



## First record of the *Cyrtodactylus brevipalmatus* group (Squamata: Gekkonidae) from Vietnam with description of a new species

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### Abstract

A new species of the genus *Cyrtodactylus* is described from Dien Bien Province, northwestern Vietnam based on morphological and molecular data. *Cyrtodactylus ngati* **sp. nov.** can be distinguished from remaining congeners by the following combination of characters: maximum SVL 69.3 mm; dorsal pattern consisting of six dark irregular transverse bands between limb insertions; inter-supranasals one; dorsal tubercles present on occiput, body, hind limbs and on first half of tail; 17–22 irregular dorsal tubercle rows at midbody; lateral folds clearly defined, with interspersed tubercles; 32–38 ventral scales between ventrolateral folds; 13 precloacal pores separated by a diastema of 5/5 poreless scales from a series of 7/7 femoral pores in enlarged femoral scales; precloacal and femoral pores absent in females; 1–3 postcloacal tubercles on each side; transversely enlarged median subcaudal scales absent. In the molecular analyses, the new species is shown to be the sister taxon to *C. interdigitalis* from Thailand. This is the 47<sup>th</sup> species of the genus *Cyrtodactylus* and the first member of the *C. brevipalmatus* species group recorded from Vietnam.

**Key words:** *Cyrtodactylus ngati* **sp. nov.**, morphology, phylogeny, taxonomy, northwestern Vietnam

### Introduction

*Cyrtodactylus* Gray, 1827 is the most speciose genus of the family Gekkonidae, with a total of 306 recognized species to date (Ostrowski *et al.* 2020, 2021; Schneider *et al.* 2020; Uetz *et al.* 2020). Its distribution extends throughout tropical South Asia, Indochina, the Philippines, the Indo-Australian Archipelago, and the Solomon Islands in the East (Bauer & Henle 1994). Over the last decade, Indochina (Cambodia, Laos, and Vietnam) has been a hotspot of new species discoveries with 55 new species described from these nations (e.g., Grismer *et al.* 2020; Neang *et al.* 2020; Ostrowski *et al.* 2020, 2021; Schneider *et al.* 2020; Uetz *et al.* 2020).

In Vietnam, 46 species were currently recognized, accounting for 15% of the *Cyrtodactylus* diversity recognized to date. Of those, 26 species of the genus have been described from Vietnam in the last 10 years. However, it is expected that the number of species in the genus will continue to increase as many areas in the country are still imperfectly studied.

The *Cyrtodactylus brevipalmatus* group contains three predominantly arboreal species comprising *C. brevipalmatus* Smith, 1923, *C. elok* Dring 1979, and *C. interdigitalis* Ulber, 1993 (Grismer *et al.* 2021). These species range from central Laos through Thailand to southern Peninsular Malaysia bearing diagnostic characters of spines on the dorsolateral surface of the tail, a prehensile tail, webbing on the fingers and toes, and a banded dorsal pattern (Dring 1979; Ulber 1993; Grismer 2008; Nurngsomsri *et al.* 2014; Chuaynkern *et al.* 2018; Grismer *et al.* 2021).

In August 2016 and August 2017, field surveys were conducted in areas with limestone outcrops throughout Dien Bien Province. During the field trip, four *Cyrtodactylus* specimens were collected in Dien Bien District. Morphological and molecular analyses revealed this population belongs to the *Cyrtodactylus brevipalmatus* group and is closely related to *C. interdigitalis*, at the same time showing distinct morphological differences in comparison with congeners within the group. Therefore, we describe the newly discovered population from Dien Bien District, Dien Bien Province, as a new species.

## Material and methods

**Sampling.** Field surveys were conducted in Pa Xa Lao Village, Pa Thom Commune, Dien Bien District, Dien Bien Province, northwestern Vietnam in August 2016 and August 2017. After the live specimens were photographed, they were euthanized in a closed vessel with a piece of cotton wool containing ethyl acetate (Simmons, 2002), fixed in 85% ethanol for eight hours and subsequently transferred into 70% ethanol for permanent storage. Muscle tissue samples of the collected bent-toed geckos were preserved separately in 95% ethanol. The preserved specimens and tissue samples were deposited in the collections of the Museum of Biology, Hanoi National University of Education (HNUE), the Institute of Ecology and Biological Resources (IEBR), and the Vietnam National University of Forestry (VNUF), Hanoi, Vietnam.

**Molecular data and phylogenetic analyses.** Since the new population is closely related to *C. interdigitalis* Ulber 1993, we incorporated all taxa of the *Cyrtodactylus brevipalmatus* group (*sensu* Grismer *et al.* 2021) in the analyses. Sequences of *C. elok* were downloaded from GenBank. Sequences from three vouchered specimens from Dien Bien Province (HNUE-R00111, IEBR 4829, VNUF R.2020.12), *C. brevipalmatus*, and *C. interdigitalis* were generated. Two species, *C. soni* Le, Nguyen, Le & Ziegler 2016 and *C. wayakonei* Nguyen, Kingsada, Rösler, Auer & Ziegler 2010, were used as outgroups based on the results of Grismer *et al.* (2021) (Table 1).

**TABLE 1.** *Cyrtodactylus* samples used in the molecular analyses.

Species	GenBank No.	Locality	Voucher number
<i>Cyrtodactylus brevipalmatus</i>	MW655792	Pulau Langkawi, Malaysia	LSUHC 11788
<i>Cyrtodactylus elok</i>	HM888479	Malaysia	ZMMURAN 1992
<i>Cyrtodactylus elok</i>	MF169914	-	-
<i>Cyrtodactylus interdigitalis</i>	MW655791	Petchabun, Thailand	LSUHC 11006
<i>Cyrtodactylus ngati</i> <b>sp. nov.</b>	MW655790	Dien Bien, Vietnam	HNUE R-00111
<i>Cyrtodactylus ngati</i> <b>sp. nov.</b>	MW655789	Dien Bien, Vietnam	IEBR 4829
<i>Cyrtodactylus ngati</i> <b>sp. nov.</b>	MW655788	Dien Bien, Vietnam	VNUF R.2020.12
<i>Cyrtodactylus soni</i>	KX430033	Ninh Binh, Vietnam	IEBR R.2016.4
<i>Cyrtodactylus wayakonei</i>	KJ817438	Luang Nam Tha, Laos	ZFMK 91016

DNA was extracted using DNeasy Blood and Tissue kit (Qiagen, Germany) following the manufacturer's instruction. Extracted DNA was amplified by 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 seconds, 45°C for 45 seconds, 72°C for 60 seconds; and the 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% 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 in both directions.

After sequences were aligned by Clustal X v2 (Thompson *et al.* 1997), data were analyzed using maximum parsimony (MP) implemented in PAUP\*4.0b10 (Swofford 2001), maximum likelihood as implemented in IQ-TREE (Nguyen *et al.* 2015) and Bayesian inference (BI) as implemented in MrBayes v3.2 (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. All characters were equally weighted and unordered. For the maximum likelihood (ML) analysis, we used IQ-TREE v.1.6.7.1 (Nguyen *et al.* 2015a) with a single model and 10,000 ultrafast bootstrap replications (UFB). The optimal model for nucleotide evolution was determined using Modeltest 3.7 (Posada & Crandall 1998).

For the Bayesian analysis, we used the optimal model determined by Modeltest with parameters estimated by MrBayes 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 values (PP) for all nodes in the final majority rule consensus tree were provided. We regard BP  $\geq 70\%$  and UFB and PP of  $\geq 95\%$  as strong support and values of  $<70\%$  and  $< 95\%$ , respectively, as weak support (Hillis & Bull 1993; Minh *et al.* 2013; Ronquist *et al.* 2012).

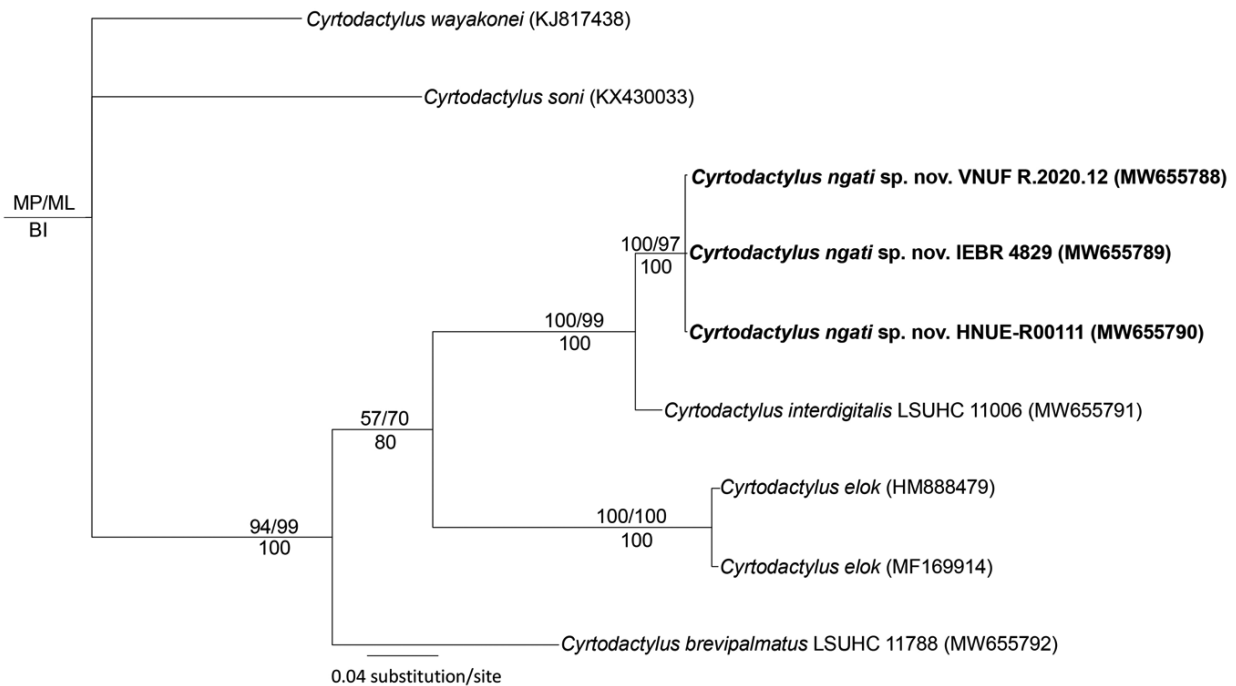
The optimal model for nucleotide evolution was set to TPM1uf+I for ML and combined Bayesian analyses as selected by Modeltest v3.7. The cutoff point for the burn-in function was set to 38 in the Bayesian analysis, as  $-\ln L$  scores reached stationarity after 38,000 generations in both runs. Uncorrected pairwise divergences were calculated in PAUP\*4.0b10.

**Morphological characters.** Measurements were taken with an Etopoo digital caliper to the nearest 0.1 mm. Abbreviations are as follows: snout-vent length (SVL), from tip of snout to anterior margin of cloaca; tail length (TaL), from posterior margin of cloaca to tip of tail; trunk length (TrunkL), from posterior edge of forelimb insertion to anterior edge of hind limb insertion; maximum head height (HH), from occiput to underside of jaws; head length (HL), from tip of snout to the posterior margin of the retroarticular; maximum head width (HW); greatest diameter of orbit (OD); snout to orbit distance (SE), from tip of snout to anterior margin of orbit; orbit to ear distance (EyeEar), from anterior edge of ear opening to posterior margin of the orbit; ear length (EarL), maximum diameter of ear; maximum rostral width (RW); maximum rostral height (RH); maximum mental width (MW); maximum mental length (ML); forearm length (ForeaL), from base of palm to elbow in a flexed position; crus length (CrusL), from base of heel to knee in a flexed position; length of finger IV (LD4A); length of toe IV (LD4P).

Scale counts were taken using a stereo microscope (Olympus SZ61), bilateral scale counts were given as left/right: supralabials (SL) and infralabials (IL) counted from the first labial scale to the corner of mouth; nasal scales surrounding nares, from rostral to labial (excluding rostral and labial), i.e. nasorostral, supranasal, postnasals (N); intersupranasals (IN) (scales between supranasals); postmentals (PM); dorsal tubercle rows (DTR) counted transversely across the center of the dorsum from one ventrolateral fold to the other (excluding ventral scales); granular scales surrounding dorsal tubercles (GST); ventral scales in longitudinal rows at midbody (V) counted transversely across the center of the abdomen from one ventrolateral fold to the other; number of scales along the midbody from mental to anterior edge of cloaca (SLB); number of scale rows around midbody (SR); femoral pores (FP); precloacal pores (PP); postcloacal tubercles (PAT); subdigital lamellae on fourth finger (LD4); subdigital lamellae on fourth toe (LT4); gulars bordering the postmentals (GP); femoral pores on the left side (FPl); femoral pores on the right side (FPr).

## Results

**Phylogenetic analyses.** The alignment contained no internal gap and the final matrix consisted of 657 aligned characters. Of these, 146 were parsimony informative. MP analysis of the dataset recovered a single most parsimonious tree with 349 steps (Consistency index = 0.81; Retention index = 0.76). The topology recovered by the BI analysis was different from that generated by Grismer *et al.* (2021), probably due to the use of two different loci with ND2 being more informative in resolving deeper nodes. In the latter, *Cyrtodactylus elok* clustered with *C. brevipalmatus* with strong support from both ML and BI, while in our analyses *C. elok* was grouped with *C. interdigitalis* and the new species with insignificant statistical values (BP = 57; UFB = 70; PP = 80). The new population from Dien Bien Province was strongly supported as the sister taxon to *C. interdigitalis* from Thailand (BP = 100; UFB = 99; PP = 100). The two species were separated by approximately 3.8% in pair-wise genetic distance based on a fragment of COI. Based on these data and the morphological data presented below, we hypothesize that the new population from Dien Bien Province is a new species and describe it below.



**FIGURE 1.** Phylogram based on the Bayesian analysis. Number above and below branches are MP/ML bootstrap and ultrafast bootstrap values and Bayesian posterior probabilities (>50%), respectively.

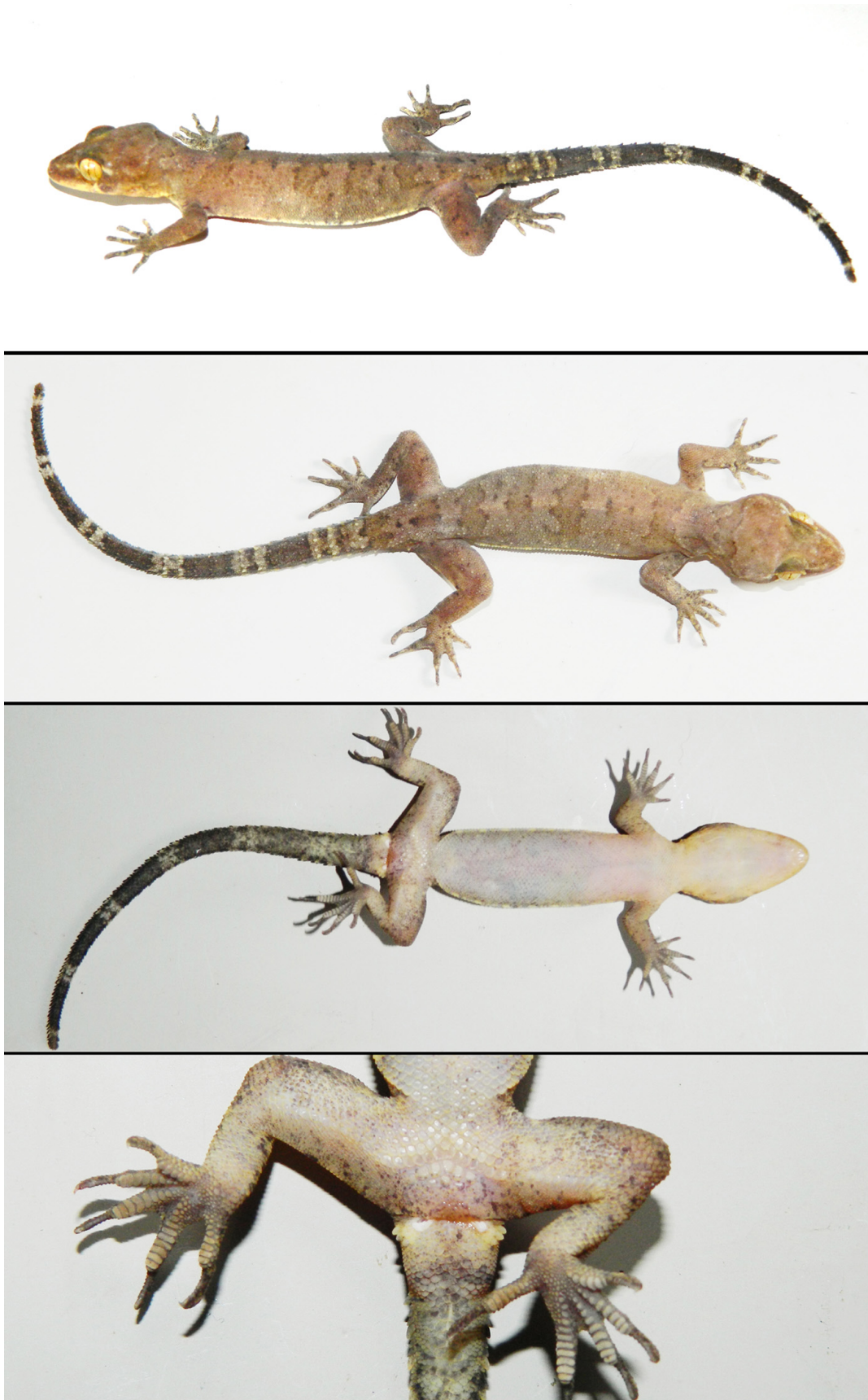
### *Cyrtodactylus ngati* sp. nov.

(Figs. 2–3)

**Holotype.** HNUE-R00111 (Field number PT.2017.215), adult male, collected on 17 August 2017 by D.T. Le, D.T. Truong, H.Q. Nguyen, N.H. Nguyen, and A.N. Nguyen, in the karst forest near Pa Thom Cave, Pa Xa Lao Village, Pa Thom Commune, Dien Bien District, Dien Bien Province, Vietnam (21°17'N; 102°54'E, 695 m a.s.l.).

**Paratypes.** IEBR 4829 (Field number PT.2016.07), adult female, VNUF R.2020.12 (Field number PT.2016.06), adult female, collected on 27 August 2016; HNUE-R00112 (Field number PT.2017.187), subadult female, collected on August 2017, the same data as the holotype.

**Diagnosis.** The new *Cyrtodactylus* species can be distinguished from remaining congeners by the following combination of morphological characters: maximum SVL 69.3 mm; dorsal pattern consisting of six dark irregular transverse bands between limb insertions; intersupranasal single; dorsal tubercles present on occiput, body, hind limbs and on first half of tail; 17–22 irregular dorsal tubercle rows at midbody; lateral folds clearly defined, with interspersed tubercles; 32–38 ventral scales between ventrolateral folds; 13 precloacal pores separated by a diastema of 5/5 poreless scales from 7/7 femoral pores in enlarged femoral scales; precloacal and femoral pores absent in females; 1–3 postcloacal tubercles on each side; median subcaudal scales not transversely enlarged.



**FIGURE 2.** Dorsolateral, dorsal, ventral views and cloacal region of the adult male holotype of *Cyrtodactylus ngati* sp. nov. (HNUE-R00111) in life. Photos: D.T. Le



**FIGURE 3.** Dorsal and ventral views of the adult female paratype of *Cyrtodactylus ngati* **sp. nov.** (VNUF R.2020.12) in life. Photos: D.T. Le

**Description of holotype.** Adult male, SVL 66.5 mm; body elongate (TrunkL/SVL 0.43); head elongate (HL/SVL 0.30), relatively wide (HW/HL 0.62), depressed (HH/HL 0.36), distinguished from neck; loreal region concave; snout long (SE/HL 0.37), obtuse anteriorly, longer than diameter of orbit (OD/SE 0.50); scales on snout small, round or oval, granular, bigger than those in frontal and parietal regions; orbit large (OD/HL 0.19), pupils vertical; supraciliaries with spinous scales posteriorly; ear oval-shaped, small (EarL/HL 0.03); rostral wider than high with a straight medial suture, bordered with first supralabial and nostril on each side; supranasals in contact with each other; nostril opening oval, surrounded by supranasal, rostral, first supralabial, and two enlarged postnasals; mental triangular, slightly wider than long (ML/MW 0.68); two enlarged postmentals; 10/9 supralabials; 8/9 infralabials; dorsal scales granular; dorsal tubercles round, conical, present from occipital region to dorsum and half of tail, tubercles in 18 irregular rows at midbody, larger at midbody, each surrounded by nine granular scales; ventrolateral body folds well defined, with interspersed tubercles; ventral scales smooth, round, midventral scales three times larger than the granules on dorsum, 38 longitudinal ventral scale rows at midbody; gular region with homogeneous, small and smooth scales; 168 ventral scales from mental to cloacal slit; precloacal groove absent; enlarged precloacal scales present; 13 contiguous precloacal pores, separated by 5/5 poreless scales and 7/7 femoral pores (FPI+PP+FPr: 7+13+7); enlarged precloacal and femoral scales present.

Fore- and hind limbs moderately slender (ForeL/SVL 0.13, CrusL/SVL 0.16); enlarged tubercles on dorsal surface of forelimbs absent, but covered with slightly enlarged granules; hind limbs with distinctly developed tubercles dorsally; fingers and toes basally webbed; 16/16 lamellae under fourth finger; 12/13 lamellae under fourth toe.

Tail longer than SVL (TaL 74.1 mm); 3/2 postcloacal tubercles; dorsal surface of tail bearing distinct tubercles on anterior one-half of tail; lateral rows of spinose scales present; median subcaudal scales slightly enlarged, flat, smooth.

**TABLE 2.** Measurements (in mm) and morphological characters of the type series of *Cyrtodactylus ngati* **sp. nov.** (for other abbreviations see material and methods).

Character	HNUE-R00111 (Holotype)	IEBR 4829 (Paratype)	VNUF R.2020.12 (Paratype)	HNUE-R00112 (Paratype)
Sex	adult male	adult female	adult female	subadult female
SVL	66.5	68.1	69.3	46.6
TaL	74.1	77.9	83.2	54.6
HH	7.4	7.2	6.6	5.1
HL	20.1	20.4	20.7	16.1
HW	12.6	12.0	11.8	8.8
OD	3.8	4.1	3.4	2.6
SE	7.5	7.6	6.9	5.0
EyeEar	5.8	5.5	5.9	4.4
EarL	0.8	0.8	0.7	0.3
TrunkL	28.8	29.8	30.2	19.7
ForeL	9.2	10.0	10.1	6.5
CrusL	10.8	11.1	11.8	7.8
LD4A	5.7	5.4	6.6	3.8
LD4P	6.6	6.4	7.2	4.7
RW	2.8	2.6	2.6	1.7
RH	1.5	1.4	1.5	0.8
MW	2.2	2.1	2.5	1.4
ML	1.5	1.5	1.5	0.9
SL	10/9	10/10	10/8	10/9
IL	8/9	9/9	9/8	9/9
N	3/3	3/3	3/3	3/3
IN	1	1	1	1
PM	2	2	2	2
GP	6	6	6	6
DTR	18	18	17	22
GST	9	9	9	9
V	38	36	35	32
SLB	168	164	178	158
SR	117	112	110	106
FPI+FPr	7+7	0	0	0
PP	13	0	0	0
PAT	3/2	1/2	1/1	1/2
LD4	16/16	16/16	16/17	16/16
LT4	12/13	16/14	17/14	17/14

**TABLE 3.** Morphological comparisons between *Cyrtodactylus ngati* sp. nov. and its congeners from Laos and neighboring countries in the Indochina region (compiled after Luu et al. 2014; Nazarov et al. 2014; Nguyen et al. 2014; Panitvong et al. 2014; Pauwels et al. 2014; Pauwels & Sumontha 2014; Schneider et al. 2014a, b; Nurngsomsri et al. 2014; Grismer et al. 2015; Sumontha et al. 2015; Luu et al. 2015; Luu et al. 2016a,b,c; Le et al. 2016; Luu et al. 2017; Nguyen et al. 2017; Pauwels et al. 2018; Chuaynkern et al. 2018; Nazarov et al. 2018; Murdoch et al. 2019; Pham et al. 2019; Sithivong et al. 2019; Schneider et al. 2020; Ostrowski et al. 2020, 2021). Abbreviations are as follows: – = characters unobtainable from literature; \* = tail regenerated; max. = maximal; SVL = snout-vent length; TaL = tail length; V = ventral scales; EFS = enlarged femoral scales; FP = femoral pores; PP = precloacal pores; LD4 = subdigital lamellae on fourth finger; TL4 = subdigital lamellae on fourth toe; FPI = femoral pores on the left side; FPr = femoral pores on the right side.

Taxa	SVL (mm)	TaL (mm)	V	EFS	FP	PP (in males)	PP (in females)	LD4	LT4	Color pattern of dorsum	Enlarged subcaudals
<i>Cyrtodactylus ngati</i> sp.nov.	66.5–69.3	54.6–83.2	32–38	present	present	7+13+7 (FPI+PP+FPr)	0	16–17	12–17	banded	present
<i>C. angularis</i>	80.0–92.0	92–95.2	40–45	present	absent	3	3	18–19	18–19	banded	present
<i>C. astrum</i>	46.4–108.3	99.0*–109.0*	31–46	–	present	31–38 (FP+PP)	–	–	20–24	banded	present
<i>C. auralensis</i>	75.9–84.3	70.5–96	40–42	present	absent	8–9	–	–	19–21	banded	present
<i>C. auribalteatus</i>	82.8–98.1	106.5–138.7	38–40	5–7	4–5 (in males)	6	absent	–	18–21	banded	present
<i>C. badenensis</i>	59.3–74.1	58.6–82.4	25–29	absent	absent	0	0	–	18–22	banded	present
<i>C. bansocensis</i>	71.0–74.0	98.5–103.5	34–35	present	present	34 (FP+PP)	unknown	16–19	18–21	banded	present
<i>C. bichnganae</i>	95.3–99.9	96.3–115.6	30–31	11–13	18	10	8	18–20	16–20	banded	present
<i>C. bidoupimontis</i>	74.0–86.3	75.0–86.0	38–43	6–8	absent	4–6	0	15–20	18–23	banded	absent
<i>C. bobrovi</i>	75.2–96.4	80.8–90.3	40–45	0	0	5	0	19–21	21–22	banded	absent
<i>C. bokorensis</i>	77.5–93	105–120	42–48	present	absent	7–9	0	–	18–20	banded	present
<i>C. brevipalmatus</i>	64.0–72.0	77.0	35–44	present	present	6+9–10+7 (FPI+PP+FPr)	6+9+7 (FPI+PP+FPr)	–	13–20	blotched	present
<i>C. buchardi</i>	60.0–65.0	46.0–54.0	30	absent	absent	9	0	14	12	blotched	absent
<i>C. bugiamapensis</i>	58.6–76.8	65.3–83.0	36–46	6–10	absent	7–8	0–7	15–17	17–20	blotched	absent
<i>C. calamei</i>	75.0–89.3	86.1–107.5	39–42	present	present	35–39 (FP+PP)	38 (FP+PP)	16–18	18–20	banded	present
<i>C. caovansungi</i>	90.4–94.0	120.0	38–44	8	6	9	0	22	23–25	banded	present
<i>C. cardamomensis</i>	72–84.1	78–107.8	36–43	present	absent	9–10	0	–	17–19	banded	present

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TABLE 3. (Continued)

Taxa	SVL (mm)	TaL (mm)	V	EFS	FP	PP (in males)	PP (in females)	LD4	LT4	Color pattern of dorsum	Enlarged subcaudals
<i>C. cattienensis</i>	43.5–69.0	51.0–64.7	28–42	3–8	absent	6–8	0	12–16	14–19	banded	absent
<i>C. chanhomeae</i>	69.9–78.8	74.4–74.7	36–38	present	present	32 (FP+PP)	34 (FP+PP)	18–20	21–23	banded	present
<i>C. chauquangensis</i>	90.9–99.3	97.0–108.3	36–38	absent	absent	6	7	16–18	19–23	banded	present
<i>C. chungi</i>	66.6–68.6	62.8*–82.2*	30–31	4–6	absent	7	6 (pitted)	15–18	17–20	banded	absent
<i>C. condorensis</i>	52.0–84.0	80.8–111.0	32–40	present	absent	0–4	0	15–18	17–23	banded	present
<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
<i>C. cucdongensis</i>	55.8–65.9	22.1–27.8	35–44	present	absent	5–6	4–6	8–11	15–20	banded	absent
<i>C. cucphuongsensis</i>	96.0	79.3*	42	14	absent	0	–	21	24	banded	present
<i>C. darevskii</i>	84.6–100.0	95.0–113.0	38–46	present	present	38–44 (FP+PP)	24–34	17–20	18–22	banded	present
<i>C. doisuthep</i>	62.5–90.5	61.6*–107.6	29–35	present	absent	6	0	6–8	11–13	banded	present
<i>C. dumuii</i>	76.2–84.2	100.2*	40	present	present in males/absent in females	6+5–6+6–7 (FPI+PP+FPPr)	0–7	16	19	banded	present
<i>C. eisenmanae</i>	76.8–89.2	91.0–103.8	44–45	4–6	absent	0	0	18–20	17–18	banded	present
<i>C. elok</i>	54.8–83	64.8–84	41–52	absent	absent	8	0	–	11–19	banded	absent
<i>C. erythrops</i>	78.4	83.0*	28	present	present	10+9+9 (FPI+PP+FPPr)	–	16	20	blotched	present
<i>C. gialaiensis</i>	50.1–62.8	42.2*–63.6*	38–45	absent	absent	9–10	0–8	14–15	15–17	banded	absent
<i>C. grismeri</i>	68.3–95.0	111.3–115.1	33–38	absent	–	0	0	16–18	16–19	banded	present
<i>C. hinnannoensis</i>	83.6–100.6	76.1–108.3*	35–48	present	present	36–44 (FP+PP)	0–28 (FP+PP)	16–21	19–22	banded	present
<i>C. houaphanensis</i>	75.8	59.1*	35	absent	absent	6	?	17	19–21	banded	present
<i>C. huongsonensis</i>	73.4–89.8	90.5	41–48	7–9	15–17	10+6+7 (FPI+PP+FPPr)	8	17–19	20–23	banded	present
<i>C. huynhi</i>	54.8–79.8	61.5–78.6	43–46	3–5	3–8	7–9	0–8	14–17	17–21	banded	absent

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TABLE 3. (Continued)

Taxa	SVL (mm)	TaL (mm)	V	EFS	FP	PP (in males)	PP (in females)	LD4	LT4	Color pattern of dorsum	Enlarged subcaudals
<i>C. interdigitalis</i>	59.0–80.0	71.0–90.0	36–42	present	present	7–8+14–16+7–9	0	17–22	16–20	banded	absent
<i>C. intermedius</i>	61.0–85.0	80.0–110.0	40–50	6–10	–	8–10	–	20	22	banded	present
<i>C. inthanon</i>	83.5–87.3	51.7*–102.0*	39–34	present	present	6+5+6 (FP+PP)	5–6+5+4–5 (FP+PP)	7–11	12–13	banded	present
<i>C. irregularis</i>	72.0–86.0	66.0–74.0	38–45	7–8	–	5–7	0–6	15–16	18–19	blotched	absent
<i>C. jaegeri</i>	60.0–68.5	82.4–83.4	31–32	17–19	present	44 (FP+PP)	21	17–19	20–23	banded	present
<i>C. jarujini</i>	85.0–90.0	105.0–116.0	32–38	present	present	52–54 (PP+FP)	0	15–17	18–19	blotched	present
<i>C. khammouanensis</i>	70.8–73	83.0–95.0	32–38	present	present	40–44 (PP+FP)	0–17	18–20	20–23	banded	present
<i>C. khelangensis</i>	72.8–95.3	max. 96.0*	32–35	present	present	6+2–5+6–7 (FPI+PP+FPr)	2+6+1 (FPI+PP+FPr)	18	22	banded	present
<i>C. kingsadai</i>	83.0–94.0	max. 117.0	39–46	9–12	0–7	7–9	4–8	19–21	21–25	banded	present
<i>C. laangensis</i>	74.4–82.2	88.8–115.5	37–40	present	absent	8–9	0	–	18–20	banded	Present
<i>C. leegrimeri</i>	57.2–86.3	83.0–131.5	30–40	present	absent	3–5	0	10–14	–	banded	present
<i>C. lekaguli</i>	80.5–103.5	115.0–125.0	31–43	present	present	30–36 (PP+FP)	0	–	20–25	banded	present
<i>C. lomyenensis</i>	57.7–71.2	72.2–86.1	35–36	17–18	present	39–40 (PP+FP)	32 (PP+FP)	16–19	19–23	banded	present
<i>C. martini</i>	64.4–96.2	76.0–101.2	39–43	14–18	absent	4	0	19–23	22–24	banded	present
<i>C. muangfuangensis</i>	79.6–83.9	81.9*–102.6	31–37	present	present	8+6+7 (FPI+PP+FPr)	5–9+6+5–8 (FPI+PP+FPr (pitted scales))	16–19	18–23	banded	present
<i>C. multiporus</i>	81.0–98.0	97.0–105.0	30–38	present	present	58–60 (PP+FP)	0	18–20	18–22	banded	present
<i>C. ngoiensis</i>	62.9–95.3	77.4–101.8	38–43	7–10	14 (male)	7	7 (pitted)	16–18	19–20	banded	present

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TABLE 3. (Continued)

Taxa	SVL (mm)	TaL (mm)	V	EFS	FP	PP (in males)	PP (in females)	LD4	LT4	Color pattern of dorsum	Enlarged subcaudals
<i>C. nigriocularis</i>	82.7–107.5	70.6–121	42–49	absent	absent	0–2	0	–	17–21	uniformly brown	present
<i>C. oldhami</i>	63.0–68.0	69*–70*	34–38	present	absent	1–4	–	–	–	striped and spotted	present
<i>C. otai</i>	85.2–90.6	89.7–97.6	38–43	absent	absent	7–8	0	16–19	19–22	banded	absent
<i>C. pageli</i>	76.2–81.8	85.4*–113.2*	41–44	absent	absent	4	4	19–23	19–23	banded	present
<i>C. phetchaburiensis</i>	57.5	70.8	33	present	absent	2–3	0	9–10	11–11	Blotched or striped	present
<i>C. phonghakebangensis</i>	78.5–96.3	98.0–110.0	32–42	present	present	32–42 (PP + FP)	0–41 (PP + FP)	15–20	18–26	banded	present
<i>C. phumyensis</i>	63.5–66.8	73.2*–74.6*	33–40	present	absent	5–7 (Pitted)	6 (Pitted)	18–19	18–21	Banded/ blotched	present
<i>C. phuocbinhensis</i>	46.0–60.4	76.1	43–47	5	absent	7	0	16–21	17–19	blotched	absent
<i>C. phuococensis</i>	59.9–84.2	80–94	40–42	present	absent	6–7	0	–	17–19	–	present
<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
<i>C. puhensis</i>	79.2	82.59	36	present	absent	5	–	18	23	banded	present
<i>C. quadrivirgatus</i>	39.0–67.0	77.0	40	present	absent	4	4	–	–	striped	absent
<i>C. ranongensis</i>	56.9–59.6	66.0–67.1	35–40	present	0	0	0	17	18	blotched	absent
<i>C. roesteri</i>	51.1–75.3	63.4–101.0	34–40	7–10	present	20–28 (PP + FP)	17–22 (PP + FP)	17–19	17–21	banded	present
<i>C. rufford</i>	68.3–72.5	94.5–96.8	27–29	present	present (in males)	42–43 (FP+PP)	unknown	19–20	18–19	banded	present
<i>C. saiyok</i>	56.7–61.0	66.7–67.5	23–24	present	absent	5	–	–	16–17	banded	present
<i>C. samroirot</i>	63.2–66.9	78.8–87.5	33–34	present	absent	7	6	18	19	banded	absent
<i>C. sangi</i>	49.9–56.3	47.9*	37	present	absent	6	4	–	–	banded	present

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TABLE 3. (Continued)

Taxa	SVL (mm)	TaL (mm)	V	EFS	FP	PP (in males)	PP (in females)	LD4	LT4	Color pattern of dorsum	Enlarged subcaudals
<i>C. sanook</i>	72.9–79.5	104.2	27–28	present	absent	3–4	absent	–	19–20	banded	present
<i>C. septimontium</i>	68.4–84.8	74.7*–119	38–42	present	absent	7–8	7–8	–	17–20	banded	present
<i>C. sommerladi</i>	58.8–80.3	58.8*–89.4	31–39	present	present	20–26 (FP+PP)	17–21 (FP+PP)	16–19	17–24	banded	present
<i>C. soni</i>	88.7–103.0	70.6–113	41–45	8–11	5–8	6–7	7–8	15–19	18–22	banded	present
<i>C. sonlaensis</i>	63.1–92.5	89.8–103.0	34–42	present	present	15+8+14 (FPI+PP+FPr)	13+7–8+14 (FPI+PP+FPr)	17–19	18–21	banded	present
<i>C. soudthichaki</i>	69.2–70.0	95.1*–95.2	32–33	present	present (in males)	29 (FP+PP)	absent	16–18	18	banded	present
<i>C. spelaeus</i>	88.9–91.0	max. 83*	36–39	absent	absent	8–9	0	19–20	22–24	banded	present
<i>C. sumonthai</i>	61.5–70.7	89.9–94.0	33–36	absent	absent	2	0	16	18	banded	present
<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
<i>C. taybacensis</i>	77.6–97.5	97.1–104.1	30–38	present	absent	11–13	5–15	17–19	16–20	banded	Present
<i>C. taynguyenensis</i>	60–85	66–94	42–49	absent	absent	6	0	13–18	17–21	blotched	absent
<i>C. teyniei</i>	89.9	ca. 110.0	38	23	absent	unknown	13	17–18	19–20	blotched	present
<i>C. thathomensis</i>	70.3–75.5	79–96	30–36	absent	absent	10	12	16–17	18–20	banded	present
<i>C. thirakhupti</i>	72.0–79.6	99.1	37–40	present	absent	absent	absent	16	20	banded	present
<i>C. thuongae</i>	57.3–77.6	max. 78.1	29–44	2–5	0–3	0–1	0	14–17	14–20	blotched	absent
<i>C. thylacodactylus</i>	44.5–74.6	74*–100	36–42	present	absent	7–9	0	–	15–18	banded	Present
<i>C. tigroides</i>	74.3–83.2	108.5–117.0	34	present	present	6+8+7 (FPI+PP+FPr)	5+9+7 (FPI+PP+FPr)	18–19	20–22	banded	present
<i>C. vilaphongi</i>	60.9–86.1	61.2–68.1	34–36	0	–	–	0	18–19	18–20	banded	absent
<i>C. wangkulangkulae</i>	73.9	98.7	38	absent	absent	0	0	9–11	10–11	banded	present
<i>C. wayakonei</i>	72.0–86.8	76.8–89.0	31–35	absent	absent	6–8	7	17–18	19–20	banded	absent
<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
<i>C. zieglerei</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

**Coloration in life.** Background coloration light yellowish brown, with dark brown dorsal pattern; dorsal surface of head with irregular dark brown blotches; an irregularly shaped dark nuchal loop present, edged in dark brown, butterfly-shaped; six dark transversal bands between limb insertions, somewhat irregularly shaped, somewhat muted in color; tubercles at midbody greyish brown; dorsal surface of limbs with dark spots; dorsal surface of original tail dark grey with light bands, and dark narrow ring within the latter; ventral surface of head, body and limbs cream; subcaudal region dark grey with light bands (see Fig. 2).

**Sexual dimorphism and variation.** The females differ from males by the absence of hemipenial swellings at the tail base as well as femoral and precloacal pores. For further morphological characters of the paratypes see Table 2 and Fig. 4.

**Comparisons.** We compared *Cyrtodactylus ngati* **sp. nov.** with other congeners from Vietnam and neighboring countries in the mainland Indochina region, including Laos, Cambodia, and Thailand based on examination of specimens (see Appendix) and data from literature (Luu *et al.* 2014; Nazarov *et al.* 2014; Nguyen *et al.* 2014; Panitvong *et al.* 2014; Pauwels *et al.* 2014; Pauwels & Sumontha 2014; Schneider *et al.* 2014 a,b; Nurngsomsri *et al.* 2014; Grismer *et al.* 2015; Luu *et al.* 2015; Sumontha *et al.* 2015; Pauwels *et al.* 2016; Le *et al.* 2016; Luu *et al.* 2016a,b,c, 2017; Nguyen *et al.* 2017; Chuaynkern *et al.* 2018; Pauwels *et al.* 2018; Nazarov *et al.* 2018; Murdoch *et al.* 2019; Pham *et al.* 2019; Sitthivong *et al.* 2019; Schneider *et al.* 2020; Ostrowski *et al.* 2020, 2021). The new species can be differentiated from other known species of the genus *Cyrtodactylus* by morphological characters (see Table 3). Below we compared the new species with the *Cyrtodactylus brevipalmatus* group data obtained from Smith (1923); Dring (1979); Ulber (1993); Nurngsomsri *et al.* (2014); and Chuaynkern *et al.* (2018).

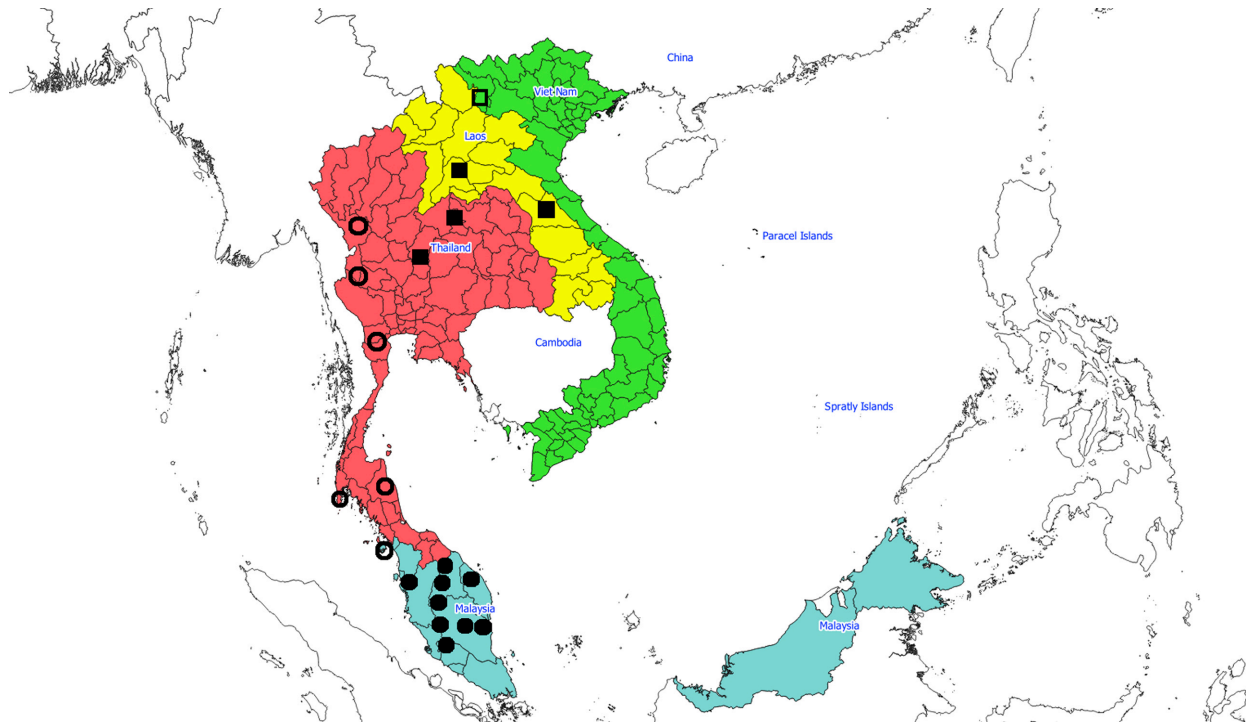
**TABLE 4.** Comparisons of *Cyrtodactylus ngati* **sp. nov.** with other species from the *Cyrtodactylus brevipalmatus* group (data obtained from Smith (1923); Dring 1979; Ulber 1993; Nurngsomsri *et al.* 2014; Chuaynkern *et al.* 2018; and own data of this study). N = number of specimens; FPl = femoral pores on the left side; FPr = femoral pores on the right side.

Character	<i>Cyrtodactylus ngati</i> <b>sp. nov.</b>	<i>C. interdigitalis</i>	<i>C. elok</i>	<i>C. brevipalmatus</i>
N	4	7	4	2
Maximal SVL (mm)	<b>69.3</b>	59–80	54.8–83	64–72
Tail length	74.1	71–89	64.8–84	77
Ventral scales	32–38	36–42	41–52	35–44
Enlarged femoral scales	yes	yes	no	yes
Femoral pores in males (FPl + FPr)	7+7	7–8+7–9	no	6+7
Femoral pores in females (FPl + FPr)	no	no	no	6+7
Precloacal pores (in males)	<b>13</b>	14–16	8	9–10
Precloacal pores (in females)	no	no	no	9
Color pattern of dorsum	banded	banded	banded	blotched
Number of body bands	<b>6</b>	3	3	3
Tubercles on forelimbs	<b>no</b>	yes	no	yes
Enlarged subcaudal scales	<b>yes</b>	no	no	yes
Tail circular (-) or square (+) in cross section	(-)	(-)	(+)	(-)
Tubercles across midbody	17–22	16–22	6–10	14–18
Tubercles on flank absent (-) or present (+)	(+)	(+)	(-)	(+)
Tubercles of dorsolateral caudal rows large (-) or small (+)	(+)	(+)	(-)	(+)

In comparison with the species from the *brevipalmatus* group, comprising *C. interdigitalis* Ulber, *C. elok* Dring, and *C. brevipalmatus* (Smith), the new species can be distinguished from *C. interdigitalis* by its smaller size (maximum SVL 69.3 mm *versus* 80.0 mm), having fewer precloacal pores (13 *versus* 14–16), more body bands (6 *versus* 3), the absence of tubercles on forelimbs (*versus* present), the presence of dark narrow ring in each light tail band (*versus* absent), and the presence of slightly enlarged subcaudal scales (*versus* absent); from *C. elok* by its smaller

size (maximum SVL 69.3 mm *versus* 83.0 mm), having fewer ventral scales (32–38 *versus* 52), more body bands (6 *versus* 3), more precloacal pores in males (13 *versus* 8), the presence of enlarged femoral scales and femoral pores in males (*versus* absent), and the presence of slightly enlarged subcaudal scales (*versus* absent); from *C. brevipalmatus* by having more femoral pores in males (13 *versus* 9 or 10), more body bands (6 *versus* 3), the absence of precloacal pores in females (*versus* present), and dorsal pattern banded (*versus* blotched). For more details see Table 4.

**Distribution.** *Cyrtodactylus ngati* **sp. nov.** is currently known only from the type locality in Dien Bien Province, Vietnam (Fig. 4).



**FIGURE 4.** Distribution map of the *Cyrtodactylus brevipalmatus* species group: square, *C. ngati* **sp. nov.**; solid black squares, *C. interdigitalis*; circles, *C. brevipalmatus*; solid black circles, *C. elok*.

**Etymology.** We name this new species in honor of our colleague, Assoc. Prof. Dr. Ngat Nguyen Le, Hanoi National University of Education, Vietnam, in recognition of his contribution to herpetological research in Vietnam. As common names, we suggest Ngat’s Bent-toed Gecko (English) and Thần lằn ngón ngật (Vietnamese).

**Ecological notes.** Specimens were found between 19:00 and 21:00, on limestone cliffs and in rock crevices, approximately 1–2 m above the ground. The surrounding habitat was disturbed evergreen forest of small hardwoods and shrubs on the mountain slope. The humidity was approximately 74–76% and the air temperature ranged from 23 to 26°C (Fig. 5).

All other members of the *Cyrtodactylus brevipalmatus* group are arboreal, have prehensile tails carried above their back in a coiled position, and usually are found only on vegetation (Grismer *et al.* 2020). This is the first member of the group that apparently lacks a prehensile tail and occurs on karst. Grismer *et al.* (2020) demonstrated that an arboreal habitat preference was the ancestral condition for the *C. brevipalmatus* group and these findings represent the first record of a potential transition of an arboreal habitat to a karst habitat preference in *Cyrtodactylus*.

## Discussion

This is the first member of the *Cyrtodactylus brevipalmatus* group discovered in Vietnam. Except for *C. ngati*, other taxa within the group are arboreal and distributed from central Laos through Thailand to southern Peninsular Malaysia (Grismer *et al.* 2008, 2020, 2021). Similar to the molecular results, *C. ngati* resembles *C. interdigitalis* morphologically, especially in dorsal pattern and the tubercles on the dorsolateral surface of tail. However, the new species can be distinguished from the latter by the number of precloacal-femoral pores, the presence of slightly enlarged median subcaudal scales, and light dorsal tail band pattern.



**FIGURE 5.** Macrohabitat (top) and microhabitat (below) of *Cyrtodactylus ngati* **sp. nov.** Photo: D.T. Le

The level of diversity within the *C. brevipalmatus* group is currently underestimated. Potentially new species have been recorded in central Laos, northern Peninsular Malaysia, and southwestern Thailand (Grismer *et al.* 2021). Through additional surveys within the range of countries this species group inhabits, it is likely that new species will be discovered. Our finding brings the number of *Cyrtodactylus* reported from Vietnam to 47 species. The type locality of the new species is not situated inside any protected area and it is vulnerable to habitat loss and degradation. Further study with a focus on population assessment and threat evaluation should be undertaken to better understand the conservation status of the species.

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## APPENDIX. Comparative specimens examined.

- Cyrtodactylus bichnganae*. Vietnam: Son La: Son La City: TBU PAT.250, TBU NT.2014.01.
- C. bobrovi*. Vietnam: Hoa Binh: Ngoc Son – Ngo Luong: IEBR A.2015.29 (holotype), IEBR A.2015.30, VFM 2015.1, VNMN A.2015.61 (paratypes).
- C. bugiamapensis*. Vietnam: Binh Phuoc: Bu Gia Map: IEBR A.2011.3, ZFMK 92323 (paratypes).
- C. cattienensis*. Vietnam: Dong Nai: Cat Tien: IEBR A.0856 (holotype); Ba Ria – Vung Tau: Nui Dinh: IEBR A.0845, VNUH 2008.0520, IEBR A.0843–A.0844 (paratypes).
- C. cucdongensis*. Vietnam: Khanh Hoa: Ninh Hoa: IEBR A.2013.104 (holotype), ZFMK 95513–95515, IEBR A.2013.105 (paratypes).
- C. gialaiensis*. Vietnam: Gia Lai: Chu Se: VNUF R.2017.1 (holotype), ZFMK 100810, IEBR A.2017.4, VNUF A.2017.4–5 (paratypes).
- C. huongsonensis*. Vietnam: Hanoi: Huong Son: IEBR A.2011.3 (holotype), ZFMK 92293 (paratype).
- C. jaegeri*. Laos: Khammouane Province: Thakhek: IEBR A.2013.55 (holotype), NUOL R-2013.1 (paratype).
- C. jarujini*. Thailand: Nong Khai Province: Bung Ban: ZMB 50648 (holotype).
- C. lomyenensis*. Laos: Khammouane Province: Huong Son: IEBR A.2011.3 (holotype), ZFMK 92293 (paratype).
- C. otai*. Vietnam: Hoa Binh: Hang Kia—Pa Co NR: IEBR A.2015.26 (holotype), IEBR A.2015.27–28, ZFMK 96721, VNMN A.2015.60 (paratypes).
- C. pageli*. Laos: Vientiane Province: Vang Vieng: IEBR A.2010.36 (holotype), IEBR A.2010.37, MTD 48025, MHNG 2723.91, NUOL 2010.3–2010.7, ZFMK 91827 (paratypes).
- C. pseudoquadrivirgatus*. Vietnam: Thua Thien-Hue: A Luoi: ZFMK 83895 (holotype).
- C. roesleri*. Vietnam: Quang Binh Province: Phong Nha – Ke Bang: ZFMK 89377 (holotype), IEBR A.0932, MHNG 2713.79, VNUH 220509, ZFMK 86433, 89378 (paratypes).
- C. rufford*. Laos: Khammouane: Gnommalath: VFU R.2015.14 (holotype), IEBR R.2015.35, NUOL R-2015.15 (paratypes).

- C. soudthichaki*. Laos: Khammouane: Thakhek: VFU R.2015.18 (holotype), IEBR A.2015.34, NUOL R-2015.5 (paratypes).
- C. teyniei*. Laos: Borikhamxay Province: near Ban Na Hin: NEM 0095 (holotype); Khammouane Province: Ban Na Than: KM2012.14–2012.15.
- C. wayakonei*. Laos: Luang Nam Tha Province: Vieng Phoukha: IEBR A.2010.01 (holotype), ZFMK 91016, MTD 47731, NUOL 2010.1 (paratypes).