-3') and VR1-d (5'-TAGACTTCTGGGTGGCCRAARAAYCA-3') (Ivanova *et al.* 2006).

PCR products were visualized using electrophoresis through a 2% low melting-point agarose gel stained with ethidium bromide. Successful amplifications were purified to eliminate PCR components using GeneJET™ PCR Purification kit (ThermoFisher Scientific, Lithuania). Purified PCR products were sent to FirstBase (Malaysia) for sequencing.

After sequences were aligned by Clustal X ver. 2 (Thompson *et al.* 1997), data were analyzed using maximum parsimony (MP) as implemented in PAUP*4.0b10 (Swofford 2002), maximum likelihood (ML) in IQ-TREE ver. 1.6.7.1 (Nguyen *et al.* 2015), and Bayesian inference (BI) in MrBayes ver. 3.2 (Ronquist *et al.* 2012). For MP analysis, heuristic analysis was conducted with 100 random taxon addition replicates using tree-bisection and reconnection (TBR) branch swapping algorithm, with no upper limit set for the maximum number of trees saved. Bootstrap support (BP) was calculated using 1000 pseudo-replicates and 100 random taxon addition replicates. $BP \geq 70$ was considered strong support for the clade (Hillis & Bull 1993). All characters were equally weighted and unordered. For the maximum likelihood (ML) analysis, the analysis was run with a single model and 10 000 ultrafast bootstrap replications using the command `iqtree -s matrix.nex -m TIM+I+G -bb 10000`. Ultrafast bootstrap $\geq 95\%$ was regarded as significant (Nguyen *et al.* 2015) The optimal model for nucleotide evolution was determined using Modeltest ver. 3.7 (Posada & Crandall 1998).

For BI analysis, we used the optimal model on an unpartitioned data set determined by Modeltest with parameters estimated by MrBayes ver. 3.2.1. Two independent analyses with four Markov chains (one cold and three heated) were run simultaneously for 10 million generations with a random starting tree and sampled every 1000 generations. Log-likelihood scores of sample points were plotted against generation time to determine stationarity of Markov chains. Trees generated before log-likelihood scores reached stationarity were discarded from the final analyses using the burn-in function. The posterior probability (PP) values for all clades in the final majority rule consensus tree were provided. $PP \geq 95\%$ were deemed strong support for a clade (Ronquist *et al.* 2012). The optimal model for nucleotide evolution was set to TIM+I+G for ML and combined Bayesian analyses as selected by Modeltest ver. 3.7. The cutoff point for the burn-in function was set to 30 in the Bayesian analysis, as -lnL scores reached stationarity after 30 000 generations in both runs. Uncorrected pairwise divergences were calculated in PAUP*4.0b10.

Morphological characters

Measurements were taken with a digital calliper to the nearest 0.1 mm.

Abbreviations

- AG = trunk length or axilla-groin distance, from posterior edge of forelimb insertion to anterior edge of hindlimb insertion
- ED = ear diameter, measured vertically

EyeEar	=	eye to ear distance, from anterior edge of ear opening to posterior margin of orbit
ForeaL	=	forearm length, from base of palm to elbow
HH	=	maximum head height, from occiput to underside of jaws
HL	=	head length, from tip of snout to process of the lower jaw
HW	=	maximum head width
Interorb	=	interorbital distance
MH	=	mental height
MW	=	mental wide
OD	=	greatest diameter of orbit, measured horizontally
RH	=	rostral height
RW	=	rostral wide
SE	=	snout to eye distance, from tip of snout to anterior margin of orbit
SnOrb	=	snout to orbit distance, from the tip of the snout to the anteriormost margin of the orbit
SVL	=	snout-vent length, from tip of snout to anterior margin of cloaca
TaL	=	tail length, from posterior margin of cloaca to tip of tail
TibiaL	=	tibia length, ventral from the posterior surface of the knee to the heel

Scale counts

DTR	=	dorsal tubercle rows
EFS	=	enlarged femoral scales
EPS	=	enlarged precloacal scales
FP	=	femoral pores
GST	=	granular scales surrounding dorsal tubercles
IL	=	infralabials
IN	=	postrostrals or internasals
N	=	nasal scales surrounding naris
NSF	=	number of subdigital lamellae on the fourth finger
NST	=	number of subdigital lamellae on the fourth toe
ParaTub	=	paravertebral tubercles, number of paravertebral tubercles between the limbs insertions immediately left of the vertebral column
PM	=	postmentals
PP	=	precloacal pores, deep pores with waxy exudates
PPi	=	pitted precloacal scales, flat depressions without waxy exudates
SL	=	supralabials
V	=	ventral scales in longitudinal rows at midbody between the ventrolateral skin folds

Bilateral scale counts were given as left/right.

Results

Based on the molecular data, *Cyrtodactylus chungii* sp. nov. is placed in a clade with *C. cattienensis* s. str. (Fig. 2). Besides the many similarities like the closed neck band, an X-shaped shoulder band, 5 or 6 irregular transverse dorsal bands (vs 4–6) and 11 or 12 transverse bands on the tail (vs 4–12) it was found that there are still distinct differences. The new species can be distinguished from *C. cattienensis* s. str. by a median row of slightly enlarged subcaudal scales, dark brown transversal bands of the tail narrower than the light brown spaces (vs wider transversal bands than the light spaces), by the presence of pitted, enlarged precloacal scales in the female (6 vs absence), by the higher number of tubercle rows on the tail (6 vs 4), which are strongly to slightly keeled (vs anteriorly keeled tubercle) and by the relatively strongly keeled tubercles on the hindlimbs (vs smooth tubercles).

Phylogenetic analyses

The alignment contained no gaps and the final matrix consisted of 652 aligned characters. Of these, 244 were parsimony informative. The MP analysis of the dataset recovered a single most parsimonious tree with 1328 steps (CI = 0.35; RI = 0.65). The topology derived from BI was largely similar to those of Luu *et al.* (2017) and Pauwels *et al.* (2018). Although the phylogenetic tree supported by Pauwels *et al.* (2018) is better resolved, most of the deep nodes in this study are insignificantly supported. There are a few discrepancies between our phylogenetic hypothesis and that of Pauwels *et al.* (2018), in particular, the position of *Cyrtodactylus phuocbinhensis* Nguyen, Le, Tran, Orlov, Lathrop, Macculloch, Le, Jin, Nguyen, Nguyen, Hoang, Che, Murphy & Zhang, 2013. This species was supported as the sister species to *C. sangi* Pauwels, Nazarov, Bobrov & Poyarkov, 2018 + *C. cattienensis* Geissler, Nazarov, Orlov, Böhme, Phung, Nguyen & Ziegler, 2009 in our BI and ML analyses (Fig. 2), but it was shown as the basal taxon of a large clade, including *C. kingsadai* Ziegler, Phung, Le & Nguyen, 2013, *C. taynguyenensis* Nguyen, Le, Tran, Orlov, Lathrop Macculloch, Le, Jin, Nguyen, Nguyen, Hoang, Che, Murphy & Zhang, 2013, *C. takouensis* Ngo & Bauer, 2008 among others with also high statistical values from both BI and ML in Pauwels *et al.* (2018: fig. 2). In our study, however, we incorporated more species and used different outgroups than did in Pauwels *et al.* (2018), and these changes might have caused the differences.

The phylogenetic results show that the new species from Ta Kou Mountain, Binh Dinh Province was recovered as the sister taxon to *C. cattienensis* s. str. with a high statistical support (all equal to 100%) in all analyses (Fig. 2). In terms of genetic divergences, the new species is separated from *C. cattienensis* s. str. with uncorrected p-distance of 9.4–9.5%. It is also significantly divergent from other species within the *C. irregularis* species group with the pairwise divergence of 14.2–18.3%. Genetic divergences between other species in the group are shown in the distance matrix (Supplementary File 1).

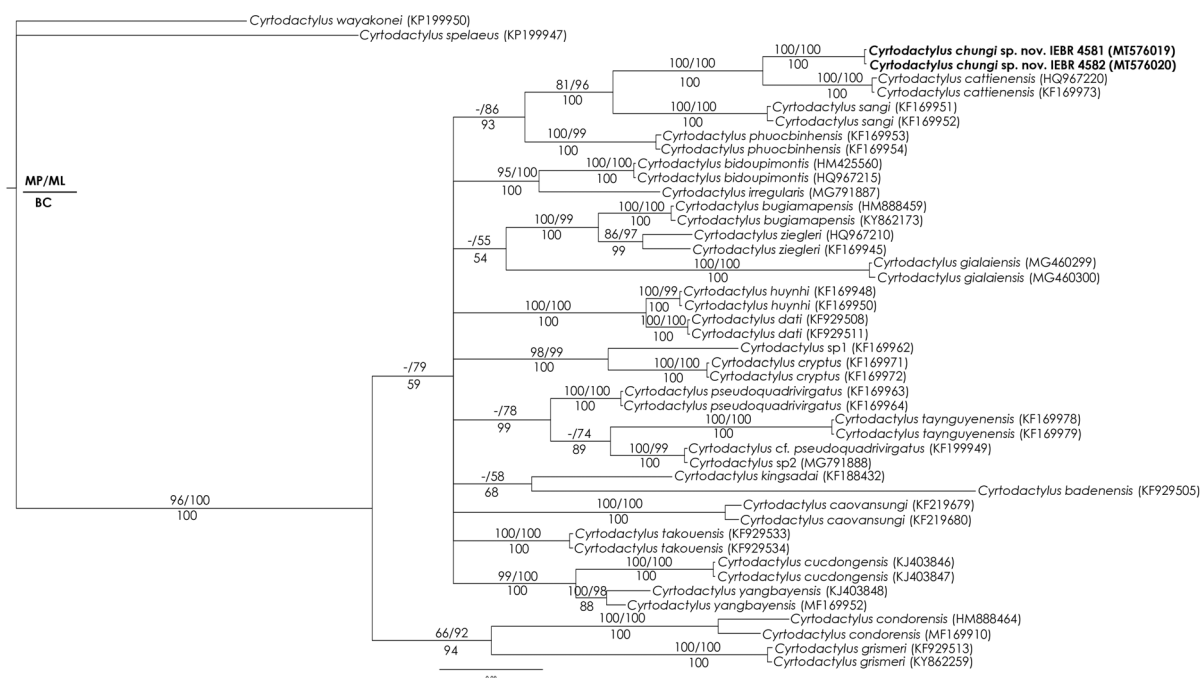


Fig. 2. Phylogram based on the Bayesian analysis. Number above and below branches are MP/ML bootstrap values and Bayesian posterior probabilities (> 50%), respectively.

Morphological analyses

Class Reptilia Laurenti, 1768
Order Squamata Oppel, 1811
Family Gekkonidae Gray, 1825
Subfamily Gekkoninae Gray, 1825
Genus *Cyrtodactylus* Gray, 1827

***Cyrtodactylus chungii* sp. nov.**

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Figs 3–8

Diagnosis

The new species can be distinguished from other members of the genus *Cyrtodactylus* by a combination of the following characters (Table 1): relatively small body size (SVL up to 68.5 mm); a continuous neckband; 5 or 6 irregular transverse dorsal bands; 11 or 12 bands on original tail; keeled tubercles present on dorsum, posterior limbs and tail; 17 or 18 irregular dorsal tubercle rows; 30 or 31 ventral scale rows; ventrolateral skin folds indistinct; an angular series of seven precloacal pores in male and six pitted, enlarged precloacal scales in female, each series separated by a diastema of undifferentiated scales from 4–6 enlarged, poreless femoral scales; median subcaudals slightly enlarged; 17–20 subdigital lamellae under the fourth toe.

Etymology

Specific epithet ‘*chungii*’ is in honor of Prof. Dr Ngo Dac Chung, College of Education, Hue University, in recognition of his outstanding contributions to training of many herpetologist generations from Hue University. For the common names we suggest Chung’s Bent-toed Gecko (English) and Thạch sùng ngón chúng (Vietnamese).

Type material (Figs 3–8)

Holotype

VIETNAM • ♂; Southern Vietnam, Ham Thuan Nam District, Binh Thuan Province, Ta Kou Nature Reserve; 10°48.868' N, 107°53.523' E; 424 m a.s.l.; 20 Jun. 2017; T.M. Phung leg.; Field No. BT2017.1; sequence with GenBank accession number MT576019; IEBR 4581.

Paratype

VIETNAM • 1 ♀; same collection data as for holotype; Field No. BT2017.2; sequence with GenBank accession number MT576020; IEBR 4582.

Description of holotype

Adult male, snout-vent length (SVL) 66.6 mm; tail length (TL) 62.7 mm (45.1 mm regenerated); head distinct from neck, relatively long (HL: 20.1 mm; HL/SVL ratio 0.32), HW 13.3 mm (HW/HL ratio 0.66), HH 7.8 mm (HH/HL ratio 0.4); loreal region slightly bulged; snout elongated and rounded (SE: 7.6; SE/HL ratio 0.38); eye diameter 4.4 mm, more than half of snout-eye distance (OD/SE ratio 0.58); median snout scales small and rounded; eyes relatively small compared to head (OD/HL ratio 0.22); anterior supraciliaries large and rounded, posterior supraciliaries small and tapered; ear openings relatively small (ED: 0.75 mm; ED/HL ratio 0.04), vertical and oval in shape; eye to ear distance slightly longer than eye diameter (EyeEar/ED ratio 1.39); rostral wider than high (RH: 1.65 mm; RW: 3.3 mm; RW/RH ratio 2), with an inverse, Y-shaped median suture, surrounded by first supralabial, two nostrils, two supranasals and internasal; lateral nostrils elongated, oval and

Table 1. Measurements (in mm) and morphological characters of type series of *Cyrtodactylus chungii* sp. nov. * = regenerated or broken tail; bilateral meristic characters are given as left/right.

characters	IEBR 4581 (holotype)	IEBR 4582 (paratype)
Sex	♂	♀
SVL	66.6	68.55
TL	62.75* (45.1*)	82.15*
AG	27.5	28.8
ForeaL	10.2	10.2
TibiaL	11.2	11.2
HH	7.8	7.7
HL	20.1	20.4
HW	13.3	12.4
OD	4.4	4.4
EyeEar	6.1	5.8
SE	7.6	27.5
SnOrb	4.3	4.75
InterOrb	4.6	5.35
ED	0.75	0.75
RH	1.65	1.35
RW	3.3	3.4
MH	1.7	2.0
MW	2.6	2.7
SL	12/11	12/11
IL	9/9	8/9
N	4/5	4/4
IN	1	3
PM	2	2
DTR	18	17
ParaTub	24	27
GST	9–11	10–11
V	31	30
PPi/PP	0/7	6/0
EPS	45	41
FP	0	0
EFS	6/4	6/6
NSF	16/15	18/18
NST	17/17	20/20

surrounded by rostral, first supralabial, three postnasals and one supranasal; supranasals separated by one internasal; eye separated from supralabials by 3 or 4 scale rows; mental triangular, wider than high (MW: 1.75 mm; MH 2.6 mm; MW/MH ratio 1.49), surrounded by first two infralabials and posteriomediaally by postmentals; supralabials 10/9; infralabials 9/9; body slender and short (AG/SVL ratio 0.41); ventrolateral skin folds not developed; dorsal scales granular, heterogeneous in shape and size; dorsal tubercles present in posterior part of head, extremities, dorsum and first third of tail; postocular tubercles irregularly distributed, rounded, flat and about three times size of surrounding granular scales; median dorsal tubercles about five times as large as granular scales, oval, and not keeled; posterior dorsal tubercles keeled and on sacral region very strongly keeled up to base of tail; 18 irregular transversal dorsal tubercle rows; 24 paravertebral tubercles; each tubercle surrounded by 9 or 10 granular scales; ventrals smooth, oval and slightly imbricate, in 31 longitudinal rows; gular scales homogeneous; dorsal surfaces of upper and lower arms without tubercles, but occasionally enlarged granular scales; left thigh with series of 6 enlarged femoral scales separated by diastema of 6 smaller scales from precloacal scales; right thigh with series of 3 enlarged femoral scales separated by diastema of 8 smaller scales from precloacal scales and single enlarged femoral scale distally; no femoral pores; 45 enlarged precloacal scales arranged in diamond shape, with angled series of 7 pore-bearing scales (3 right, 1 angled, 3 left); 15 posteriorly enlarged scales and 21 anteriorly enlarged scales; two postcloacal tubercles on each side; scales on palms and soles rounded to oval, smooth and arched; fore- and hindlimbs moderately long (ForeaL/SVL ratio 0.15; Tibia/SVL ratio 0.17) relatively narrow; toes and fingers narrow and curved at interphalangeal joint; slightly transparent, pointed and curved claws, bordered ventrally by large lamella and dorsally by small, narrow scale; subdigital lamellae proximally larger, widened and merge basally into smaller scales of palm and sole surfaces; distal lamellae smaller, more elongated and distally increasingly imbricate; right fourth finger with 15 subdigital lamellae (6 proximal, 9 distal); left fourth finger with 16 subdigital lamellae (5 proximal, 11 distal); right and left fourth toe with 17 subdigital lamellae each (6 proximal, 11 distal); base of tail with small granular supracaudals and strongly keeled, rounded tubercles; last two thirds of tail regenerated, scales heterogeneously arranged and shaped; tubercles of original part arranged in 6 transverse rows (8/-/4/4/4/4) in a distance of 6–7 granular scale rows; tubercles slightly keeled; subcaudals of original part oval, rounded and imbricate; median subcaudals about two to three times larger than the lateral scales, but not transversely enlarged, or arranged in definable rows.

Coloration in preservative (Figs 5–8)

Ground color of head, neck, limbs and tail grey to light brown; dorsal surface of head brown with irregular, small, dark brown spots; two larger dark brown blotches located in posterior interorbital area and two other dark brown blotches in occiput area; skin above eyes dark grey, blue to black; rostral dark brown; supralabials and infralabials also brown, turning to cream at adjacent areas; a distinct dark brown stripe in loreal region, reaching to third supralabial; nuchal loop dark brown, in V-shape, extending from posterior corner of eye to the neck, edged in light grey; tubercles on head, limbs, dorsum and tail light to dark brown; tubercles on lateral skin fold white to gray; dorsal surfaces of limbs with small, irregularly distributed, dark brown spots; dorsal surface of toes and fingers dark brown spotted with light grey; dorsum with 5 irregular transverse dark brown bands; first band over the shoulder region, X-shaped; dark and light brown spots present between transverse bands and on flanks; ventral scales of body light grey to cream; lateral sides of head, below postocular stripe, and ventrolateral margins of flanks slightly white to cream; anterior part of tail with two transverse, dark brown bands dorsally with dark brown spots in interspaces; dark, transverse dorsal bands separated from underside of tail by light brown, whitish spotted sides of tail; tail light grey to cream ventrally and marbled brown on the original part; regenerated part of tail grey to light brown, marbled.

Coloration in life

Ground color of dorsal surface of head, limbs and dorsum bright-yellow; transverse body and tail bands darker; lateral head and belly with bright-yellow spots; marbling of surface of limbs darker; ventral surface white to light blue (Figs 3–4).

Sexual dimorphism and variation

The morphological characteristics of the female IEBR 4582 correspond well with the holotype (IEBR 4581) and differ only in a few details. The female has some slightly keeled tubercles on the dorsal surface of the forelimbs. Dorsal tubercles are keeled from the posterior insertion of the forelimbs. The two supranasals are separated by two internasals. Another internasal is inserted between the rostral and the two internasals. Two inverse sutures are X-shaped from the lower edges of the internasal and do not form a median suture. The tail is original. The median subcaudals are about twice as large as the supracaudals and extend to the tip of the tail. The two dark brown spots of the occiput are longer and larger. The neck band is also V-shaped but pointed posteriorly. The dorsal surfaces of the forearms and hindlimbs with fine, irregular, transverse stripes. Dorsum with 6 transverse, irregular bands. The first band, between the insertion of the forelimbs, is clearly X-shaped over the shoulder region. Between the neck band and the first body band is an oval, dark brown spot. The dorsal tubercles are clearly lighter. The dorsal side of the tail bears 11–12 transverse, dark brown bands, which completely enclose only the last third. Between these bands are irregular, fine, light brown to brown stripes and dots. The first two thirds of the underside of the tail are marbled light grey to brown. The last third resembles the dorsal side.

Comparison

We compared the new species with its 19 congeners from the *Cyrtodactylus irregularis* complex based on an examination of specimens (Table 2) and data obtained from the literature (Smith 1921a, 1921b; Ziegler *et al.* 2002, 2013; Heidrich *et al.* 2007; Orlov *et al.* 2007; Nazarov *et al.* 2008, 2012; Ngo & Bauer 2008; Rösler *et al.* 2008; Geissler *et al.* 2009; Ngo & Chan 2010; Ngo 2013; Nguyen *et al.* 2013; Schneider *et al.* 2014; Luu *et al.* 2017; Pauwels *et al.* 2018; Neang *et al.* 2020; Ostrowski *et al.* 2020). The new species can be distinguished from all other *Cyrtodactylus* species from Vietnam by morphological characteristics (see Table 3).

In comparison with the species from the *C. irregularis* complex *Cyrtodactylus chungii* sp. nov. is distinguished from *C. caovansungi* Orlov, Nguyen, Nazarov, Ananjeva & Nguyen, 2007, *C. kingsadai* Ziegler, Phung, Le & Nguyen, 2013, *C. takouensis* Ngo & Bauer, 2008 and *C. yangbayensis* Ngo & Chan, 2010 by the absence of transversely enlarged subcaudals.

The new species can be distinguished from *C. cryptus* Heidrich, Rösler, Vu, Böhme & Ziegler, 2007, *C. gialaiensis* Luu, Tran, Nguyen, Le & Ziegler, 2017, *C. pseudoquadrivirgatus* Rösler, Nguyen, Vu, Ngo & Ziegler 2008 and *C. taynguyenensis* Nguyen, Le, Tran, Orlov, Lathrop Macculloch, Le, Jin, Nguyen, Nguyen, Hoang, Che, Murphy & Zhang, 2013 by the presence of enlarged femoral scales.

The new species can be distinguished from *C. bidoupimontis* Nazarov, Poyarkov, Orlov, Phung, Nguyen, Hoang & Ziegler, 2012 by its smaller size (SVL of 66.6–68.5 vs 74.0–86.3 mm), fewer ventral scale rows (30–31 vs 38–43) and enlarged femoral scales (4–6 vs 8–10), more precloacal pores in the male (7 vs 4–6), the presence of 6 pitted precloacal scales in the female (vs absence) and by the different dorsal color pattern (irregular transversal bands vs irregular transversal bands with light borders).

Cyrtodactylus chungii sp. nov. differs from *C. bugiamapensis* Nazarov, Poyarkov, Orlov, Phung, Nguyen, Hoang & Ziegler, 2012 by having fewer ventral scale rows (30–31 vs 36–46) and enlarged femoral scales (4–6 vs 6–8), and by the different dorsal color pattern (irregular transversal bands vs round spots forming irregular transverse bands).



Fig. 3. *Cyrtodactylus chungi* sp. nov. in life. Top: holotype, ♂ (IEBR 4581). Bottom: paratype, ♀ (IEBR 4582). Photos T.M. Phung.

Table 2. Morphological comparisons between *Cyrtodactylus chungii* sp. nov. and its congeners of the *C. irregularis* complex (after Smith 1921a, 1921b; Ziegler *et al.* 2002, 2013; Heidrich *et al.* 2007; Orlov *et al.* 2007; Nazarov *et al.* 2008, 2012; Ngo & Bauer 2008; Rösler *et al.* 2008; Geissler *et al.* 2009; Ngo & Chan 2010; Ngo 2013; Nguyen *et al.* 2013; Schneider *et al.* 2014; Luu *et al.* 2017; Pauwels *et al.* 2018; Neang *et al.* 2020; Ostrowski *et al.* 2020). Symbols: / = data not available in literature; – = characteristic does not exist; + = characteristic exists but is not uniquely determined; * = broken or regenerated tail.

Species	SVL (mm)	TL (mm)	V	EFS	FP	PP (♂)	PP (♀)	LT4	Color pattern of dorsum	Enlarged subcaudals
<i>Cyrtodactylus chungii</i> sp. nov.	66.6–68.5	62.7*–82.1	30–31	4–6	–	7	6 (pitted)	17–20	banded	absent
<i>C. bidoupimontis</i>	74.0–86.3	75.0–86.0	38–43	8–10	–	4–6	0	18–23	banded	absent
<i>C. bugiamapensis</i>	58.6–76.8	65.3–83.0	36–46	6–8	–	7–11	0–7 (pitted)	17–20	blotched	absent
<i>C. caovansungi</i>	90.4–94.0	120.0	38–44	8	6	9	0	23–25	banded	transversally
<i>C. cattienensis</i>	43.5–69.0	51.0–64.7	28–42	3–8	–	6–8	0	14–19	banded	absent
<i>C. cryptus</i>	62.5–90.8	63.5–88.4	47–50	–	–	9–11	–	20–23	banded	absent
<i>C. cucdongensis</i>	55.8–65.9	22.1–27.8	35–44	5–9	–	5–6	4–6 (pitted)	15–20	banded	absent
<i>C. dati</i>	57.3–77.6	50.3–78.1	42–48	2–7	0–7	0–6	/	14–20	blotched	absent
<i>C. gialaiensis</i>	50.1–62.8	42.2–63.6*	38–45	–	–	9–10	0–8 (pitted)	25–17	banded	absent
<i>C. huynhi</i>	54.8–79.8	61.5–78.6	43–46	3–5	3–8 (♂)	7–9	0–8 (pitted)	17–21	banded	absent
<i>C. irregularis</i>	72.0–86.0	66.0–74.0	38–45	7–8	–	5–7	0–6	18–20	blotched	absent
<i>C. kingsadai</i>	83.0–94.0	117.0	39–46	9–12	0–7	7–9	4–8	21–25	banded	transversal
<i>C. phnomchiensis</i>	76.1–80.7	56.9–79.1	45–54	0–8	–	4–5	1–7 (pitted)	20–23	banded	absent
<i>C. phumyensis</i>	63.5–66.8	73.2*–74.6*	33–40	5–7	–	5–7 (1 pitted)	6 (pitted)	18–21	banded/ blotched	absent
<i>C. phuocbinhensis</i>	46.0–60.4	76.1	43–47	5	–	7	–	17–19	banded	absent
<i>C. pseudoquadrivirgatus</i>	48.6–83.3	55.7–82.3	41–57	–	–	5–9	5–10	16–25	blotched	absent
<i>C. sangi</i>	49.9–56.3	40.8–47.9*	37	4	–	7	4 (pitted)	18–22	banded	absent
<i>C. takouensis</i>	74.7–81.1	77.7–91.0	39–40	3–5	0–2	3–4	–	18–20	banded	transversally
<i>C. taynguyenensis</i>	60.0–85.0	66.0–94.0	42–49	–	–	6	–	17–21	blotched	absent
<i>C. yangbayensis</i>	78.5–92.3	91.3–109.1	39–46	5–16	0–2 V	6–8	–	15–17	banded	variable/ not transversal
<i>C. ziegleri</i>	84.6–93.0	95.0–107.0	33–39	8–10	0–6	5–8	0–8	18–21	banded	absent

Table 3. Morphological comparisons between *Cyrtodactylus chungii* sp. nov. and its other congeners from Vietnam (after S.N. Nguyen *et al.* 2006, 2014, 2017; Ngo 2008a, 2008b; Ngo *et al.* 2008, 2010, 2017; Rösler *et al.* 2008; Ngo & Grismer 2010, 2012; Ziegler *et al.* 2010; Luu *et al.* 2011; Ngo & Chan 2011; Nazarov *et al.* 2012; Phung *et al.* 2014; Grismer *et al.* 2015, 2017; T.Q. Nguyen *et al.* 2015, 2017; Le *et al.* 2016; Pauwels *et al.* 2018; Murdoch *et al.* 2019; Pham *et al.* 2019). Symbols: / = data not available in literature; – = characteristic does not exist; + = characteristic exists but is not uniquely determined; * = broken or regenerated tail.

Species	SVL (mm)	TL (mm)	V	EFS	FP	PP (♂)	PP (♀)	LT4	Color pattern of dorsum	Enlarged subcaudals
<i>Cyrtodactylus chungii</i> sp. nov.	66.6–68.5	62.75*–82.15	30–31	4–6	–	7	6 (pitted)	17–20	banded	absent
<i>C. badensis</i>	59.3–74.1	58.6–82.4	25–29	–	–	0	0	18–22	banded	transversal
<i>C. bichnganae</i>	95.3–99.9	96.3–115.6	30–31	11–13	18 (♂)	10	8 (pitted)	16–20	banded	transversal
<i>C. bobrovi</i>	75.2–96.4	80.8–90.3	40–45	0	0	5	0	21–22	banded	absent
<i>C. chauquangensis</i>	90.9–99.3	97.0–108.3	36–38	–	–	6–7	6–7	19–23	banded	absent
<i>C. condorensis</i>	52.0–84.0	80.8–111.0	26–40	+	–	4–7	–	17–23	blotched	transversal
<i>C. cucphuongensis</i>	96.0	79.3*	42	14	–	0	/	24	banded	transversal
<i>C. eisenmanae</i>	76.8	91.0–103.8	44–45	4–6	–	–	–	17–18	banded	transversal
<i>C. grismeri</i>	68.3–95.0	111.3–115.1	33–38	–	/	–	–	16–19	banded	transversal
<i>C. honreensis</i>	72.4–88.9	84.2–106.5	40–42	–	–	7–8	–	17–19	banded	transversal
<i>C. huongsonensis</i>	73.4–89.8	90.5	41–48	7–9	15–17	6	8	20–23	banded	transversal
<i>C. intermedius</i>	61.0–85.0	80.0–100.0	40–50	6–10	–	8–10	–	22	banded	transversal
<i>C. leegrimeri</i>	80.6–92.0	58.0–99.0	27–35	+	–	4	0	18–20	blotched	transversal
<i>C. martini</i>	64.4–96.2	76.0–101.2	39–43	14–8	–	4	–	22–24	banded	present
<i>C. nigritocularis</i>	82.7–107.5	70.6–121.0	42–49	–	–	0–2	–	17–21	uniform brown	transversal
<i>C. otai</i>	85.2–90.6	89.7–97.6	38–43	–	–	7–8	–	19–22	banded	present
<i>C. phongnhakebangensis</i>	78.5–96.3	98.0–110.0	32–42	+	+	32–42 (PP+PF)	0–41 (PP+FP)	18–26	banded	transversal
<i>C. phuquocensis</i>	62.2–85.8	80.5–103.1	38–43	10–16	–	7–9	–	15–18	banded	transversal
<i>C. puhensis</i>	79.2	82.59	36	+	–	5	/	23	banded	transversal
<i>C. roesleri</i>	51.1–75.3	63.4–101.0	34–40	7–10	+	20–28 (PP+FP)	17–22 (PP+FP)	17–19	banded	transversal
<i>C. septimontium</i>	59.5–89.8	/	37–46	12–16	–	6–8	–	17–10	banded	transversal
<i>C. soni</i>	88.7–103.0	70.6–113.0	41–45	8–11	6–8 (♂)	6–7	7–8 (pitted)	18–22	banded	transversal
<i>C. sonlaensis</i>	63.1–83.2	33.3*–103.0	34–42	15–17	14–15 (♂)	8	–	18–21	banded	transversal
<i>C. taybacensis</i>	77.6–97.5	97.1–104.1	30–38	11–13	–	11–13	5–15 (pitted)	16–20	banded	transversal



Fig. 4. *Cyrtodactylus chungii* sp. nov., in life paratype, ♀ (IEBR 4582). Photos T.M. Phung.



Fig. 5. *Cyrtodactylus chungii* sp. nov., holotype, ♂ (IEBR 4581) and paratype, ♀ (IEBR 4582). Views in preservative. Top: dorsal view. Bottom: ventral view. Photos T. Ziegler.

Cyrtodactylus chungi sp. nov. differs from *C. cucdongensis* Schneider, Phung, Le, Nguyen & Ziegler, 2014 by its larger size (SVL 66.6–68.5 vs 55.8–65.9 mm), fewer ventral scale rows (30–31 vs 35–44) and enlarged femoral scales (4–6 vs 5–9).

Cyrtodactylus chungi sp. nov. differs from *C. dati* Ngo, 2013 by having fewer ventral scale rows (30–31 vs 42–48) and by the different dorsal color pattern (irregular transverse bands vs irregular dark blotches).

Cyrtodactylus chungi sp. nov. differs from *C. huynhi* Ngo & Bauer, 2008 by having fewer ventral scale rows (30–31 vs 43–46) and by the absence of femoral pores (vs 3–8).

Cyrtodactylus chungi sp. nov. differs from *C. irregularis* (Smith, 1921) by its smaller size (SVL of 66.6–68.5 vs 72.0–86.0 mm), having fewer ventral scale rows (30–31 vs 38–45) and enlarged femoral scales (4–6 vs 7–8), and by the different dorsal color pattern (irregular transverse bands vs transverse bands with uneven margins in white binding, some bands can fall into separated spots).

Cyrtodactylus chungi sp. nov. differs from *C. phnomchiensis* Neang, Henson & Stuart, 2020 by its smaller size (SVL 66.6–68.5 vs 76.1–80.7 mm), having fewer ventral scale rows (30–31 vs 45–54) enlarged femoral scales (4–6 vs 0–8), precloacal pores in males (7 vs 4–5) and subdigital lamellae under the fourth to (17–20 vs 20–23) and by the different dorsal color pattern (irregular transverse brown bands vs dark brown body bands bordered by yellowish white or light brown bands).



Fig. 6. *Cyrtodactylus chungi* sp. nov., holotype, ♂ (IEBR 4581). Cloacal region in preservative. Photo T. Ziegler.

Cyrtodactylus chungi sp. nov. differs from *C. phumyensis* Ostrowski, Do, Lee, Ngo, Pham, Nguyen, Nguyen & Ziegler, 2020 by having fewer ventral scale rows (30–31 vs 33–40), the absence of pitted precloacal scales in the male (absent vs 1), more paravertebral tubercles (24–27 vs 20–23) and by the different dorsal color pattern (irregular transverse bands vs anteriorly irregularly spotted and posteriorly banded).

Cyrtodactylus chungi sp. nov. differs from *C. phuocbinhensis* Nguyen, Le, Tran, Orlov, Lathrop Macculloch, Le, Jin, Nguyen, Nguyen, Hoang, Che, Murphy & Zhang, 2013 by its larger size (SVL 66.6–68.5 mm vs 46.0–60.4 mm), having fewer ventral scale rows (30–31 vs 43–47), the presence of 6 pitted precloacal scales in the female (vs absence) and the different dorsal color pattern (irregular transversal bands vs stripes).

Cyrtodactylus chungi sp. nov. differs from *C. ziegleri* Nazarov, Orlov, Nguyen & Ho, 2008 by its smaller size (SVL of 66.6–68.5 vs 84.6–93.0 mm), having fewer ventral scale rows (30–31 vs 33–39) and enlarged femoral scales (4–6 vs 8–10).

Cyrtodactylus chungi sp. nov. is most similar to *C. sangi* Pauwels, Nazarov, Bobrov & Poyarkov, 2018. However, the new species can be distinguished from *C. sangi* by its larger size (SVL 66.6–68.5 vs 49.9–56.3 mm), having fewer ventral scale rows (30–31 vs 37) and by the different dorsal color pattern (irregular transversal bands with a closed neck band vs irregular transversal bands and pattern with an interrupted neck band).



Fig. 7. Head views in preservative of *Cyrtodactylus chungi* sp. nov. from Ta Kou Nature Reserve, Binh Thuan Province, Vietnam. On the left: holotype, ♂ (IEBR 4581); on the right: paratype, ♀ (IEBR 4582). Top: lateral view. Bottom left: dorsal view. Bottom right: ventral view. Photos T. Ziegler.

Distribution

Cyrtodactylus chungi sp. nov. is currently known only from the type locality in Ta Kou Nature Reserve, Binh Thuan Province, Vietnam (Fig. 1).

Natural history

Specimens were found at night between 20:00 and 22:00, on granite rock nearby a forest path, about 0.5–1.0 m above the ground, at elevations between 400 and 500 m a.s.l. The surrounding habitat was evergreen forest of medium and small hardwoods mixed with shrubs and vines. The humidity was approximately 68–72% and the air temperature ranged from 26.8 to 31.6°C (Fig. 9).

Discussion

In our phylogenetic analyses, *Cyrtodactylus chungi* is recovered as the sister taxon to *C. cattienensis* s. str. with the genetic divergence of more than 9%. Although superficially similar, the new species differs in color pattern and scalation characters. The new species is recovered as a member of the *Cyrtodactylus irregularis* species group, which consists of *C. bidoupimontis* Nazarov, Poyarkov, Orlov, Phung, Nguyen, Hoang & Ziegler, 2012, *C. bugiamapensis* Nazarov, Poyarkov, Orlov, Phung, Nguyen, Hoang & Ziegler, 2012, *C. caovansungi* Orlov, Nguyen, Nazarov, Ananjeva & Nguyen, 2007, *C. cattienensis* Geissler, Nazarov, Orlov, Böhme, Phung, Nguyen & Ziegler, 2009, *C. cryptus* Heidrich, Rösler, Vu, Böhme & Ziegler, 2007, *C. cucdongensis* Schneider, Phung, Le, Nguyen & Ziegler, 2014, *C. dati* Ngo, 2013, *C. gialaiensis* Luu, Dung, Nguyen, Le & Ziegler, 2017, *C. huynhi* Ngo & Bauer, 2008, *C. irregularis*



Fig. 8. *Cyrtodactylus chungi* sp. nov., paratype, ♀ (IEBR 4582). Head views in preservative. Top: lateral view. Bottom left: dorsal view. Bottom right: ventral view. Photos T. Ziegler.

(Smith, 1921), *C. kingsadai* Ziegler, Phung, Le & Nguyen, 2013, *C. phnomchiensis* Neang, Henson & Stuart, 2020, *C. phumyensis* Ostrowski, Do, Lee, Ngo, Pham, Nguyen, Nguyen & Ziegler, 2020, *C. phuocbinhensis* Nguyen, Le, Tran, Orlov, Lathrop Macculloch, Le, Jin, Nguyen, Nguyen, Hoang, Che, Murphy & Zhang, 2013, *C. pseudoquadrivirgatus* Rösler, Nguyen, Vu, Ngo & Ziegler, 2008, *C. sangi* Pauwels, Nazarov, Bobrov & Poyarkov, 2018, *C. takouensis* Ngo & Bauer, 2008, *C. taynguyenensis* Nguyen, Le, Tran, Orlov, Lathrop Macculloch, Le, Jin, Nguyen, Nguyen, Hoang, Che, Murphy & Zhang, 2013, *C. yangbayensis* Ngo & Chan, 2010 and *C. ziegleri* Nazarov, Orlov, Nguyen & Cuc, 2008.

The *C. irregularis* group has been split into a northern *C. pseudoquadrivirgatus* clade (A), including *C. cryptus*, *C. pseudoquadrivirgatus*, *C. taynguyenensis*, and a southern *C. irregularis* clade (B), consisting of the remaining taxa, based on two nuclear genes, RPL35 and Rag1 (S.N. Nguyen *et al.* 2017). *C. chungi* was found within the distribution of clade B, which is characterized by enlarged femoral scales. However, group A lacks this character. Accordingly, this group is characterized by small femoral scales. Similar to the results based the single mitochondrial COI reported by S.N. Nguyen *et al.* (2017), our analyses and previous studies based on the same gene have not been able to fully resolve the phylogenetic relationships within the *C. irregularis* group, especially the deep nodes of the phylogeny, although species in the group are highly diverged from each other in terms of genetic distance. In addition, substantial discrepancies between phylogenetic relationships derived from nuclear and mitochondrial markers (see S.N. Nguyen *et al.* 2017) emphasize the need to include additional molecular data to investigate the complicated evolutionary history of the group. Moreover, the *C. irregularis* species group still includes unsolved taxonomic issues, such as an obvious cryptic taxon sister to *C. irregularis* and the *C. pseudoquadrivirgatus* species group apparently containing more than one species.

The new species was discovered in Ta Kou Nature Reserve, Binh Thuan Province, from where *C. takouensis* was described (Ngo & Bauer 2008). The latter species, which distinctly differs in morphology (color pattern and scalation) and by genetic divergence (16.4%), also seems to inhabit a



Fig. 9. Habitat of *Cyrtodactylus chungi* sp. nov. in Ta Kou Nature Reserve, Binh Thuan Province. Photo C.T. Pham.

different microhabitat, because it was found in a cave in deciduous forest, whereas *C. chungii* was found on rocks in the evergreen forest.

The Ta Kou Nature Reserve is located in the Binh Thuan Province, coastal southern central of Vietnam. It is like an isolated island on land with endangered species, e.g., *Trachypithecus germaini* (Milne-Edwards, 1876) and *Pygathrix nigripes* (Milne-Edwards, 1871), and two new species of geckos were discovered, namely *Cyrtodactylus takouensis* Ngo & Baur, 2008 and *Gekko takouensis* Ngo & Gamble, 2010 (Uetz *et al.* 2020). A major threat to the local fauna is habitat loss by agricultural extension and tourism development.

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Supplementary material

Supplementary file 1. Distance matrix. <https://doi.org/10.5852/ejt.2021.731.1203.3403>

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Autor(en)/Author(s): Ostrowski Sabrina, Le Minh Duc, Ngo Hanh Thi, Pham Cuong The, Phung Trung My, Nguyen Truong Quang, Ziegler Thomas

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