







**Research article**

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**The discovery of two new species in the *Cyrtodactylus irregularis* group highlights that hidden diversity remains in the largest clade of the mega-diverse genus *Cyrtodactylus***

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**Abstract.** The *Cyrtodactylus irregularis* group, originally considered to consist of only one taxon, has been split into 26 species. We herein present the distribution of all species within the group in Cambodia, Laos and Vietnam and describe two new species based on integrative analyses. *Cyrtodactylus chumuensis* sp. nov. is discovered from Dak Lak Province and distinguished from the remaining taxa by more than 11.86% genetic divergence and by the following distinct morphological characters: size medium (SVL 67.5 mm); enlarged femoral scales on each thigh 4–5, femoral pores 0–2 in males; precloacal pores 6–7 in males; ventral scale rows 43–45; lamellae under toe IV 17–21. *Cyrtodactylus arndti* sp. nov. is described from Binh Dinh Province and genetically differentiated from its congeners by a minimum of 11.42% and by the following characters: adult size medium (SVL 73.4–80.8 mm); enlarged femoral scales on each thigh 5–11; femoral pores 0–2 in males; 6 precloacal pores in males, females with 6 pitted precloacal pores; ventral scale rows 26–38; lamellae under toe IV 17–22; subcaudal scales transversely enlarged. Additionally, we highlight the potential cryptic diversity with the taxon currently regarded as *C. pseudoquadrivirgatus* and understudied areas in Vietnam where new species will likely be discovered.

**Keywords.** *Cyrtodactylus chumuensis* sp. nov., *Cyrtodactylus arndti* sp. nov., molecular phylogeny, taxonomy, Vietnam.

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## Introduction

The genus *Cyrtodactylus* Gray, 1827 is the most diverse gecko genus with 324 currently recognized species (Uetz *et al.* 2022). The members of *Cyrtodactylus* are known from tropical South Asia, southern China, Indochina, the Philippines, the Indo-Australian Archipelago and the Solomon Islands (Wood *et al.* 2012; Grismer *et al.* 2015, 2021). Species in the genus can adapt to different habitat types, including limestone karst, granitic montane, and lowland evergreen forests, caves, and swamps (Grismer *et al.* 2021). As a result of increased scrutiny in recent years, new taxa have been described in several morphologically conservative species complexes of *Cyrtodactylus*. A special case is the *Cyrtodactylus irregularis* group, which was originally considered to consist of only one taxon, *Gymnodactylus peguensis* var. *irregularis* Smith, 1921. Remarkably, a total of 25 species have been discovered within this group over the last 20 years (Ngo *et al.* 2022; Uetz *et al.* 2022). Of these, only *C. phnomchiensis* Neang, Henson & Stuart, 2020 is found in Cambodia, *C. buchardi* David, Teynié & Ohler, 2004 in Laos, and *C. cryptus* Heidrich, Rösler, Thanh, Böhme & Ziegler, 2007 in both Laos and Vietnam whereas the remaining 23 species are known only from Vietnam: *C. badenensis* Sang, Orlov & Darevsky, 2006; *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. chungii* Ostrowski, Do, Le, Ngo, Pham, Nguyen, Nguyen & Ziegler, 2021; *C. cucdongensis* Schneider, Phung, Le, Nguyen & Ziegler, 2014; *C. culaochamensis* Ngo, Grismer, Pham & Wood, 2020; *C. dati* Ngo, 2013; *C. gialaiensis* Luu, Tran, Nguyen, Le & Ziegler, 2017; *C. huynhi* Ngo & Bauer, 2008; *C. irregularis sensu stricto*, *C. kingsadai* Ziegler, Phung, Le & Nguyen, 2013; *C. orlovi* Do, Phung, Ngo, Le, Ziegler, Pham & Nguyen, 2021; *C. phumyensis* Ostrowski, Le, Ngo, Pham, Phung, Nguyen & Ziegler, 2020; *C. phuocbinhensis* Nguyen, Le, Tram, Orlov, Lathrop, MacCulloch, Le, Jin, Nguyen, Nguyen, Hoang, Che, Murphy & Zhang, 2013; *C. pseudoquadrivirgatus* Rösler, Vu, Nguyen, Ngo & Ziegler, 2008; *C. raglai* Nguyen, Duong, Grismer & Poyarkov, 2021; *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. zieglerei* Nazarov, Orlov, Nguyen & Ho, 2008 (Uetz *et al.* 2022).

We herein present data on the distribution of known taxa in the *C. irregularis* group and discuss potential cryptic diversity based on our updated molecular analyses. In addition, we also describe two new species collected during our recent fieldwork in Dak Lak and Binh Dinh provinces in south-central Vietnam based on integrative taxonomy, viz. combination of morphological and genetic evidence.

## Material and methods

### Sampling

Field surveys were conducted in June 2014 in M'Drak District, Dak Lak Province and in August 2016 in Van Canh District, Binh Dinh Province, Vietnam. Specimens were collected between 19:00 and 22:00 h (Fig. 1). After being photographed in life, specimens were euthanized in a closed vessel with a piece of cotton wool containing ethyl acetate (Simmons 2002), fixed in 80% ethanol for five hours, and later transferred to 70% ethanol for permanent storage. Tissue samples were preserved separately in 70% ethanol prior to fixation. Voucher specimens referred to in this paper were deposited in the collections of the Institute of Ecology and Biological Resources (IEBR), Hanoi, Vietnam and the Zoologisches Forschungsmuseum Alexander Koenig (ZFMK), Bonn, Germany.

### Molecular data and phylogenetic analysis

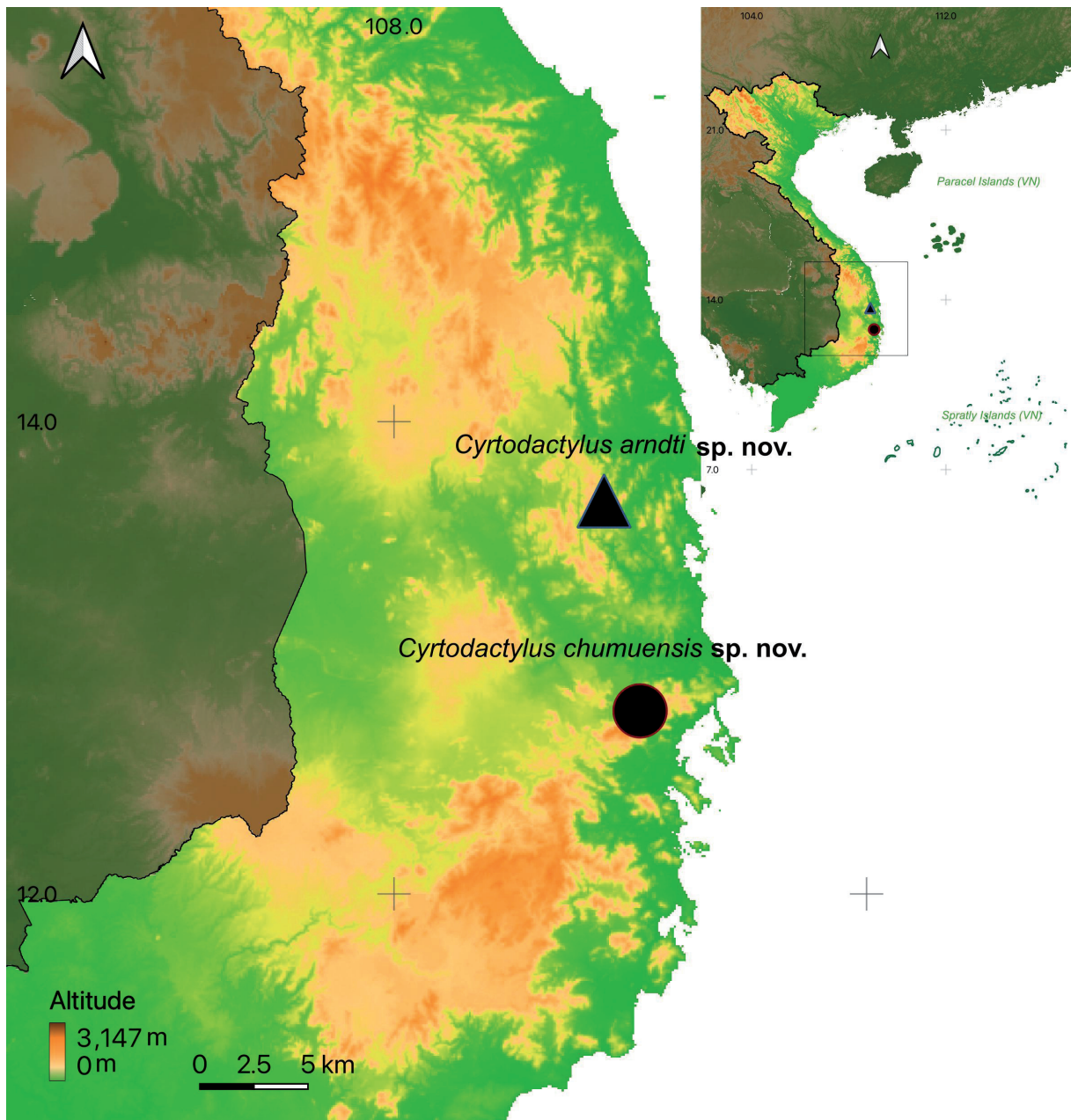
All recognized species of the *Cyrtodactylus irregularis* species complex were included in the study, except *C. buchardi* and true *C. pseudoquadrivirgatus* (Table 1). Sequences of the species were downloaded from GenBank. Five new samples from two distinct populations were incorporated into the analysis, comprising of two from Dak Lak Province IEBR R.4928, IEBR R.4929 (field numbers PMT01 and PMT02) and three from Binh Dinh Province IEBR R.5077, IEBR R.4930, and ZFMK 103910 (field numbers BD.2016.85, BD.2016.141, and BD.2016.142). Four taxa, *C. condorensis* Smith, 1921, *C. grismeri* Ngo, 2008, *C. spelaeus* Nazarov, Poyarkov, Orlov, Nguyen, Milto, Martynov, Konstantinov & Chulisov, 2014 and *C. wayakonei* Nguyen, Kingsada, Rösler, Auer & Ziegler, 2010 were used as an outgroup based on their phylogenetic relationships to the *C. irregularis* species group as reported by Luu *et al.* (2016a) and Grismer *et al.* (2021).

DNA was extracted using DNeasy Blood and Tissue kit (Qiagen, Germany) following the manufacturer's instruction. Extracted DNA was amplified by HotStarTaq 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<sup>-1</sup> and 2 µl of DNA). PCR condition's were 95°C for 15 minutes to activate the taq; with 40 cycles at 95°C for 30 s, 45°C for 45 s, 72°C for 60 s; and a final extension at 72°C for 6 minutes. A fragment of the mitochondrial gene, cytochrome c oxidase subunit 1 (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 % agarose gel stained with ethidium bromide. Successful amplifications were purified to eliminate PCR components using GeneJET™ PCR Purification kit (ThermoFischer Scientific, Lithuania). Purified PCR products were sent to FirstBase (Malaysia) for sequencing in both directions.

Afterwards, sequences were aligned by ClustalX ver. 2.1 (Thompson *et al.* 1997) with default settings. Data were analyzed using Bayesian inference (BI) as implemented in MrBayes ver. 3.2.7 (Ronquist *et al.* 2012), maximum likelihood as implemented in IQ-TREE ver. 1.6.8 (Nguyen *et al.* 2015), and Maximum Parsimony (MP) implemented in PAUP\*4.0b10 (Swofford 2001). For MP analysis, a 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 was calculated using 1000 pseudo-replicates (BP) and 100 random taxon addition replicates. All characters were equally weighted and unordered. For the ML analysis, we employed a single model and 10000 ultrafast bootstrap replications (UFB). The optimal model for nucleotide evolution was determined using jmodeltest ver. 1.2.4 (Darriba *et al.* 2012).

For the Bayesian analyses, we used the optimal model determined by jmodeltest with parameters estimated by MrBayes ver. 3.2.7. Two independent analyses with four Markov chains (one cold and three heated) were run simultaneously for  $10^7$  generations with a random starting tree and sampled every 1000 generations. Loglikelihood scores of sample points were plotted against generation time



**Fig. 1.** Type locality of *Cyrtodactylus chumuensis* sp. nov. in Dak Lak Province (black circle) and *Cyrtodactylus arndti* sp. nov. in Binh Dinh Province (black triangle), Vietnam.

**Table 1** (continued on next page). Samples of *Cyrtodactylus* Gray, 1827 used in the molecular analyses. Abbreviations: CBC = Royal University of Phnom Penh, Cambodia; IEBR = Institute of Ecology and Biological Resources, Vietnam; ITBCZ = Institute of Tropical Biology Collection and Zoology, Vietnam; KIZ = Kunning Institute of Zoology, Germany; NAP and ZMMU = Zoological Museum of Moscow University, Russia; PNKB = Phong Nha-Ke Bang, Vietnam; ROM = Royal Ontario Museum, Canada; UNS = United States National Museum, USA; VNMN = Vietnam National Museum of Nature, Vietnam; VNUF = Vietnam National University of Forestry, Vietnam; ZFMK = Zoologisches Forschungsmuseum Alexander Koenig, Germany.

Species	GenBank No.	Locality	Voucher number
<i>Cyrtodactylus spelaeus</i>	KP199947	Laos: Kasi	ZMMU R-13980-3
<i>C. wayakonei</i>	KP199950	Laos: Luang Nam Tha	ZMMU R-13981-1
<i>C. badenensis</i>	KF929505	Vietnam: Tay Ninh Prov.	KIZ13689
<i>C. bidoupimontis</i>	HM425560	Vietnam	NAP-01121
<i>C. bidoupimontis</i>	HQ967215	Vietnam: Lam Dong Prov.	ZMMU NAP-00080
<i>C. bugiamapensis</i>	HM888459	Vietnam: Binh Phuoc Prov.	ZMMU R-13093-2
<i>C. bugiamapensis</i>	KY862173	Vietnam: Binh Phuoc Prov.	KIZ33
<i>C. caovansungi</i>	KF219679	Vietnam: Ninh Thuan Prov.	ITBCZ 932
<i>C. caovansungi</i>	KF219680	Vietnam: Ninh Thuan Prov.	ITBCZ 1113
<i>C. cf. cattienensis</i>	HQ967220	Vietnam: Dong Nai Prov.	ZMMU NAP-00117.1
<i>C. cf. cattienensis</i>	KF169973	Vietnam: Dong Nai Prov.	ROM37887
<i>C. cf. cattienensis</i>	MG791892	Vietnam: Ba Ria – Vung Tau Prov.	ZMMU R-14509
<i>C. condorensis</i>	HM888464	Cambodia: Kong Tang Island	ZMMU RAN 1987
<i>C. condorensis</i>	MF169910	Vietnam: Ba Ria – Vung Tau Prov.	UNS 0431
<i>Cyrtodactylus chumuensis</i> sp. nov.	OQ152319	Vietnam: Dak Lak Prov.	IEBR R. 4928
<i>Cyrtodactylus chumuensis</i> sp. nov.	OQ152320	Vietnam: Dak Lak Prov.	IEBR R. 4929
<i>C. chungi</i>	MT576019	Vietnam: Binh Thuan Prov.	IEBR 4581
<i>C. chungi</i>	MT576020	Vietnam: Binh Thuan Prov.	IEBR 4582
<i>C. cryptus</i>	KF169971	Vietnam: Quang Binh Prov.	PNKB3
<i>C. cryptus</i>	KF169972	Vietnam: Quang Binh Prov.	PNKB4
<i>C. cucdongensis</i>	KJ403846	Vietnam: Khanh Hoa Prov.	IEBR A.2013.104
<i>C. cucdongensis</i>	KJ403847	Vietnam: Khanh Hoa Prov.	ZFMK 95513
<i>C. dati</i>	KF929508	Vietnam: Binh Phuoc Prov.	ITBCZ2537
<i>C. dati</i>	KF929511	Vietnam: Binh Phuoc Prov.	ITBCZ2540
<i>C. gialaiensis</i>	MG460299	Vietnam: Gia Lai Prov.	VNUF R.2017.1
<i>C. gialaiensis</i>	MG460300	Vietnam: Gia Lai Prov.	VNUF R.2017.4
<i>C. grismeri</i>	KF929513	Vietnam: An Giang Prov.	ITBCZ 684
<i>C. grismeri</i>	KY862259	Vietnam: An Giang Prov.	ITBCZ 685
<i>Cyrtodactylus arndti</i> sp. nov.	OQ152316	Vietnam: Binh Dinh Prov.	IEBR R.5077
<i>Cyrtodactylus arndti</i> sp. nov.	OQ152317	Vietnam: Binh Dinh Prov.	IEBR R.4930

**Table 1** (continued).

Species	GenBank No.	Locality	Voucher number
<i>Cyrtodactylus arndti</i> sp. nov.	OQ152318	Vietnam: Binh Dinh Prov.	ZFMK 103910
<i>C. huynhi</i>	KF169948	Vietnam: Dong Nai Prov.	ITBCZ513
<i>C. huynhi</i>	KF169950	Vietnam: Dong Nai Prov.	ITBCZ530
<i>C. irregularis</i>	MG791887	Vietnam: Lam Dong Prov.	ITBCZ-10025
<i>C. kingsadai</i>	KF188432	Vietnam: Phu Yen Prov.	IEBR A.2013.3
<i>C. phnomchiensis</i>	MT066405	Cambodia: Kampong Thom Prov.	CBC 3003
<i>C. phnomchiensis</i>	MT066406	Cambodia: Kampong Thom Prov.	CBC 3004
<i>C. phumyensis</i>	MT210158	Vietnam: Binh Dinh Prov.	ZFMK 103153
<i>C. phumyensis</i>	MT210161	Vietnam: Binh Dinh Prov.	IEBR 4579
<i>C. phuocbinhensis</i>	KF169953	Vietnam: Ninh Thuan Prov.	ITBCZ1518
<i>C. phuocbinhensis</i>	KF169954	Vietnam: Ninh Thuan Prov.	ITBCZ1529
<i>C. pseudoquadrivirgatus</i>	KF169963	Vietnam: Thua Thien Hue Prov.	ITBCZ3001
<i>C. pseudoquadrivirgatus</i>	KF169964	Vietnam: Thua Thien Hue Prov.	ITBCZ3002
<i>C. cf. pseudoquadrivirgatus</i>	KP199949	Vietnam: Da Nang Prov.	ZMMU-R-13095-2
<i>C. cf. pseudoquadrivirgatus</i>	MG791888	Vietnam: Quang Tri Prov.	ZMMU R130952
<i>C. raglai</i>	MW675653	Vietnam: Khanh Hoa Prov.	ZMMU R16688
<i>C. sangi</i>	KF169951	Vietnam: Ninh Thuan Prov.	ITBCZ1150
<i>C. sangi</i>	KF169952	Vietnam: Ninh Thuan Prov.	ITBCZ965
<i>Cyrtodactylus</i> sp.	KF169962	Vietnam: Da Nang Prov.	ITBCZ2532
<i>C. takouensis</i>	KF929533	Vietnam: Binh Thuan Prov.	ITBCZ2527
<i>C. takouensis</i>	KF929534	Vietnam: Binh Thuan Prov.	ITBCZ2528
<i>C. taynguyenensis</i>	KF169978	Vietnam: Gia Lai Prov.	ROM32119
<i>C. taynguyenensis</i>	KF169979	Vietnam: Gia Lai Prov.	ROM32120
<i>C. yangbayensis</i>	KJ403848	Vietnam: Khanh Hoa Prov.	VNMN03373
<i>C. yangbayensis</i>	MF169952	Vietnam: Khanh Hoa Prov.	UNS 0476
<i>C. cf. ziegleri</i>	HQ967210	Vietnam: Dak Lak Prov.	ZMMU R-13116-3
<i>C. cf. ziegleri</i>	KF169945	Vietnam: Dak Lak Prov.	UNS5007
<i>C. cf. ziegleri</i>	KF169977	Vietnam: Dak Nong Prov.	VNMN2016

to detect stationarity of the Markov chains. Trees generated prior to stationarity were removed from the final analyses using the burn-in function. The posterior probability values (PP) for all clades in the final majority rule consensus tree were provided. Nodal support was evaluated using BP as estimated in PAUP, UFB in IQ-TREE ver. 1.6.7.1, and PP in MrBayes ver. 3.2. UFB and PP  $\geq 95\%$  and BP  $\geq 70\%$  are regarded as strong support for a clade (Hillis & Bull 1993; Ronquist *et al.* 2012; Nguyen *et al.* 2015). The optimal model for nucleotide evolution was set to GTR+I+G for ML and Bayesian analyses. The cut-off point for the burn-in function was set to 47 in the Bayesian analysis, as  $-\ln L$  scores reached stationarity after 47 000 generations in both runs. Uncorrected pairwise divergences were calculated in PAUP\*4.0b10.

### **Morphological characters**

Measurements followed Ziegler *et al.* (2002) and Luu *et al.* (2015) with slight exceptions and were taken with a slide-caliper to the nearest 0.1 mm. Measurements were taken on the right side of the specimens unless otherwise indicated. Scale counts were taken using a stereo microscope (Euromex NexiusZoom). Bilateral scale counts were given as left/right or as one value (on each side), unless otherwise indicated.

### **Abbreviations**

AG	=	axilla-groin length, from insertion of posterior margin of front limbs to insertion of anterior margin of hindlimbs
BW	=	maximum width of body
CrusL	=	crus length, from heel to flexed knee
ED	=	greatest diameter of ear opening
EyeEar	=	distance between posterior margin of orbit and anterior margin of ear opening
FemurL	=	femur length, from limb insertion to knee
ForeaL	=	forearm length, from elbow flexed to base of palm
HH	=	maximum height of head posterior to orbits
HL	=	head length, from posterior margin of retroarticular process of jaw to tip of snout
HW	=	maximum width of head posterior to orbits
IND	=	internarial distance
ML	=	maximum length of mental
MW	=	maximum width of mental
OD	=	orbital diameter, greatest diameter or bony orbit
RW	=	maximum width of rostral
RH	=	maximum height of rostral
SE	=	distance between tip of snout and anterior margin of orbit
SVL	=	snout-vent length, from tip of snout to anterior margin of cloaca
TaL	=	tail length, from cloaca to end of tail

### **Scale counts**

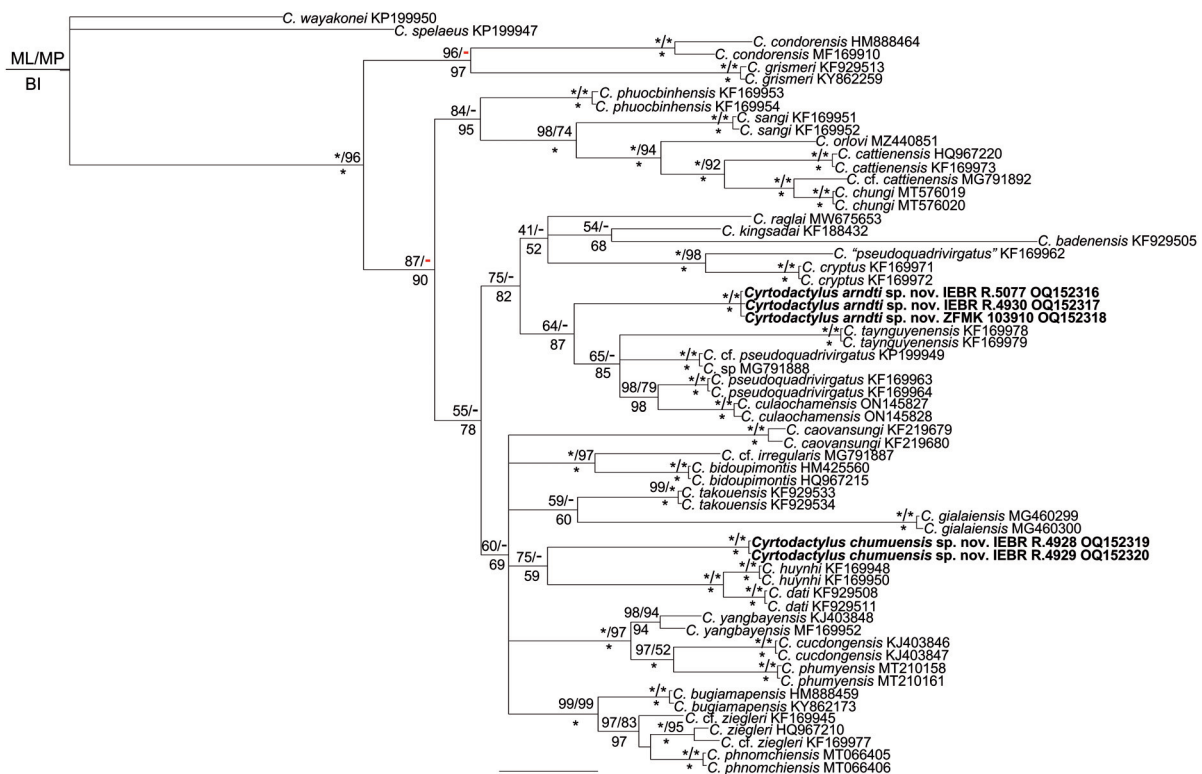
DTR	=	dorsal tubercle rows counted transversely across the midbody between ventrolateral folds
FP	=	femoral pores in males
EFS	=	enlarged femoral scales
EPS	=	distinctly enlarged precloacal scales, at the least twice as large, as the surrounding scales
GST	=	granular scales surrounding dorsal tubercles
IL	=	infralabials were counted from the first labial scale to posterior corner of mouth (except for granular scales)
IN	=	internasals
LD1	=	number of subdigital lamellae on first finger
LD4	=	number of subdigital lamellae on fourth finger
LT1	=	number of subdigital lamellae on first toe
LT4	=	number of subdigital lamellae on fourth toe
N	=	nasal scales, surrounding naris, from rostral to labial, except rostral and labial
PAT	=	postcloacal tubercles
PM	=	postmentals
PP	=	precloacal pores in males or pitted precloacal pores in females
SL	=	supralabials were counted from the first labial scale to corner of the mouth
V	=	ventral scales at midbody, counted from one ventrolateral fold to the other

## Results

### Phylogenetic analyses

The final matrix consisted of 61 terminals, consisting of five from this study and 56 from previous works. The ingroup taxa contained described species (except *C. buchardi* and true *C. pseudoquadrivirgatus*) and two undescribed populations of the *Cyrtodactylus irregularis* group. Both ML and BI produced very similar topologies based on a total of 652 aligned characters with no internal gaps and using a single model of molecular evolution (Fig. 2). In the MP analysis, 254 characters were parsimony informative. A single most parsimonious tree with 1649 steps was recovered (Consistency index = 0.25; Retention index = 0.59). The results show that *Cyrtodactylus condorensis* and *Cyrtodactylus grismeri* are nested within the *Cyrtodactylus irregularis* group in the MP analysis but placed in a separate clade in ML and BI (Fig. 2).

In our analyses, *Cyrtodactylus badenensis* is considered a member of the *Cyrtodactylus irregularis* group in both ML and BI analyses. Similar to the results reported in Ngo *et al.* (2022), *Cyrtodactylus* cf. *pseudoquadrivirgatus* was recovered in three distinct places of the tree, two closely related to *C. taynguyenensis* with 8.2 % and 10.6% genetic divergence from the latter and one as a sister taxon to *C. cryptus* with 9.3 % divergence between the two.



**Fig. 2.** Phylogram based on the Bayesian analysis. Number above and below branches are ML untrafast bootstrap/MP bootstrap values and Bayesian posterior probabilities, respectively. Dashes denote bootstrap values < 50%. Asterisk denotes 100% value. Red dashes show that *C. condorensis* (Smith, 1921) and *C. grismeri* Ngo, 2008 are nested within the *Cyrtodactylus irregularis* group in the MP analysis.



Moreover, two unnamed taxa from M'Drak District, Dak Lak Province and Van Canh District, Binh Dinh Province, Vietnam are nested within the *Cyrtodactylus irregularis* complex without any clear sister. *Cyrtodactylus arndti* sp. nov. is placed as a member in a clade consisting of *C. badenensis*, *C. culaochamensis*, *C. cryptus*, *C. kingsadai*, *C. pseudoquadrivirgatus*, *C. taynguyenensis*, *C. cf. pseudoquadrivirgatus*, *Cyrtodactylus* sp. (MG791888), and *C. raglai* without nodal support (UFB = 75, BP < 50, and PP=82) and also without any clear sister species. Genetically, *Cyrtodactylus chumuensis* sp. nov. is divergent from other members in *Cyrtodactylus irregularis* group by at least approximately 11.86 %. *Cyrtodactylus arndti* shows a minimum genetic distance of 11.42–11.42% to other members in *Cyrtodactylus irregularis* complex (Supp. file 1).

### Taxonomy

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

#### *Cyrtodactylus chumuensis* sp. nov.

urn:lsid:zoobank.org:act:F6A019B5-B1ED-4976-8C1D-803CC0D91DD9

Figs 3–5; Table 2

### Diagnosis

The new species can be distinguished from remaining congeners of the *irregularis* species group by a combination of the following characters: maximum SVL 67.5 mm; dorsal pattern with 6 irregularly shaped and short longitudinal stripes on the neck; nuchal band thin, interrupted, reaching the posterior margin of the orbits; the absence of transversely enlarged median subcaudal scales; 4 or 5 enlarged femoral scales on each thigh, 17–19 distinctly enlarged precloacal scales; males with 0 or 1 femoral pore on each thigh, 6 or 7 precloacal pores in a continuous series, ^-shaped; ventral scales 43–45; dorsal tubercles in 20 irregular longitudinal rows; precloacal groove absent; internasal scales 2; supralabials 8–14; infralabials 9–11; number of subdigital lamellae on fourth finger 16–19 and on fourth toe 19–21.

### Etymology

The new species is named after its type locality, Chu Mu Mountain in Dak Lak Province. We propose the following common names: Chu Mu Bent-toed Gecko (English), Thạch sùng ngón chù mu (Vietnamese).

### Type material (Figs 3–5)

#### Holotype

VIETNAM • ♂; Dak Lak Province, M'Drak District, Ea M'Doal Commune, Chu Mu Mountain; 12°41.330' N, 108°55.450' E; 500 m a.s.l.; 20 Jun. 2014; T.M. Phung leg.; Field No. PMT01; IEBR R.4928.

#### Paratypes

VIETNAM • 1 ♂ (subadult); Dak Lak Province, M'Drak District, Ea M'Doal Commune, Chu Mu Mountain; 12°41.321' N, 108°55.382' E; 400 m a.s.l.; 20 Jun. 2014; T.M. Phung leg.; Field No. PMT02; IEBR R.4929.

### Description of holotype

Adult male; snout-vent length SVL 67.5 mm; tail regenerated 51.4 mm in length (regenerated portion 43.7 mm); body slender, elongate (AG/SVL 0.4); head distinct from neck, elongate (HL/SVL 0.26), relatively wide (HW/HL 0.71) and depressed (HH/HL 0.36); loreal region concave; snout long, blunt

in dorsal profile (SE/HL 0.44), longer than diameter of orbit (OD/SE 0.56); scales on snout small, round or oval, granular, larger than scales on occiput; orbit large (OD/HL 0.24), pupils vertical; ear opening small, oval (ED/HL 0.06); rostral wider than high, indented medially the top, in contact with first supralabial, naris and nasorostral on each side, two internasal scales; nostril opening small, oval, surrounded by rostral, nasorostral, two supranasals and one or two postnasals; mental scale triangular, wider than high (ML/MW 0.74); two enlarged, triangular postmentals; supralabials 8/9; infralabials 9/9.

Dorsal scales granular, dorsal tubercles round, keeled, conical, in 20 irregular rows at midbody; tubercles on occiput small; tubercles surrounded by 10–12 granular scales; ventral scales smooth, round, midventral scales three times as large as dorsal granular scales, in 45 longitudinal rows at midbody between ventrolateral folds; precloacal groove absent; enlarged femoral scales 4 or 5 on each thigh, the third bearing a femoral pore (Fig. 4C); enlarged precloacal scales 17, arranged in a rhombus; precloacal pores 6, arranged in a  $\wedge$ -shaped series.

Fore and hindlimbs moderately slender (ForeaL/SVL 0.14 mm, CrusL/SVL 0.17); forelimbs dorsally covered by several slightly enlarged tubercles; dorsal hindlimbs with well-developed tubercles; two postcloacal tubercles on each side on the hemipenial swellings; phalanges without webbing; each claw sheathed by two scales, the ventral sheath larger than the upper; number of subdigital lamellae on first finger 11/11, on first toe 10/11, on fourth finger 17/17, on fourth toe 19/19.

#### Coloration in preservative

Dorsal surface of head, body and limbs light-brown with some dark-brown bands, pattern without light bordering; occiput marbled with small, irregular dark-brown blotches; rostral, mental and infralabials creamy white, supralabials dark-beige with short greyish brown vertical stripes; neck bands dark-brown,



**Fig. 3.** *Cyrtodactylus chumuensis* sp. nov., holotype, ♂ (IEBR R.4928), in life.

extending in two thin stripes along lateral sides of the snout to the orbits, broader on the neck, interrupted on the left side; two dark-brown longitudinal stripes, disconnected from the neck band extending to shoulders, one dark-brown blotch next to each stripe; dorsal pattern consisting of 6 irregular bands, each formed by two triangularly shaped blotches, shifted medially along the body axis; dorsolateral region covered with small, irregular dark-brown blotches arranged in a longitudinal row from neck to groin; a blurry dark-brown transverse band on dorsal surface of original part of the tail, regenerated part greyish beige and speckled with very small light-greyish brown blotches; dorsal surface of limbs with 3 or 4 dark-brown, blurry bands; phalanges brown with creamy white knuckles; tubercles white or dark-brown depending on position on pattern or background; venter creamy white; ventral tail greyish beige without bands. For coloration of the paratype in life that closely resembles the holotype in life see Fig. 3.

### Variation

The paratype is a subadult and therefore differs greatly in size. Its original tail showed some dark-brown irregular bands, although broken at the base. The number of precloacal pores is 7 and it lacks femoral pores. For more morphological characters see Table 2.

### Comparisons

The new species can be distinguished from all other member of *Cyrtodactylus irregularis* group from Vietnam by morphological characteristics (see Table 2).

*Cyrtodactylus chumuensis* sp. nov. differs from *C. badenensis* by having more ventral scale rows (43–45 vs 25–29 in *C. badenensis*), the presence of enlarged femoral scales (4–5 vs absent in *C. badenensis*), the presence of precloacal pores in males (6–7 vs absent in *C. badenensis*), and the absence of transversely



**Fig. 4.** *Cyrtodactylus chumuensis* sp. nov. in preservative. **A.** Holotype, ♂ (IEBR R.4928, left) and paratype, ♂ (IEBR R.4929, right). **B.** Paratype, ♂ (IEBR R.4929). **C.** Holotype, ♂ (IEBR R.4928). **A.** Dorsal view. **B.** Precloacal region with precloacal pores. **C.** Precloacal region with precloacal pores and femoral pores.

enlarged subcaudals (vs present in *C. badenensis*); differs from *C. bidoupimontis* by having a smaller size (SVL 67.5 mm vs 74.0–86.3 mm in *C. bidoupimontis*), fewer enlarged femoral scales (4 or 5 vs 8–10 in *C. bidoupimontis*), a different dorsal color pattern (irregularly banded with longitudinal stripes on the neck vs transversal bands with light borders in *C. bidoupimontis*), and a thin discontinuous nuchal band (vs well developed, widened posteriorly in *C. bidoupimontis*); differs from *C. bugiamapensis* by having fewer enlarged femoral scales (4 or 5 vs 6–10 in *C. bugiamapensis*) and the different dorsal color pattern (irregularly banded with longitudinal stripes on the neck vs unclear transversal bands formed by irregular round to oblong, dark-brown spots in *C. bugiamapensis*); differs from *C. buchardi* by having more ventral scale rows (30 vs 43–45 in *C. buchardi*), the presence of enlarged femoral scales (4–5 vs absent in *C. buchardi*), more subdigital lamellae under the fourth finger (16–19 vs 14 in *C. buchardi*), more subdigital lamellae under the fourth toe (17–21 vs 12 in *C. buchardi*); differs from *C. cattienensis* by having more ventral scale rows (43–45 vs 28–42 in *C. cattienensis*), more subdigital lamellae under the fourth finger (16–19 vs 12–16 in *C. cattienensis*), and different dorsal color pattern (irregularly banded with longitudinal stripes on the neck vs irregular dark-brown banded, first band on the shoulder x-shaped *C. cattienensis*); differs from *C. caovansungi* by having a smaller size (SVL 67.5 mm vs 90.4–94 mm in *C. caovansungi*), fewer enlarged femoral scales (4 or 5 vs 8 in *C. caovansungi*), fewer femoral pores on each thigh in males (0–1 vs 6 in *C. caovansungi*), fewer precloacal pores in males (6 or 7 vs 9 in *C. caovansungi*), fewer lamellae under the fourth finger (16–19 vs 22 in *C. caovansungi*), fewer lamellae under the fourth toe (17–21 vs 23–25 in *C. caovansungi*), and the absence of transversely enlarged subcaudal plates (vs present in *C. caovansungi*); differs from *C. chungii* by having more ventral scale rows (43–45 vs 30 or 31 in *C. chungii*), more dorsal tubercle rows (20 vs 18 in *C. chungii*), different dorsal color pattern (irregularly banded with longitudinal stripes on the neck vs irregular transversal bands with a closed nuchal band), and a thin, discontinuous nuchal band (vs continuous nuchal band in *C. chungii*); differs from *C. cryptus* by having fewer ventral scale rows (43–45 vs 47–50 in *C. cryptus*), the presence of enlarged femoral scales (vs absent in *C. cryptus*), fewer precloacal pores in males (6 or 7 vs 9–11 in *C. cryptus*), a thin, discontinuous nuchal band (vs well developed, widened posteriorly in *C. cryptus*), and different dorsal color pattern (irregularly banded with short, longitudinal stripes on the neck vs irregular transverse bands in *C. cryptus*); differs from *C. cucdongensis* by having more dorsal tubercle rows (20 vs 16–19 in *C. cucdongensis*), fewer enlarged femoral scales (4 or 5 vs 5–9 in *C. cucdongensis*), more enlarged precloacal scales (20–21 vs 6–13), and a different dorsal colour pattern (irregularly banded with short, longitudinal stripes on the neck vs irregular dark brown transverse bands); differs from *C. culaochamensis* by having a smaller size (SVL 67.5 mm vs 69.8–79.8 mm in *C. culaochamensis*), the presence of enlarged femoral scales (vs absent in *C. culaochamensis*), fewer lamellae under the first finger (11 vs 13 or 14 in *C. culaochamensis*), and fewer lamellae under the first toe (10 or 11 vs 13–15 in *C. culaochamensis*); differs from *C. dati* by having fewer femoral pores in males (0–2 vs 3 or 4 each side in *C. dati*), fewer lamellae under the first toe (10 or 11 vs 12 or 13 in *C. dati*), the presence of blotches on head (vs absent in *C. dati*), and different dorsal color pattern (irregularly banded with longitudinal stripes on the neck vs irregular dark blotches); differs from *C. gialaiensis* by the presence of enlarged femoral scales (vs absent in *C. gialaiensis*), fewer precloacal pores in males (6 or 7 vs 9 or 10 in *C. gialaiensis*), and more subdigital lamellae under the fourth finger (16–19 vs 14 or 15 in *C. gialaiensis*) as well as under the fourth toe (17–21 vs 15–17 in *C. gialaiensis*); differs from *C. huynhi* by having more dorsal tubercle rows in males (20 vs 16–18 in *C. huynhi*), fewer lamellae under first finger (11 vs 12–15 in *C. huynhi*), fewer lamellae under first toe (10 or 11 vs 13–17 in *C. huynhi*), and a thin discontinuous nuchal band (vs well developed, widened posteriorly in *C. huynhi*); differs from *C. irregularis* by having a smaller size (SVL 67.5 mm vs 72.0–86.0 mm in *C. irregularis*), more ventral scale rows (43–45 vs 37–42 in *C. irregularis*), fewer enlarged femoral scales (4 or 5 vs 7 or 8 in *C. irregularis*), and different dorsal color pattern (irregularly banded with short longitudinal stripes on the neck vs blotched in *C. irregularis*); differs from *C. kingsadai* by having a smaller size (SVL 67.5 mm vs 83.0–94.0 in *C. kingsadai*), fewer enlarged femoral scales (4 or 5 vs 9–12 in *C. kingsadai*), the absence of transversely enlarged subcaudal plates (vs present in *C. kingsadai*), and more internasals (2 vs 1 in *C. kingsadai*); differs from *C. orlovi* by having more ventral scale rows

**Table 2.** Measurements (in mm) and morphological characters of the type series of *Cyrtodactylus chumuensis* sp. nov. Bilateral meristic characters are given as (left/right). Abbreviations: \* = regenerated or broken tail; max = maximum; min = minimum.

Characters	IEBR R.4928	IEBR R.4929
	Holotype	Paratype
Sex	♂	♂
SVL	67.5	52.4
TaL	51.4*	41.5*
AG	26.7	21.3
HL	17.6	16.0
HW	12.5	10.3
HH	6.4	5.2
OD	4.25	3.6
SE	7.7	6.8
EyeEar	6.5	4.6
ED	1.0	1.2
IND	2.2	1.6
RW	2.6	2.4
RH	2.1	1.7
MW	2.3	2.1
ML	1.7	1.7
BW	13.7	9.6
ForeaL	9.7	7.6
CrusL	11.2	8.8
FemurL	11.6	7.5
SL	8/9	12/14
IL	9/9	10/11
N	4/5	4/4
IN	2	2
PM	2	2
DTR	20	20
GST	10–12	9–11
V	45	43
EFS	5/4	4/4
FP	1/1	–
EPS	17	19
PP	6	7
PAT	2/2	3/3
LD1	11/11	11/11
LT1	10/11	11/11
LD4	17/17	19/16
LT4	19/17	19/21

(43–45 vs 36–39 in *C. orlovi*); a thin, discontinuous nuchal band (vs continuous nuchal band in *C. orlovi*), and different banded pattern ranges (6 vs 3–5 in *C. orlovi*); differs from *C. phnomchiensis* by having a smaller size (SVL 67.5 vs 76.1–80.7 mm in *C. phnomchiensis*), more precloacal pores in males (6 or 7 vs 5 in *C. phnomchiensis*), and different dorsal color pattern (irregularly banded vs banded in *C. phnomchiensis*); differs from *C. phuocbinhensis* by having a larger size (SVL 67.5 mm vs 46.0–60.4 mm in *C. phuocbinhensis*), different dorsal color pattern (irregularly banded vs stripes or blotches in *C. phuocbinhensis*), and dark-brown transverse banded of the tail than light-brown interspaces (vs dark transverse banded wider than light interspaces in *C. phuocbinhensis*); differs from *C. phumyensis* by having more ventral scale rows (43–45 vs 33–41 in *C. phumyensis*), fewer enlarged femoral scales (4 or 5 vs 5–7 in *C. phumyensis*), more dorsal tubercle row (20 vs 18 or 19 in *C. phumyensis*), fewer enlarged precloacal scales (17–19 vs 21–41 in *C. phumyensis*), and different dorsal color pattern (irregularly banded with short longitudinal stripes on the neck vs anteriorly irregularly spotted and posteriorly banded in *C. phumyensis*); differs *C. pseudoquadrivirgatus* by the presence of enlarged femoral scales on each thigh (vs absent in *C. pseudoquadrivirgatus*), the presence of precloacal pores in males (0–2 vs absent in *C. pseudoquadrivirgatus*), and more enlarged precloacal scales (17–19 vs 1–12 in *C. pseudoquadrivirgatus*); differs *C. raglai* by having a smaller size (SVL 67.5 mm vs 87.5–111.7 mm in *C. raglai*), more ventral scale rows (43–45 vs 36–39 in *C. raglai*), fewer enlarged femoral scales (4 or 5 vs 9 or 10 in *C. raglai*), fewer precloacal pores in males (0–2 vs 5 in *C. raglai*), and the absence of transversely enlarged subcaudal plates (vs present in *C. raglai*); differs from *C. sangi* by having a larger size (SVL 67.5 mm vs 49.9–56.3 mm in *C. sangi*) and more ventral scale rows (43–45 vs 37 in *C. sangi*); differs from *C. takouensis* by having a smaller size (SVL 67.5 mm vs 74.7–81.1 mm in *C. takouensis*), more ventral scale rows (43–45 vs 39–40 in *C. takouensis*), more precloacal pores in males (6 or 7 vs 3 or 4 in *C. takouensis*), the absence of transversely enlarged subcaudal plates (vs present in *C. takouensis*), a thin discontinuous nuchal band (vs well developed, widened posteriorly in *C. takouensis*), and different dorsal color pattern (irregularly banded vs banded in *C. takouensis*); differs from *C. taynguyenensis* by



**Fig. 5.** Habitat of *Cyrtodactylus chumuensis* sp. nov. in the Chu Mu Mountain, M'Drak District, Dak Lak Province.

the presence of enlarged femoral scales on each thigh (vs absent in *C. taynguyenensis*); irregularly banded of the tail (vs banded in *C. taynguyenensis*), and different dorsal color pattern (irregularly banded vs blotched in *C. taynguyenensis*); differs from *C. yangbayensis* by having a smaller size (SVL 67.5 vs 78.5–92.3 mm in *C. yangbayensis*), more subdigital lamellae under the fourth toe (17–21 vs 15–17 in *C. yangbayensis*), fewer subdigital lamellae under the first toe (10–11 vs 18–20 in *C. yangbayensis*), and the absence of transversely enlarged subcaudal plates (vs present in *C. yangbayensis*); differs from *C. ziegleri* by having a smaller size (SVL 67.5 vs 84.6–93.0 mm in *C. ziegleri*), more ventral scale rows (43–45 vs 33–39 in *C. ziegleri*), and fewer enlarged femoral scales (4 or 5 vs 8–10 *C. ziegleri*).

### Distribution

*Cyrtodactylus chumuensis* sp. nov. is currently known only from the Chu Mu Mountain, M'Drak District, Dak Lak Province, Vietnam (Fig. 1).

### Natural history

Specimens were found at night between 19:00 and 22:00, on granite rock, along a rocky stream, approximately 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 (Fig. 5). The humidity was approximately 50–71% and the air temperature ranged from 27.5 to 32.1°C. Other reptile species found at the sites included *Gekko gecko* (Linnaeus, 1758), *Hemidactylus platyurus* (Schneider, 1792), *Ahaetulla prasina* (Boie, 1827), *Lycodon* sp., and *Oligodon* sp.

### *Cyrtodactylus arndti* sp. nov.

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Figs 6–9; Table 3

### Diagnosis

The new species of *Cyrtodactylus* is distinguished from remaining congeners of the *C. irregularis* species group by a combination of the following characters: SVL: 73.4–80.9 mm; dorsal pattern with 6 or 7 irregularly shaped bands; moderately broad nuchal band; original tail with irregular transverse bands; subcaudals transversely enlarged; 5–11 enlarged femoral scales; males with 0–2 pitted femoral pores, those absence in females; males with 6 precloacal pores, females with 6 pitted precloacal pores, pore-bearing scales arranged in a single  $\wedge$ -shaped series; ventral scales 26–38; dorsal tubercles in 17–20 irregular longitudinal rows; precloacal groove absent; supralabials 8–13; infralabials 8–12; number of subdigital lamellae on fourth finger 15–20 and on fourth toe 17–22.

### Etymology

We name this species in honor of our colleague, Prof. Dr. Hartmut Arndt, Institute of Zoology, University of Cologne, Germany, in recognition of his support for biodiversity research in Vietnam. As common names, we suggest Arndt's Bent-toed Gecko (English) and *Thằn lằn ngón arndt* (Vietnamese).

### Type material (Figs 6–9)

#### Holotype

VIETNAM • ♂; Binh Dinh Province, Van Canh District, near Hiep Ha Village; 13°39.858' N, 108°53.355' E; 270 m a.s.l.; 13 Aug. 2016; D.T. Do and T.V. Nguyen; Field No. BD.2016.141; IEBR R.4930.

#### Paratypes

VIETNAM • 1 ♂; Binh Dinh Province, Quy Nhon District, Quy Nhon City; 13°41.718' N, 109°10.277' E; 140 m a.s.l.; 8 Aug. 2016; D.T. Do and T.V. Nguyen; Field No. BD.2016.1; IEBR R.5219 • 2 ♂♂, 1 ♀; Binh Dinh Province, Van Canh District, near Dak Dum Village; 13°38.365' N, 108°57.863' E; 150 m a.s.l.; 11 Aug. 2016; D.T. Do and T.V. Nguyen; Field No. BD.2016.86, BD2016.87, BD.2016.88;

IEBR R.4931 to IEBR.4933 • 1 ♀; Binh Dinh Province, Van Canh District, near Hiep Ha Village; 13°39.858' N, 108°53.355' E; 270 m a.s.l.; D.T. Do and T.V. Nguyen; Field No. BD.2016.86; IEBR R.5077 • 2 ♂♂; same collection data as for preceding; Field No. BD.2016.142, BD.2016.143; ZFMK 103910, ZFMK 103911.

### Description of holotype

Adult male; snout-vent length 74.4 mm; tail regenerated, 98.15 mm in length; body slender, elongate (AG/SVL ratio 0.39); head distinct from neck, elongate, depressed (HL/SVL 0.29, HW/HL 0.67, HH/HL 0.37); loreal region concave; snout long, blunt in dorsal profile (SE/HL 0.37), longer than diameter of orbit (OD/SE 0.61); scales on snout small, round or oval, granular, larger than scales on occiput; orbit large (OD/HL 0.22); pupils vertical; ear opening small, oval (ED/HL 0.06); rostral almost twice as wide as high with an inverse Y-shaped structure, surrounded by first supralabial, naris, nasorostral on each side, and internasal; nostril opening small and oval, surrounding by rostral, nasorostral, 2 supranasals and one postnasal; mental scale triangular, wider than high (ML/MW 0.74); two enlarged, triangular postmentals; supralabials 12/12; infralabials 11/13.

Dorsal scales granular, dorsal tubercles round, keeled, conical, in 20 irregular rows at midbody; tubercles on occiput small; each tubercle surrounded by 9 or 10 granular scales; ventral scales smooth, round, midventral scales approximately 3–4 times as large as dorsal scales, slightly imbricate laterally, in 37 longitudinal rows at midbody between ventrolateral folds; precloacal groove absent; enlarged femoral scales 7 or 8 on each thigh, about twice the size of surrounding scales; enlarged precloacal scales 17, arranged in a rhombus; femoral pores absent; precloacal pores 6, arranged in ^-shaped series.

Fore and hindlimbs moderately slender (ForeaL/SVL 0.15 mm, CrusL/SVL 0.16); forelimbs dorsally covered by several slightly enlarged tubercles; dorsal surface of hindlimbs bearing well-developed tubercles; two postcloacal tubercles on each side on the hemipenal swellings; phalanges without



**Fig. 6.** *Cyrtodactylus arndti* sp. nov., holotype, ♂ (IEBR R.4930), in life.



webbing; each claw sheathed by two scales, the ventral sheath larger than the upper scale; number of subdigital lamellae on first finger 12/13, on first toe 13/13, on fourth finger 18/18, on fourth toe 22/22.

#### **Coloration in preservative**

Dorsal surface of head, body and limbs light-brown with some dark-brown pattern, without light bordering; occiput marbled with small, irregular dark-brown banded; rostral, mental, first three supralabials and first infralabials greyish brown, remaining infralabials light beige, some with greyish brown speckles or frames; nuchal band discontinuous, consisting of two stripes extending from the orbits to the neck, ending by a dark blotch on each side and a third blotch medially; dorsum with 7 irregular bands, the first two interrupted; dorsolateral region covered with round or elongate dark-brown blotches; tail with 6 dark-brown bands, fade ventrally, some small dark-brown spots arranged in a line along the lateral side of tail, tail tip dark-brown; dorsal surface of limbs with 6 or 7 irregular dark-brown bands; phalanges brown with beige knuckles; dorsal tubercles white or dark-brown depending on position; tubercles on dorsal surface of limbs and tail light-brown; venter greyish brown.



**Fig. 7.** *Cyrtodactylus arndti* sp. nov., paratypes ♂♂ (IEBR R.4931, IEBR R.4932), in life.

**Table 3** (continued on next page). Measurements (in mm) and morphological characters of the type series of *Cyrtodactylus arndti* sp. nov. Bilateral meristic characters are given as (left/right). Abbreviations: \* = regenerated or broken tail; max = maximum; min = minimum.

Characters	IEBR R.4930	IEBR R.5129	IEBR R.5077	IEBR R.4931	IEBR R.4932	IEBR R.4933	ZFMK 103910	ZFMK 103911
	Holotype	Paratype	Paratype	Paratype	Paratype	Paratype	Paratype	Paratype
Sex	♂	♂	♀	♂	♂ (sub)	♀	♂	♂
SVL	74.4	74.4	75.6	80.9	66.1	74.7	73.4	76.9
TaL	98.2*	67.1*	91.5	50.1*	75.1	85.9*	94*	68.8*
AG	28.7	30.6	31.6	34.7	24.7	27.4	27.2	26.4
HL	21.8	22.4	21.6	23.2	18.8	20.5	21.4	23.2
HW	14.5	14.4	15.1	16.2	13.5	15.1	15.1	15.3
HH	8.1	8.9	9.2	9.8	6.1	8.1	7.8	8.5
OD	4.9	4.8	5.3	6.1	4	5.1	5.2	5.3
SE	8	10.0	9.8	10	8.0	9.9	9.3	9.4
EyeEar	6.4	6.0	6.1	7.1	5.6	6.2	6.6	7.1
ED	1.4	1.8	1.9	1.8	1.4	6.2	1.9	1.1
IND	2.7	2.6	2.5	2.4	2.2	2.3	2.7	2.2
RW	4.5	3.3	4.1	3.8	3.3	3.6	3.2	3.4
RH	2.3	2.2	2.2	2.3	2.0	2.2	2.1	2.2
MW	3.1	3.0	3.0	3.1	3.0	3.2	3.1	3.1
ML	2.3	2.1	2.4	2.6	2.7	2.3	2.4	2.6
BW	14.5	15.6	16.2	17.7	12.5	15.5	15.6	14.5
ForeaL	11.4	11.5	9.9	11.4	9.9	10.3	10.3	10.8
CrusL	12.1	13.3	12.5	13.7	12.4	13.3	12.8	14.1

Table 3 (continued).

Characters	IEBR R.4930	IEBR R.5129	IEBR R.5077	IEBR R.4931	IEBR R.4932	IEBR R.4933	ZFMK 103910	ZFMK 103911
	Holotype	Paratype	Paratype	Paratype	Paratype	Paratype	Paratype	Paratype
FemurL	11.7	14.3	14.3	12.9	11.6	12.3	12.5	13.9
SL	11/13	10/9	11/11	10/10	11/11	10/10	11/10	8/12
IL	12/12	10/9	8/8	12/11	9/8	8/9	10/8	8/8
N	4/5	4/4	4/4	4/4	4/4	4/4	4/4	4/4
IN	1	1	1	1	1	2	3	2
PM	2	2	2	2	2	2	2	2
DTR	20	17	17	19	17	18	20	18
GST	9–10	10–11	9–11	10–11	9–11	10–11	9–11	9–12
V	37	26	36	36	38	36	36	36
EFS	8/7	10/10	11/11	7/7	7/7	6/5	8/10	8/7
FP	absent	1/0	0/0	1p/1p	0/1	absent	absent	absent
EPS	17	19	21	19	17	21	23	17
PP	6	6	6	6	6	6	6	6
PAT	2/2	2/2	2/2	2/2	2/2	3/3	3/2	3/3
LD1	12/13	10/10	10/11	11/11	11/11	12/12	11/11	11/10
LT1	13/13	11/11	12/14	11/11	11/12	12/13	12/12	11/11
LD4	18/18	17/16	18/18	18/18	17/15	20/19	19/18	17/17
LT4	22/22	19/19	20/21	21/22	20/19	22/22	20/21	18/17

### Sexual dimorphism and variation

The female (IEBR R.4933) differs from the males by the absence of hemipenal swellings. All male specimens have 6 preloacal pores but the females has 6 pitted scales only. Three males (IEBR R.4930, ZFMK 103910, ZFMK 103911) and the female lack femoral pores (IEBR R.5077, IEBR R.4933). For further morphological characters see Table 3.

### Comparisons

The new species can be distinguished from all other member of *Cyrtodactylus irregularis* group from Vietnam by morphological characteristics (see Table 4).

*Cyrtodactylus arndti* sp. nov. differs from *C. badenensis* by having the presence of enlarged femoral scales (5–11 vs absent in *C. badenensis*), the presence of preloacal pores in males (6 vs absent in *C. badenensis*), the presence of pitted preloacal pores in females (6 vs absent in *C. badenensis*), and different dorsal pattern (irregular bands vs banded in *C. badenensis*); differs from *C. bidoupimontis* by having the presence of pitted preloacal pores in females (6 vs absent in *C. bidoupimontis*), having moderately broad nuchal band, continuous or discontinuous band (vs well developed, widened posteriorly in *C. bidoupimontis*), different dorsal pattern (6 or 7 irregular transverse bands, colouration dark-brown on light-brown background vs 4–5 dark irregular transverse dorsal bands, usually with light borders), and the presence of transversely enlarged subcaudals vs absent in *C. bidoupimontis*; differs from *C. bugiamapensis* by having fewer preloacal pores in males (6 vs 7–11 in *C. bugiamapensis*), different dorsal color pattern (irregular, dark-brown transverse bands vs unclear transversal bands formed by irregular roundish to oblong, dark brown spots in *C. bugiamapensis*), moderately broad nuchal band, continuous or discontinuous bands (vs dark nuchal band, which can be medially divided, narrow, U-shape in *C. bugiamapensis*), and the presence of transversely enlarged subcaudals vs absent in *C. bugiamapensis*; differs from *C. buchardi* by having a larger size (SVL of 73.4–80.9 vs 60–65 in *C. buchardi*), the presence of enlarged femoral scales (5–11 vs absent in *C. buchardi*), more subdigital lamellae on first finger (15–20 vs 14 in *C. buchardi*), more subdigital lamellae on first toe (17–22 vs 12



**Fig. 8.** *Cyrtodactylus arndti* sp. nov., type series in preservative (the holotype is the third from right).

in *C. buchardi*) and the presence of transversely enlarged subcaudals vs absent in *C. buchardi*); differs from *C. caovansungi* by having a smaller size (SVL of 73.4–80.9 vs 90.4–94.0 mm), fewer femoral pores (0–2 vs 6 in *C. caovansungi*), fewer precloacal pores in males (6 vs 9 in *C. caovansungi*), the presence of pitted precloacal pores in females (6 vs absent in *C. caovansungi*), and fewer subdigital lamellae under the fourth toe (17–22 vs 23–25 in *C. caovansungi*); differs from *C. cattienensis* by having a larger size (73.4–80.9 mm vs 43.5–69.0 mm in *C. cattienensis*), the presence of pitted precloacal pores in females (6 vs absent in *C. cattienensis*), and the presence of transversely enlarged subcaudals (vs absent in *C. cattienensis*); differs from *C. chungii* by having a larger size (73.4–80.9 mm vs 66.6–68.5 mm in *C. chungii*), fewer precloacal pores in males (6 vs 7 in *C. chungii*), fewer enlarged precloacal scales (17–23 vs 41–45 in *C. chungii*), and the presence of transversely enlarged subcaudals (vs absent in *C. chungii*); differs from *C. cryptus* by having fewer ventral scale rows (26–38 vs 47–50 in *C. cryptus*), the presence of enlarged femoral scales (5–11 vs absent in *C. cryptus*), fewer precloacal pores in males (6 vs 9–11 in *C. cryptus*), the presence of pitted precloacal pores in females (6 vs absent in *C. cryptus*), and the presence of transversely enlarged subcaudals (vs absent in *C. cryptus*); differs from *C. cucdongensis* by having a larger size (SVL 73.4–80.9 mm vs 55.8–65.9 mm in *C. cucdongensis*), fewer ventral scale rows (26–38 vs 41–44 in *C. cucdongensis*), more subdigital lamellae under the first toe (11–14 vs 8–11 in *C. cucdongensis*), and the presence of transversely enlarged subcaudals (vs absent in *C. cucdongensis*); differs from *C. culaochamensis* by having fewer ventral scale rows (26–38 vs 45–50 in *C. culaochamensis*), the presence of enlarged femoral scales (5–11 vs absent in *C. culaochamensis*), fewer precloacal pores in males (6 vs 7–8 in *C. culaochamensis*), and the presence of pitted precloacal pores in females (6 vs absent in *C. culaochamensis*); differs from *C. dati* by having fewer ventral scale rows (26–38 vs 42–48 in *C. dati*), fewer femoral pores (0–2 vs 3–4 on each side in *C. dati*), different dorsal color pattern (irregular bands vs blotches in *C. dati*), and the presence of transversely enlarged subcaudals (vs absent in *C. dati*); differs from *C. gialaiensis* by having a larger size (73.4–80.9 mm vs 50.1–62.8 mm in *C. gialaiensis*), the presence of enlarged femoral scales (5–11 vs absent in *C. gialaiensis*), fewer precloacal pores in males (6 vs 9–10 in *C. gialaiensis*), and more subdigital lamellae under the fourth finger (15–20 vs 14–15 in *C. gialaiensis*); differs from *C. huynhi* by having fewer ventral scale rows (26–38 vs 43–46 in *C. huynhi*), more enlarged femoral scales (5–11 vs 3–5 in *C. huynhi*), fewer precloacal pores in males (6 vs 7–9 in *C. huynhi*), and the presence of transversely enlarged subcaudals (vs absent in *C. huynhi*); differs from *C. irregularis* by having the presence of precloacal pores in males (1–2 vs absent in *C. irregularis*), different dorsal color pattern (irregular bands vs blotched in *C. irregularis*), and the presence of transversely enlarged subcaudals (vs absent in *C. irregularis*); differs from *C. kingsadai* by having a smaller size (SVL 73.4–80.9 mm vs 83.0–94.0 mm in *C. kingsadai*), fewer ventral scale rows (26–38 vs 39–46 in *C. kingsadai*), and fewer precloacal pores in males (6 vs 7–9 in *C. kingsadai*); differs from *C. orlovi* by having a larger size in males (SVL 73.4–80.9 mm vs 61.0–68.2 mm in *C. orlovi*), the presence of pitted precloacal pores in females (6 vs absent in *C. orlovi*), and the presence of transversely enlarged subcaudals (vs absent in *C. orlovi*); differs from *C. phnomchiensis* by having fewer ventral scale rows (26–38 vs 45–54 in *C. phnomchiensis*), more precloacal pores in males (6 vs 4–5 in *C. phnomchiensis*), fewer AG/SVL ratio (0.34–0.43 vs 0.45–0.48 in *C. phnomchiensis*), and the presence of transversely enlarged subcaudals (vs absent in *C. phnomchiensis*); differs from *C. phumyensis* by having a larger size (SVL 73.4–80.9 mm vs 63.6–66.8 mm in *C. phumyensis*), and the presence of transversely enlarged subcaudals (vs absent in *C. phumyensis*); differs from *C. phuocbinhensis* by having a larger size (SVL 73.4–80.9 mm vs 46.0–60.4 mm in *C. phuocbinhensis*), fewer ventral scale rows (26–38 vs 43–47 in *C. phuocbinhensis*), fewer precloacal pores in males (6 vs 7 in *C. phuocbinhensis*), the presence of pitted precloacal pores in females (6 vs absent in *C. phuocbinhensis*); differs from *C. pseudoquadrivirgatus* by having fewer ventral scale rows (26–38 vs 41–57 in *C. pseudoquadrivirgatus*), the presence of enlarged femoral scales (5–11 vs absent in *C. pseudoquadrivirgatus*), different dorsal color pattern (irregular bands vs blotched in *C. pseudoquadrivirgatus*), and the presence of transversely enlarged subcaudals (vs absent in *C. pseudoquadrivirgatus*); differs from *C. raglai* by having a smaller size (SVL 73.4–80.9 mm vs 95–111.7 mm in *C. raglai*), more precloacal pores in males (6 vs 5 in

**Table 4** (continued on next page). Morphological comparisons between *Cyrtodactylus chumuensis* sp. nov., *Cyrtodactylus arndti* sp. nov. and 23 congeners from the *Cyrtodactylus irregularis* complex based on examination of specimens and data obtained from the literature (Ziegler *et al.* 2002; Nguyen *et al.* 2006, 2013, 2014, 2015, 2017a, 2017b, 2021; Heidrich *et al.* 2007; Nazarov *et al.* 2008, 2012; Ngo 2008, 2013; Ngo & Bauer 2008; Ngo *et al.* 2010; Rösler *et al.* 2008; Ngo & Chan 2010, 2011; Ngo & Grismer 2012; Ziegler *et al.* 2010, 2013; Luu *et al.* 2011, 2017; Phung *et al.* 2014; Le *et al.* 2016; Ostrowski *et al.* 2020, 2021; Do *et al.* 2021). Abbreviations: ? = data not available in literature; – = characteristic not present; + = characteristic present but not uniquely determined; \* = regenerated or broken tail.

Species	SVL (mm)	TaL (mm)	V	EFS	FP	PP (M)	PP (F)	LD4	LT4	Color pattern of dorsum	Subcaudals
1 <i>Cyrtodactylus chumuensis</i> sp. nov.	67.5	51.4*	43–45	4–5	0–2	6–7	?	16–19	17–21	banded	absent
2 <i>Cyrtodactylus arndti</i> sp. nov.	73.4–80.9	50.1*–91.51	26–38	5–11	0–2	6	6	15–20	17–22	banded	present
3 <i>C. badenensis</i>	59.3–74.1	58.6–82.4	25–29	absent	absent	0	0	?	18–22	banded	present
4 <i>C. bidoupinontis</i>	74.0–86.3	75.0–86	38–43	8–10	absent	4–6	0	15–20	18–23	banded	absent
5 <i>C. bugiamapensis</i>	58.6–76.8	65.3–83.0	36–46	6–10	absent	7–11	0–7	15–17	17–20	blotched	absent
6 <i>C. buchardi</i>	60.0–65.0	46.0–54.0	30	absent	absent	9	0	14	12	blotched	absent
7 <i>C. caovansungi</i>	90.4–94.0	120.0	38–44	8	6	9	0	22	23–25	banded	present
8 <i>C. cattienensis</i>	43.5–69.0	51–64.7	28–42	3–8	absent	6–8	0–8 pitted scales	12–16	14–19	banded	absent
9 <i>C. chungii</i>	66.6–68.5	62.8*–82.2	30–31	4–6	absent	7	6	?	17–20	banded	absent
10 <i>C. cryptus</i>	62.5–90.8	63.5–88.4	47–50	absent	absent	9–11	0	18–19	20–23	banded	absent
11 <i>C. cucdongensis</i>	55.8–65.9	max. 81.3	41–44	5–9	absent	5–6	4–6	13–18	15–20	banded	absent
12 <i>C. culaochamensis</i>	69.8–79.8	89.7–91.2	45–50	absent	absent	7–8	absent	18–19	20–23	banded	absent
13 <i>C. dati</i>	max 70.1	max 57.3	42–48	4–7	3–4 each	5–6	?	?	18–19	blotched	absent
14 <i>C. giataiensis</i>	50.1–62.8	?	38–45	absent	absent	9–10	0–8	14–15	15–17	banded	absent
15 <i>C. huynhi</i>	67.2–79.8	61.5–78.6	43–46	3–5	3–8	7–9	0–8 pitted scales	14–17	17–21	banded	absent
16 <i>C. irregularis</i>	72.0–86.0	66.0–74.0	38–45	7–8	absent	5–7	0–6	15–16	18–19	blotched	absent
17 <i>C. kingsadai</i>	83.0–94.0	max 117	39–46	9–12	0–4	7–9	4–8	19–21	21–25	banded	present
18 <i>C. orlovi</i>	61–77.7	Max 71.2	36–39	3–8	absent	5–6	0	15–17	16–19	banded	absent

Table 4 (continued).

Species	SVL (mm)	TaL (mm)	V	EFS	FP	PP (M)	PP (F)	LD4	LT4	Color pattern of dorsum	Subcaudals
19 <i>C. phnomchiensis</i>	76.1–80.7	56.9–79.1	45–54	0–8	absent	4–5	1–7 pitted scales	18–20	20–23	banded	absent
20 <i>C. phumyensis</i>	63.6–66.8	?	33–41	5–7	absent	5–7	6 pitted scales	18–19	18–21	banded	absent
21 <i>C. phuocbinhensis</i>	46.0–60.4	76.1	43–47	5	absent	7	0	16–21	17–19	striped/blotched	absent
22 <i>C. pseudoquadrivirgatus</i>	48.6–83.3	55.7–82.3	41–57	absent	absent	5–9	5–10	15–21	16–25	blotched	absent
23 <i>C. raglai</i>	95–111.7	113.4–135	36–39	9–10	absent	5	0	?	21–22	banded	present
24 <i>C. sangi</i>	49.9–56.3	47.9*	37	4	absent	7	4 pitted scale	?	?	banded	absent
25 <i>C. takouensis</i>	74.7–81.1	77.7–91.0	39–40	3–5	0–2	3–4	0	16–17	18–20	banded	present
26 <i>C. taynguyenensis</i>	60.0–85.0	66.0–94.0	42–49	absent	absent	6	0	13–18	17–21	blotched	absent
27 <i>C. yangbayensis</i>	78.5–92.3	91.3–109.1	39–46	5–16	0–2	6–8	0	16–19	15–17	banded	present
28 <i>C. ziegleri</i>	84.6–93.0	95.0–107.0	33–39	8–10	0–6	5–8	0–8	16–19	18–21	banded	absent

*C. raglai*) and the presence of pitted precloacal pores in females (6 vs absent in *C. raglai*); differs from *C. sangi* by having a larger size (SVL 73.4–80.9 mm vs 49.9–56.3 mm in *C. sangi*), more enlarged femoral scales (5–11 vs 4 in *C. sangi*), fewer precloacal pores in males (6 vs 7 in *C. sangi*), and more pitted precloacal pores in females (6 vs 4 in *C. sangi*); differs from *C. takouensis* by having more enlarged femoral scales (5–11 vs 3–5 in *C. takouensis*), more precloacal pores in males (6 vs 3–4), the presence of pitted precloacal pores in females (6 vs absent in *C. takouensis*), and the different dorsal color pattern (irregular bands vs banded in *C. takouensis*); differs from *C. taynguyenensis* by having more ventral scale rows (26–38 vs 42–49 in *C. taynguyenensis*), the presence of enlarged femoral scales (5–11 vs absent in *C. taynguyenensis*), the different dorsal color pattern (irregular bands vs blotched in *C. taynguyenensis*), and the presence of transversely enlarged subcaudals (vs absent in *C. taynguyenensis*); differs from *C. yangbayensis* by having the presence of pitted precloacal pores in females (6 vs absent in *C. yangbayensis*), more subdigital lamellae under the fourth toe (17–22 vs 15–17), and fewer subdigital lamellae on first toe (11–14 vs 18–20 in *C. yangbayensis*); differs from *C. ziegleri* by having a smaller size (SVL 73.4–80.9 mm vs 84.6–93.0 mm in *C. ziegleri*), the presence of transversely enlarged subcaudals (vs absent in *C. ziegleri*), and dark-brown transverse bands of the tail narrower than the light-brown interspaces (vs dark transverse bands wider than the light interspaces in *C. ziegleri*).

Differs from *C. chumuensis* sp. nov. by having a larger size (SVL 73.4–80.9 mm vs maximum 67.5 mm in *C. chumuensis*), fewer ventral scale rows (26–38 vs 43–45 in *C. chumuensis*), and the presence of transversely enlarged subcaudals (vs absent in *C. chumuensis*).

### Distribution

*Cyrtodactylus arndti* sp. nov. is currently known only from the Van Canh District, Binh Dinh Province, Vietnam (Fig. 1).



**Fig. 9.** Habitat of *Cyrtodactylus arndti* sp. nov. in Hiep Ha Village, Van Canh District, Binh Dinh Province.

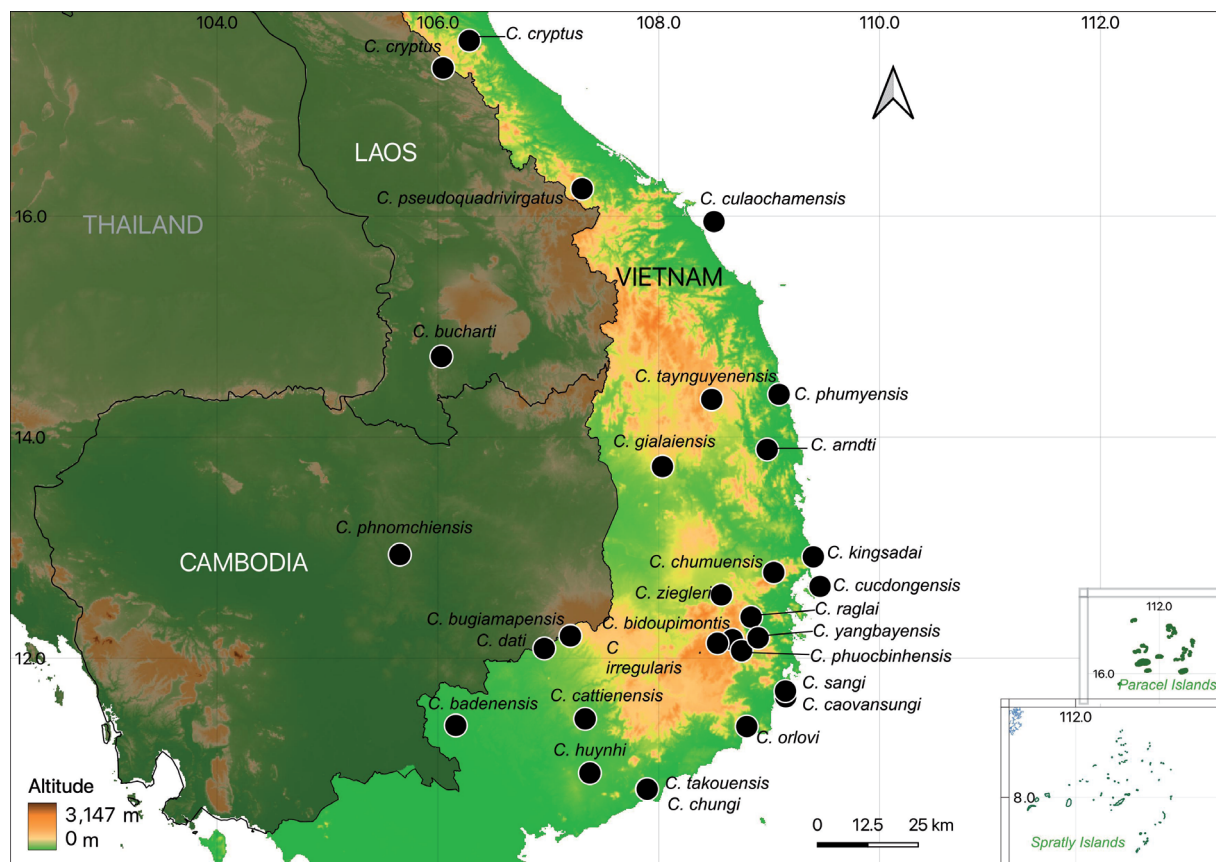


## Natural history

Specimens were found at night between 19:00 and 22:00, on trees or on granite rock, along rocky streams, about 0.6–1.5 m above the ground, at elevations between 150 and 300 m a.s.l. The surrounding habitat was evergreen forest of medium and small hardwoods mixed with shrubs and vines (Fig. 9). The humidity was approximately 40–62% and the air temperature ranged from 28.9 to 33.1°C. Other reptiles species found at the sites included *Acanthosaura coronata* (Günther, 1861) *Dixonius vietnamensis* Das, 2004, *Gekko gekko* (Linnaeus, 1758), *Gekko* sp., *Eutropis multifasciata* (Kuhl, 1820), *Boiga jaspidea* (Duméril, Bibron & Duméril, 1854), *Psammodynastes pulverulentus* (Boie, 1827), and *Trimeresurus* sp.

## Discussion

*Cyrtodactylus irregularis* was described by Smith in 1921 based on specimens collected from the Cam Ly River Valley, Langbian Plateau (now known as Lam Dong Province, Vietnam) (Smith 1921; Grismer *et al.* 2021). After its description, the name *Cyrtodactylus irregularis* was applied to all specimens of *Cyrtodactylus* collected in north-central and south-central Vietnam for more than 80 years. However, as *C. irregularis* is still being investigated, we referred to the specimens of *Cyrtodactylus* from Lac Duong, Lam Dong Province, Vietnam as *C. cf. irregularis* in this study. At the moment, the *Cyrtodactylus irregularis* group is split into 28 species (including the two species in the present study) and it is the largest group within the genus *Cyrtodactylus* (Grismer *et al.* 2021; Ngo *et al.* 2022). Most members of the *Cyrtodactylus irregularis* group are distributed in north-central and south-central Vietnam which is also known as the Truong Son Range (Fig. 10) (Grismer *et al.* 2021; Ngo *et al.* 2022). Only a few species



**Fig. 10.** Type localities of all taxa of *Cyrtodactylus irregularis* group occurring in Cambodia, Laos and Vietnam (the altitude data based on GADM database of Global Administrative Areas, 2022).

inhabit eastern Cambodia and southeast Laos, i.e., *C. buchardi*, *C. cryptus*, and *C. phnomchiensis* (David *et al.* 2004; Luu *et al.* 2016b; Neang *et al.* 2020; Grismer *et al.* 2021).

Species in this group occur in different habitat types, including granitic montane and limestone evergreen forests, and coffee farms. The adaptation ability allows its members to successfully diversify by occupying different ecological niches (Grismer *et al.* 2020; Ngo *et al.* 2022). Many areas in Cambodia, Laos, Vietnam where members of the *C. irregularis* group might occur are still poorly studied, e.g., the Central Highlands in Vietnam (Fig. 10). It is also noted that a number of species complexes and several potentially new species have been reported within the range of these broadly distributed taxa (Grismer *et al.* 2021; Ngo *et al.* 2022). For example, there exist three *C. pseudoquadrivirgatus* clades with high genetic divergence from each other as shown by this and previous studies. *Cyrtodactylus pseudoquadrivirgatus* was described by Rösler *et al.* (2008) from A Luoi, Thua Thien Hue Province; Huong Hoa, Quang Tri Province; Ba Na Nature Reserve, Da Nang Province; Kon Plong, Kon Tum Province. Thus, further studies are required to determine the actual distribution of the *C. irregularis* group by sequencing and examining the type specimens (i.e., *C. pseudoquadrivirgatus*, *C. irregularis*) to show whether it is in fact a species complex, viz. containing multiple taxa.

Similar to those relationships reported by Grismer *et al.* (2021) using ND2, the phylogeny supported by BI and ML in our study showed that *C. grimeri* belongs to the *C. condorensis* group although the former was placed in both the *C. irregularis* and *C. condorensis* groups in the barcoding study by Brennan *et al.* (2017) using a combination of COI and ND2. Moreover, the phylogenetic position of *C. badenensis* is still unclear. Grismer *et al.* (2021) considered *C. badenensis* the sister species to the *C. condorensis* group in their ML analysis but this placement was not supported in the BEAST analysis, using the mitochondrial gene ND2 and tRNAs. However, it was supported as a member of or sister to the *C. irregularis* group in this study and in several previous studies using COI gene or combining mito-nuclear data in both ML and BI analyses (i.e., Brennan *et al.* 2017; Nguyen *et al.* 2017; Grismer *et al.* 2021; Ostrowski *et al.* 2021). In addition, the species was not recognized as representative of the *C. irregularis* group based on morphological characters. It has a different dorsal pattern compared to that of remaining species within the *C. irregularis* group. Instead of an irregular brown dorsal pattern on a beige background and the occiput marbled in the same color, *C. badenensis* shows regular white transverse bands on a black background and a yellow occiput (Nguyen *et al.* 2006). *Cyrtodactylus badenensis* is tentatively placed in the *C. irregularis* group in the present study pending more comprehensive molecular study. Furthermore, *C. buchardi* was considered a member of *C. irregularis* in Grismer *et al.* (2021), but the authors who described this species suggested that *C. buchardi* is more closely related to the *C. angularis* group and especially to *C. papilionoides* based on five morphological characters (David *et al.* 2004; Grismer *et al.* 2021). Unfortunately, its phylogenetic placement has not been determined due to the lack of DNA samples. Thus, the status of *C. buchardi* is still controversial and should be addressed in future studies. *Cyrtodactylus phuocbinhensis* was strongly supported as the sister species to *C. sangi* Pauwels, Nazarov, Bobrov & Zhang and *C. cattienensis* Geissler, Nazarov, Orlov, Böhme, Phung, Nguyen & Ziegler, 2009 and *C. chungi* Ostrowski, Le, Ngo, Pham, Phung, Nguyen & Ziegler, 2021 and *C. orlovi* Do, Phung, Ngo, Le, Ziegler, Pham & Nguyen, 2021 with strong nodal support in our BI analysis (Fig. 2), although Pauwels *et al.* (2018) suggested that *C. phuocbinhensis* belongs to a large clade, encompassing all other members of *Cyrtodactylus irregularis* group by high statistical values in both BI and ML analyses. In our study, however, we used different outgroups and incorporated more species than did Pauwels *et al.* (2018), and these changes might have caused the topological differences.

Importantly, knowledge on the distribution of *Cyrtodactylus* is still limited. Almost all species of *Cyrtodactylus* are only known from their type localities. According to the IUCN Red List, several species of this genus are facing severe extinction risks, as there are three species listed as Critically Endangered (CR), three species as Endangered (EN), and six species as Vulnerable (VU). Of these, two species listed as CR, *C. gialaiensis* and *C. takouensis*, one as EN, *C. caovansungi*, and two as VU, *C. badenensis* and *C. huynhi*, belong to the *Cyrtodactylus irregularis* group. Therefore, urgent research is needed not only

for resolving taxonomic issues but also for providing a better understanding of the population status, threats, and distribution of species within the largest group within the mega-diverse *Cyrtodactylus*.

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### **Supplementary material**

**Supp. file 1.** Uncorrected (p) distance matrix showing percentage pairwise genetic divergence (COI) between *Cyrtodactylus chumuensis* sp. nov., *Cyrtodactylus arndti* sp. nov. and closely related species of *Cyrtodactylus* Gray, 1827. <https://doi.org/10.5852/ejt.2023.875.2141.9087>