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Two new cryptic species of the *Cyrtodactylus irregularis* complex (Squamata: Gekkonidae) from southern Vietnam

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Abstract

We describe two new species of the *Cyrtodactylus irregularis* complex both based on phylogenetic analysis of 654 bp of COI mtDNA gene and morphological analyses of voucher specimens from Binh Phuoc and Lam Dong provinces, southern Vietnam. *Cyrtodactylus bugiamapensis* **sp. nov.** is described from the monsoon tropical forests of Bu Gia Map National Park, Binh Phuoc Province, and is distinguished from the remaining representatives of the *C. irregularis* complex by a combination of the following characters: (1) size medium, with a maximum SVL of 76.8 mm; (2) original tail relatively thin, longer than body; (3) presence of enlarged femoral scales without femoral pores; (4) preclocal groove lacking; (5) 36–46 longitudinal rows of ventral scales at midbody; (6) males with 7–11 precloacal pores in an angular continuous series; (7) absence of enlarged subcaudals; (8) dorsal pattern consisting of a dark neck band which can be medially divided, and irregular dark brown spots with bright white edges. *Cyrtodactylus bidoupimontis* **sp. nov.** is described from mountainous evergreen tropical forests of Bidoup – Nui Ba National Park, Lam Dong Province, and is most similar to *C. irregularis* sensu stricto from which it is distinguished by a combination of the following characters: (1) absence of enlarged, strongly keeled conical tubercles on the dorsal tail-base; (2) presence of flat rounded smooth to weakly keeled dorsal tubercles; (3) pallid dorsal head surface pattern lacking distinct dark brown irregular spots with light edges; and (4) elongated limbs. Phylogenetic analyses revealed the presence of a number of cryptic allopatric species within the *C. irregularis* complex. Long geological history and complicated relief of the Lang Bian plateau and surrounding areas might have shaped the present diversity within the *C. irregularis* complex. COI DNA-barcoding appears to be a useful tool to reveal cryptic diversity within the genus *Cyrtodactylus*.

Key words: Squamata, Gekkondidae, *Cyrtodactylus bugiamapensis* **sp. nov.**, *Cyrtodactylus bidoupimontis* **sp. nov.**, southern Vietnam, taxonomy

Introduction

Vietnam has been one of the regions of the most numerous discoveries of new *Cyrtodactylus*, the most speciose genus of gekkonids to date (e.g., Kluge 2001; Uetz *et al.* 2011). Twenty-five species are reported from that country to date, of which 22 have been described in the past decade: *C. badenensis* Nguyen, Orlov & Darevsky, *C. bichnganae* Ngo & Grismer, *C. cattienensis* Geissler, Nazarov, Orlov, Böhme, Phung, Nguyen & Ziegler, *C. caovansungi* Orlov, Nguyen, Nazarov, Ananjeva & Nguyen, *C. chauquangensis* Hoang, Orlov, Ananjeva, Johns,

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Hoang & Dau, *C. condorensis* (Smith), *C. cryptus* Heidrich, Rösler, Vu, Böhme & Ziegler, *C. cucphuongensis* Ngo & Chan, *C. eisenmanae* Ngo, *C. grismeri* Ngo, *C. hontreensis* Ngo, Grismer & Grismer, *C. huongsonensis* Luu, Nguyen, Do & Ziegler, *C. huynhi* Ngo & Bauer, *C. intermedius* (Smith), *C. irregularis* (Smith), *C. martini* Ngo, *C. nigriocularis* Nguyen, Orlov & Darevsky, *C. paradoxus* (Darevsky & Szczerbak), *C. phongnhakebangensis* Ziegler, Rösler, Herrmann & Vu, *C. phuquocensis* Ngo, Grismer & Grismer, *C. pseudoquadrivirgatus* Rösler, Vu, Nguyen, Ngo & Ziegler, *C. roesleri* Ziegler, Nazarov, Orlov, Nguyen, Vu, Dang, Dinh & Schmitz, *C. takouensis* Ngo & Bauer, *C. yangbayensis* Ngo & Chan, and *C. ziegleri* Nazarov, Orlov, Nguyen & Ho.

Cyrtodactylus irregularis was described by Smith (1921) from the mountains of Lang Bian near Dalat. For almost one century all *Cyrtodactylus* found in southern and central Vietnam were attributed to this species on the basis of the following character combination: small subcaudal scales, low number of femoral (no more than 6 on each side) and precloacal pores (no more than 9) and irregular dorsal pattern. Several new species already have been described from this taxonomically most complicated *Cyrtodactylus* group in the past years, such as *C. cattienensis*, *C. pseudoquadrivirgatus*, and *C. ziegleri* (Nazarov *et al.* 2008, Rösler *et al.* 2008, Geissler *et al.* 2009). Although the monophyly of this group of *Cyrtodactylus* has not been tested so far, due to the great morphological similarity and biogeographic relationship of these taxa to the southern part of the Annamite Mountains (Truong Son Mt.) and neighbouring areas in southern and central Vietnam, we herein treat the *Cyrtodactylus irregularis* complex as a putatively monophyletic group. In their extensive review of the taxonomy of the *C. irregularis* complex, Nazarov *et al.* (2008) already have pointed to as yet undescribed taxa within this complex. Recent field research in southern Vietnam has led to new discoveries within the *C. irregularis* complex. Based on comprehensive morphological and molecular comparisons we herein describe two new cryptic species of the *C. irregularis* complex from Binh Phuoc and Lam Dong provinces.

Material and methods

Field work was conducted in the Vietnamese Provinces of Binh Phuoc (Bu Gia Map National Park), and Lam Dong (Bidoup – Nui Ba National Park, Bidoup sector). Specimens were anaesthetized, ethanol-fixed and subsequently deposited in the collections of the Institute of Ecology and Biological Resources (IEBR), Hanoi, Vietnam; Institute of Tropical Biology (ITB), Ho Chi Minh City, Vietnam; Vietnam National Museum of Nature (VNMN), Hanoi, Vietnam; Zoologisches Forschungsmuseum Alexander Koenig (ZFMK), Bonn, Germany; Zoological Institute, St. Petersburg (ZISP), Russian Academy of Sciences, Russia; Zoological Museum, Moscow State University (ZMMU), Moscow. For localities and specimens studied see Fig. 1 and Tables 1–2.

Morphology. For the morphological descriptions and comparisons, the following measurements (taken with caliper rule to the nearest 0.1 mm) and scalation characters were used (after Darevsky & Szczerbak 1997; Bauer 2002, 2003; Bauer *et al.* 2002, 2003; Ziegler *et al.* 2002; David *et al.* 2004; Nguyen *et al.* 2006; Hoang *et al.* 2007; Nazarov *et al.* 2008):

Snout-vent length (SVL, from tip of snout to vent); tail length (TailL, from vent to tip of tail); head length (HeadL, distance between retroarticular process of jaw and snout-tip); head width (HeadW, maximum width of head); head height (HeadH, maximum height of head, from occiput to underside of jaws); orbital diameter (OrbD, greatest diameter of orbit); snout to eye distance (SnEye, distance between anteriormost point of eye and tip of snout); ear length (EarL, longest dimension of ear); trunk length (TrunkL, distance from axilla to groin measured from posterior edge of forelimb insertion to anterior edge of hindlimb insertion); shoulder length (LS); forearm length (ForeaL, from base of palm to elbow); femur length (FemurL); crus length (Crus L, from base of heel to knee); length of finger IV (LF4); length of toe IV (LT4); eye to ear distance (EyeEar, distance from anterior edge of ear opening to posterior corner of eye); scales across the belly in the middle of the body (V); number of scales along the midbody from mental shield to anterior edge of cloaca (SLB), supralabials (SL); infralabials (IL); precloacal pores (PP); femoral pores (FP); enlarged femoral scales (EFS); number of basal and distal subdigital lamellae under fourth finger (SDL4A); number of basal and distal subdigital lamellae under fourth toe (SDL4P), number of longitudinal rows of enlarged tubercles in the middle of dorsum between ventrolateral folds (TubL); number of transversal rows of enlarged tubercles between occipital region and middle of sacrum along the middle of dorsum (TubW); number of scales along middle of head, between occiput sinus and supranasals (SLH); scales across head, between top of ear openings (SAH).

All scale counts were taken on the right side of the body. For asymmetrical characters counts are given in left/right order.

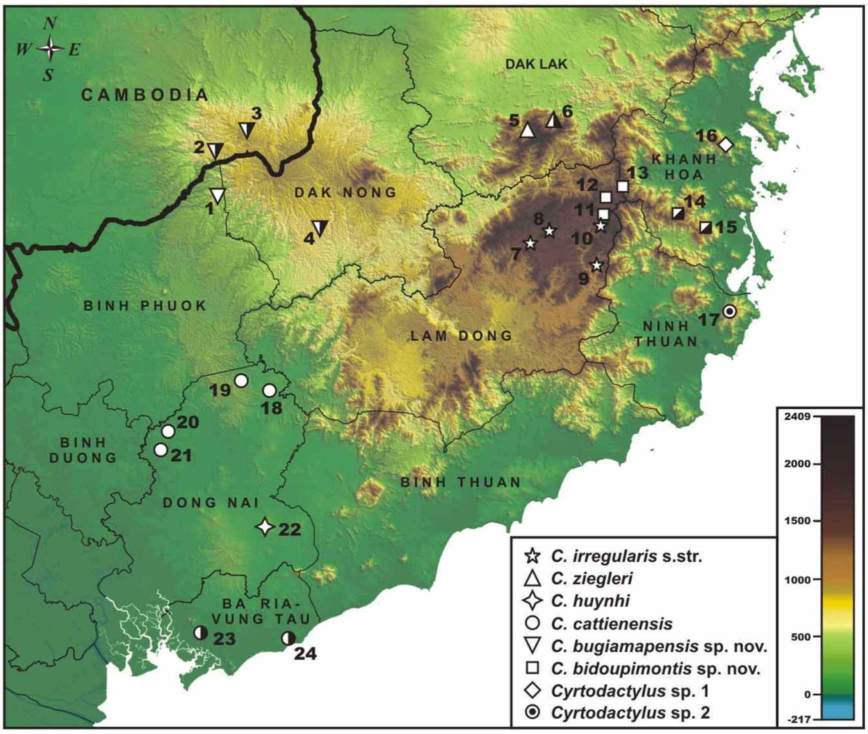

FIGURE 1. Distribution of *Cyrtodactylus irregularis* species complex members in southern Vietnam and localities studied. Empty icons denote species' type localities or localities of specimens which have been studied by molecular means; half-filled icons denote localities of specimens that have either been referred to the corresponding species on the basis of photographs, or for which the locality and taxonomic status is uncertain and requires further confirmation. Localities information: ***Cyrtodactylus bugiamapensis* sp. nov.**: 1 – Vietnam, Binh Phuoc Prov., Bu Gia map Distr., Bu Gia Map comm., Bu Gia Map National Park, Dak Ka stream valley (ZMMU R-13366, R-13367; ZISP 26323; ZFMK 92323); 2 – Cambodia, Mondolkiri Prov., O'Rang distr. (FMNH 262987); 3 – Cambodia, Mondolkiri Prov., Keo Seima Distr., (FMNH 262988); 4 – Vietnam, Dak Nong Prov., Dak R'Lap Distr.; Dao Nghia comm., Dao Nghia National Park (IEBR 404); ***C. ziegleri***: Vietnam, Dak Lak Prov., Krong Bong Distr.: 5 – Khue Ngoc Dien comm., Chu Yang Sin National Park, NW slope of Chu Yang Sin Mt., alt. 900 m a.s.l. (ZISP 24492-24497; ZMMU 12611-1, 12611-2; ITBCZ 482–485); 6 – Hoa Le and Yang Mao comm. border, Chu Yang Sin National Park, NE slope of Chu Yang Sin Mt., alt. 1000 m a.s.l. (ZMMU R-13143); ***C. irregularis* s. str.**: Lam Dong Prov.: 7 – Cam Ly river valley, Ta Nung comm., Da Lat Distr. (BMNH 1932.1.4.1, 1946.3.23.3, 1946.3.23.4); 8 – Nui Ba (Lang Bian Mt.), Bidoup – Nui Ba National Park, Xa Lat comm., Lac Duong Distr.; 9 – Rung Tong Da Lat, Lac Xuan comm., Don Duong Distr. (field number NLO 36031-36033); 10 – Bidoup Mt., Bidoup – Nui Ba National Park, Da Chais comm., Lac Duong Distr.; ***Cyrtodactylus bidoupimontis* sp. nov.**: Lam Dong Prov.: 11 – N slope of Bidoup Mt., env. of Klong Klanh (= Long Lanh) village, Bidoup – Nui Ba National Park, Da Chais comm., Lac Duong Distr.; 12 – Da Nhim river valley, env. of Giang Ly forest station, Bidoup – Nui Ba National Park, Da Chais comm., Lac Duong Distr. (ZMMU R-13368, R-13369; ZISP 26325-26326); 13 – S slope of mt. Hon Giao, env. of Hon Giao forest station, Bidoup – Nui Ba National Park, border of Da Chais comm., Lac Duong and Khanh Vinh Distr. of Khanh Hoa Prov. (field number NAP-01321-22; NAP-01413-14); Khanh Hoa Prov.: 14 – Hon Ba Mt., Khanh Phu comm., Khanh Vinh Distr. (ZMMU R-11445); 15 – Suoi Cat (= Sui Cat), Suoi Cat comm., Cam Lam Distr. (BMNH 1931.6.12.3); ***Cyrtodactylus* sp. 1**: 16 – Ba Ho cascade, Vinh Phuong and Vinh Luong distr. border, Nha Trang, Khanh Hoa Prov. (ZMMU R-13090-1); ***Cyrtodactylus* sp. 2**: 17 – Nui Chua mt., Nui Chua National Park, border of Vinh Hai comm. of Ninh Hai Distr. and Bac Son comm. of Thuan Bac Distr., Ninh Thuan Prov. (ZMMU R-11503-2); ***C. cattienensis***: Dong Nai Prov.: 18 – env. of Cat Tien National Park headquarters, Dac Lua comm., Tan Phu Distr. (IEBR 656; A.0854-A.0856; ZFMK 88090-88095; ZMMU R-11444-; R-11926; R-11189; ZISP 25216-17); 19 – env. of Bau Sau forestry station, Cat Tien National Park, Dac Lua comm., Tan Phu Distr. (field number NAP-00111; NAP-00115-117); 20 – memorial, Dong Nai National Park., Ma Da comm., Vinh Cuu Distr. (VNUH 2008.09.07; field number NAP-01525–30); 21 – 7th road, Dong Nai National Park, border of Hieu Liem and Ma Da comm., Vinh Cuu Distr. (field number NAP-00704; NAP-03185–88); ***C. huynhi***: 22 – Nui Chua Chan, Xuan Truong and Suoi Cat comm., Xuan Loc Distr., Dong Nai Prov. (UNS 0215; 0256-57; 0325-29); ***C.* cf. *cattienensis***: Ba Ria – Vung Tau Prov.: 23 – Nui Dinh Mt., border of Tan Hoa and Chau Pha comm., Tan Thanh Distr. (IEBR A.0843-A.0845; VNUH 2008.0520); 24 – Binh Chau – Phuoc Buu N.P., Binh Chau and Bung Rieng comm. of Xuyen Moc Distr. (field number NAP-03141).

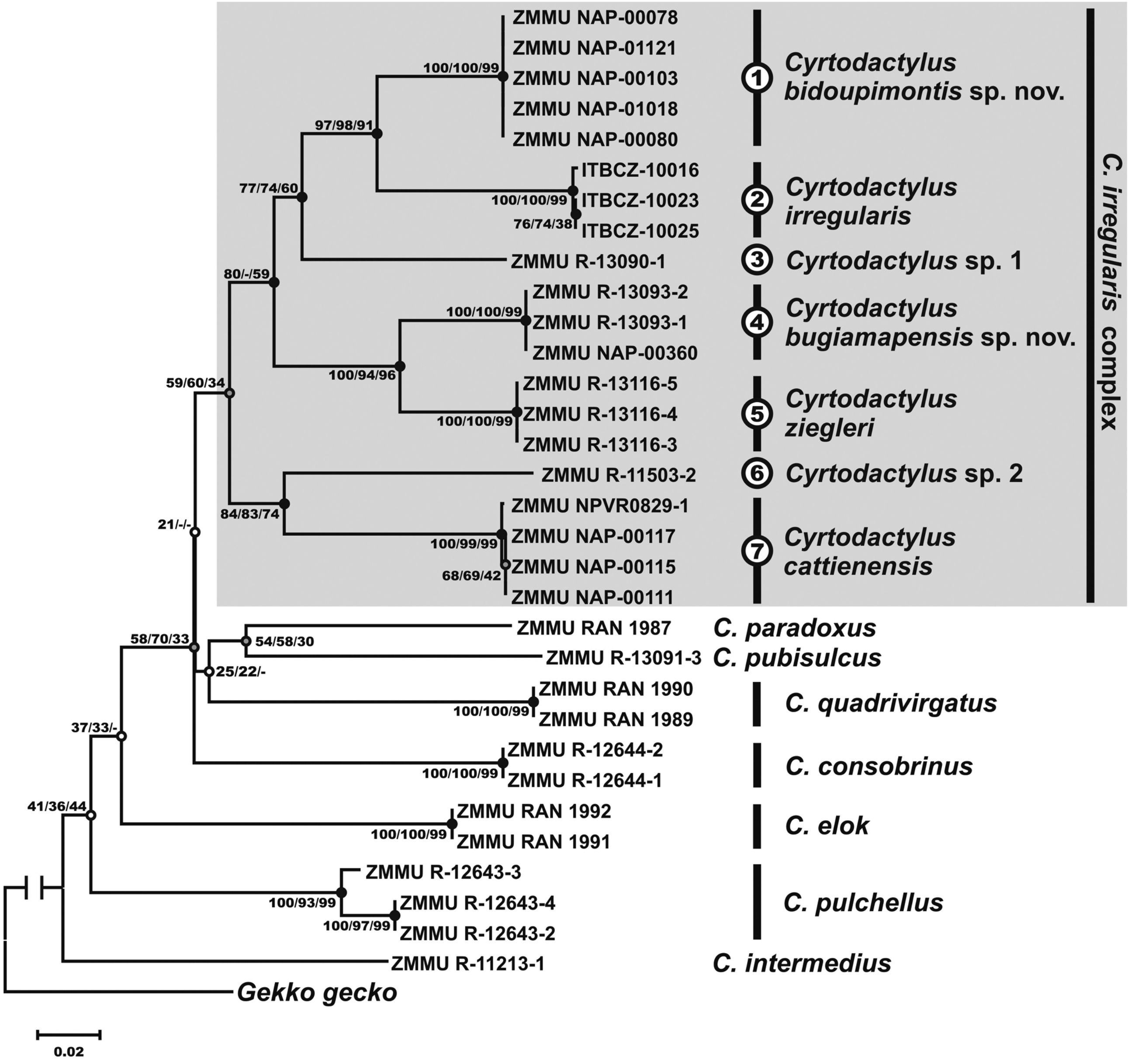

FIGURE 2. ML-tree of studied *Cyrtodactylus* species based on the analysis of 602 bp of COI mtDNA gene. Node colour indicates support value: black for well-supported and sufficiently supported nodes, grey for moderately or poorly supported nodes and white for unresolved nodes with low or no support. Bootstrap support values are shown above or below tree nodes for NJ/ML/MP analyses respectively. Species of the *C. irregularis* species complex are marked with grey.

Molecular comparisons. In the molecular analyses we included samples of 14 *Cyrtodactylus* species from Southeast Asia with the main focus on representatives of the *C. irregularis* complex from southern Vietnam. For the species of this complex (i.e., *C. irregularis*, *C. ziegleri*, *C. cattienensis* and as yet undescribed taxa) we tried to include several populations where possible. For other congeners from Southeast Asia studied here (*C. consobrinus*, *C. elok*, *C. intermedius*, *C. paradoxus*, *C. pubisulcus*, *C. pulchellus*, *C. quadrivirgatus*, and some undescribed taxa) we included 1 or 2 specimens per taxon or population. All specimens studied in the framework of this paper are listed in Tables 1–2. *Gekko gecko* from Nha Trang (Khanh Hoa Province, southern Vietnam) was used as outgroup within the phylogenetic analyses.

DNA extraction, PCR and sequencing. Total genomic DNA was extracted from ethanol-preserved muscle or liver tissues using a glass-fiber automatic DNA isolation protocol following Ivanova *et al.* (2006) or using standard phenol–chloroform extraction procedures (Hillis *et al.* 1996) followed with isopropanol precipitation. We amplified 655 bp of Cytochrome oxidase I (COI), a mitochondrial marker proved to be useful for species identification in reptiles and widely used as a barcoding marker for vertebrates (Hebert & Gregory, 2005; Smith *et* *al.*, 2008; Solovyeva *et al.* 2011). Primers used both for PCR and sequencing were the VF1-d (5'-TTCTCAACCAACCACAARGAYATYGG-3') and the VR1-d (5'-TAGACTTCTGGGTGGCCRAARAAYCA-3') (Ivanova *et al.* 2006). The obtained fragments were sequenced in both directions for each sample, and a consensus sequence was generated. PCRs were performed in 25 µl reactions using ca. 50 ng genomic DNA, 10 pmol of each primer, 15 nmol of each dNTP, 50 nmol additional MgCl 2, Taq PCR buffer (10 mM Tris-HCl, pH 8.3, 50 mM KCl, 1.1 mM MgCl 2 and 0.01% gelatine) and 1 U of Taq DNA polymerase. The PCR conditions were: an initial denaturation step at 95° C for 3 min; 5 cycles at 95° C for 30 s, annealing at 45° C for 1 min, extension at 72° C for 2 min followed with 35 cycles at 95° C for 30 s, annealing at 51 for 1 min, extension at 72° C for 2 min and final extension of 5 min at 72° C. PCR products were loaded onto 1% agarose gels, stained with GelStar gel stain (Cambrex), and visualized in a Dark reader transilluminator (Clare Chemical). If results were satisfying, products were purified using 2 µl, from a 1:4 dilution of ExoSapIt (Amersham), per 5 µl of PCR product prior to cycle sequencing. A 10 µl sequencing reaction included 2 µL of template, 2.5 µl of sequencing buffer, 0.8 µl of 10 pmol primer, 0.4 µl of BigDye Terminator version 3.1 Sequencing Standard (Applied Biosystems) and 4.2 µl of water. The sequence reaction was 35 cycles of 10 s at 96° C, 10 s at 50° C and 4 min at 60° C. Cycle sequencing products were purified by ethanol precipitation. Sequence data collection and visualization were performed on an ABI 3730xl automated sequencer (Applied Biosystems). Obtained sequences are accessible at BOLD systems website (http://www.boldsystems.org) and are deposited in GenBank under accession numbers HM425553, HM425560, HM888459, HM888464-HM888472, HM888478-HM888479, HQ543943-HQ543944, HQ577272, HQ967191-HQ967193, HQ967196-HQ967205, HQ967210-HQ967225.

TABLE 1. Specimens and localities of *Cyrtodactylus* used within our molecular analysis.

Species	Collection Number	N	E	h (m)	Locality .
Cyrtodactylus bidoupimontis **sp. nov.**	ZMMU R-13368; R-13369-1- 13369-4	12°10'	108°40'	1600-1920	Vietnam, Lam Dong Prov., Lac Duong Dist., Bidoup-Nui Ba Reserve
C. irregularis	ITB 10016 (to be deposited at ZFMK), ITB 10023, ITB 10025	-	-	1471	Vietnam, Lam Dong Prov., Bidoup
Cyrtodactylus sp.1	ZMMU R-13090-1	12°22'	109°07'		Vietnam, Khanh Hoa Prov., Ba Ho cascade
Cyrtodactylus bugiamapensis **sp. nov.**	ZMMU R-13366; R-13367-1-5	12°12'	107°12'	354	Vietnam, Binh Phuoc Prov., Bu Gia Map NP, Dak-A river valley
C. ziegleri	ZMMU R-13116-3, 13116-4, 13116-5	12°25'	108°20'	900	
Cyrtodactylus sp.2	ZMMU R-11503-2	11°41'	109°10'	230	Vietnam, Ninh Thuan Prov., Nui Chua Mt.
C. cattienensis	ZMMU R-11444	21'			
C. paradoxus	ZMMU RAN 1987	10°35'	103°17'	-	Cambodia, Koh Tang Island
C. pubisulcus	ZMMU R-13091-3	1°28'	110°09'	-	Malaysia, Borneo, Sarawak
C. quadrivirgatus	ZMMU RAN`1989, 1990	-	-	-	Malaysia, without precise locality IF
C. consobrinus	ZMMU R-12644-1, 12644-2	-	-	-	Malaysia, without precise locality
C. elok	ZMMU RAN`1991, 1992	-	-	-	Malaysia, without precise locality
C. pulchellus	ZMMU R-12643-2, 12643-3, 12643-4	-	-	-	Malaysia, without precise locality
C. intermedius	ZMMU R-11213-1	10°50'	103°58'	-	Cambodia, Phnom Bakor National Park.

TABLE 2. Uncorrected *p*-distance (percentage) between COI sequences of studied *Cyrtodactylus* species (below diagonal), within group mean *p*-distances (on diagonal) and calculation errors (above diagonal).

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
1 *C. irregularis*	**0.16**	1.41	1.48	1.51	1.66	1.77	1.81	1.78	1.80	1.92	1.82	1.89	1.83	1.77	2.05
2 *Cyrtodactylus bidoupimontis* **sp. nov.**	9.78	**0.00**	1.51	1.50	1.55	1.66	1.82	1.79	1.74	1.87	1.83	1.89	1.81	1.73	1.96
3 *Cyrtodactylus* sp. 1	12.75	12.91	-	1.56	1.58	1.79	1.71	1.80	1.87	1.97	1.79	1.90	1.91	1.71	2.01
4 *C. ziegleri*	14.87	14.20	13.03	**0.00**	1.14	1.64	1.72	1.70	1.80	1.89	1.67	1.73	1.88	1.75	1.98
5 *Cyrtodactylus bugiamapensis* **sp. nov.**	16.04	13.85	12.91	7.39	**0.00**	1.65	1.77	1.81	1.95	1.92	1.72	1.91	1.94	1.77	1.95
6 *C. cattienensis*	19.36	15.93	17.61	15.29	14.79	**0.06**	1.61	1.67	1.84	1.94	1.89	1.82	1.80	1.87	1.95
7 *Cyrtodactylus* sp. 2	18.47	17.14	17.14	16.31	15.96	13.82	-	1.95	1.93	1.91	1.77	1.87	1.91	1.83	1.88
8 *C. consobrinus*	19.33	17.84	17.14	16.49	17.37	16.23	20.19	**0.00**	1.90	1.96	1.92	1.96	1.81	1.82	1.97
9 *C. elok*	20.50	18.54	19.01	19.84	21.83	19.45	21.36	19.48	**0.00**	1.78	1.91	1.84	1.68	1.83	1.98
10 *C. intermedius*	22.38	21.13	21.60	21.95	21.83	21.10	19.01	21.13	17.61	-	1.83	1.95	1.77	1.81	1.90
11 *C. paradoxus*	17.76	18.54	17.14	16.31	15.73	18.75	17.84	19.95	19.72	20.19	-	1.75	1.90	1.75	1.97
12 *C. pubisulcus*	18.94	19.01	18.54	18.78	19.48	17.87	17.14	19.25	19.01	20.66	15.96	-	1.92	1.77	2.05
13 *C. pulchellus*	20.50	18.39	20.19	19.76	21.83	19.16	19.56	19.41	17.84	17.53	20.27	19.87	**1.56**	1.89	1.91
14 *C. quadrivirgatus*	19.33	17.37	16.20	18.25	18.54	19.48	19.48	18.31	19.25	19.95	17.84	17.84	20.50	**0.00**	1.94
15 *Gekko gecko*	25.98	24.18	24.18	25.18	26.06	23.24	23.24	23.24	25.82	22.30	22.54	26.06	22.54	24.65	-

Phylogenetic analysis. Final alignment used for phylogenetic analysis contained 654 bp of COI gene for 31 specimens belonging to approximately 14 *Cyrtodactylus* species (summarized in Tab. 1). Sequences were aligned by eye using BioEdit Sequence Alignment Editor 5.0.9 (Hall, 1999). Phylogenetic analyses were conducted in PAUP version 4.0b4a (Swofford 1998) and MEGA5 (Tamura *et al.* 2011) software. Uncorrected genetic distances (*p*-distance) between sequences were calculated in MEGA5. Optimal Neighbour-Joining (NJ) trees were constructed in MEGA5 based on evolutionary distances obtained using the Maximum Composite Likelihood method (Tamura *et al.* 2004) with transitions, transversions and all three codon-positions included into the analysis. MODELTEST v.3.06 (Posada & Crandall 1998) was used to estimate the optimal evolutionary models to be used for the data set analysis. The preferred model was (GTR + I + G), as suggested by the Akaike information criterion (AIC). The proportion of invariable sites, I = 0.55, for among-site rate variation followed a gamma distribution, with the shape parameter α = 1.32. The MP and ML analyses were conducted with the program PAUP version 4.0b4a (Swofford 1998), using a heuristic search and the closest step-wise sequence addition algorithm. Most-parsimonious trees were generated with 100 random-addition sequences and the tree-bisection-reconnection (TBR) algorithm, for branch swapping. For the maximum parsimony (MP) analysis we preformed ten random-addition replicates. Transitions and transversions were equally weighted, and gaps were treated as missing data. Confidence in tree topology was tested by non-parametric bootstrap analysis (Felsenstein, 1985) with 1000 replicates for the MP and NJ analyses. We performed a heuristic ML search (Felsenstein 1981) with ten random-addition sequence replicates and TBR branch swapping was performed with the (GTR + I + G) model. Branches with bootstrap values 70% or greater were regarded as sufficiently resolved (Huelsenbeck & Hillis 1993).

Results

Sequence and statistics. The studied COI mtDNA fragment consisted of 654 sites in which 390 sites were conserved, 264 variable and 259 of them were potentially parsimony-informative; the transition–transversion bias was estimated as 2.55 (all data given for ingroups only). Substitution pattern and rates were estimated under the Kimura (1980) 2-parameter model (+G+I). MP analysis yielded 40 most parsimonious trees of 779 steps, a consistency index of 0.406 and retention index of 0.839. The ML analysis produced a topology with maximum Log likelihood -3609.3398. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories; +*G*, parameter = 1.5409). Nucleotide frequencies were A = 22.8%, T = 25.2%, C = 32.0%, and G = 19.9%.

Sequence divergence. According to the results of our analysis intraspecific variation of the studied COI-fragment is quite low with maximum value of within group *p*-distance found among populations of *C. pulchellus* (*p* = 1.56%), whereas among populations of other *Crytodactylus* species intraspecific variation was minimal (less than 0.06%) or zero (see Tab. 1). On the contrary we report on high interspecific differentiation between Southeast Asian *Cyrtodactylus* species accessed in this research: the minimal uncorrected genetic *p*-distance is found between *C. ziegleri* and *Cyrtodactylus* sp. from Bu Gia Map National Park (*p* = 7.39%) and the maximum distance is found between *C. intermedius* and *C. irregularis* (*p* = 22.38%). Maximum genetic distance between the outgroup and ingroup species was observed between *Gekko gecko* and *C. pubisulcus* (*p* = 26.06%), and minimal – between *Gekko gecko* and *C. intermedius* (*p* = 22.30%). Slightly overlapping values of genetic distances in ingroup and outgroup comparisons indicate deep divergence within *Cyrtodactylus* and also may be a result of fragment saturation.

Phylogenetic relationships. The primary purpose of the phylogenetic analysis in this paper was the molecular diagnosis of biodiversity within the taxonomically complicated genus *Cyrtodactylus*. Diagnosing different species only from morphological characters is often problematic in *Cyrtodactylus* due to interspecific variation and limited sample sizes available for researchers. Thus development of molecular markers suitable for DNA-barcoding and species identification in *Cyrtodactylus* is a quite relevant task; our paper is one of the first steps in this direction. Though resolving phylogeny of the genus *Cyrtodactylus* would require more genes and taxa to be studied, the 654-bp fragment of COI analyzed in this paper demonstrates phylogenetic signal which is strong enough to provide significant support values for some nodes in the resultant tree. These phylogenetic patterns are briefly discussed below.

All analyses resulted in essentially similar topologies. They differed only in associations at poorly supported nodes. The ML tree (Fig. 2) infers the following set of phylogenetic relationships among studied *Cyrtodactylus* species:

1) The monophyly of *Cyrtodactylus* is poorly supported, with *C. intermedius* being the most distant lineage which forms the outgroup in relation to other species studied. Phylogenetic relationships on the genus level are poorly resolved, with nodes of basal splits within *Cyrtodactylus* having moderate or statistically insignificant bootstrap values (BS < 50%). However, phylogenetic relationships between closely related species or species groups are well-resolved with high bootstrap-values (BS > 75%). Thus, the studied COI fragment appears to be a suitable marker for species identification and phylogenetic inference on species group-level but cannot be applied for resolving evolutionary relationships between distantly-related species groups in *Cyrtodactylus* and more conservative genetic markers should be used here (see also Discussion).

2) The phylogenetic position of *C. elok* and *C. pulchellus* is not resolved. These species form two basal lineages with small bootstrap support values. Within Malaysian *C. pulchellus* a distinct phylogenetic structuring is observed.

3) Other *Cyrtodactylus* species included in this study, i.e., the Southeast Indochinese species *C. consobrinus*, *C. paradoxus*, *C. pubisulcus*, *C. quadrivirgatus*, and representatives of the *C. irregularis* complex form a moderately-supported monophyletic group (bootstrap for ML BS = 70%).

4) Within the Southeast Indochinese species clade the basal split is unresolved: the phylogenetic position of *C. consobrinus* and *C. quadrivirgatus* is unclear. *C. pubisulcus* from Java and *C. paradoxus* from offshore islands of Kien Giang Province, southern Vietnam, form a moderately supported monophyly (ML BS = 58%). Representatives of the *C. irregularis* complex (former *C. irregularis* sensu lato) form a monophyletic group with significant BS support value (ML BS = 60%).

5) In the present study we were able to assess phylogenetic relationships within the southern cluster of the *C. irregularis* complex (sensu Nazarov *et al.*, 2008), populations of the northern cluster were not included in the analysis. All studied populations grouped into seven distinct lineages of apparently specific status (uncorrected *p*-distance between lineages > 7.0%; lineages 1–7 (Fig. 2); the monophyly of every lineage is well supported (BS > 99%):

a) The first group encompasses populations from mountainous forests at altitudes of 1500–1900 m a.s.l. from the eastern edge of the Lang Bian plateau (slopes of Bidoup, Gia Rich and Hon Giao mountains) on the border between Lam Dong and Khanh Hoa provinces (Bidoup sector of Bidoup – Nui Ba National Park, Lam Dong, Lang Bian plateau, southern Vietnam) described here as *Cyrtodactylus bidoupimontis* **sp. nov.**

b) The second group includes the population from Nui Ba (= Lang Bian) mountain (environs of Da Lat, Nui Ba sector of Bidoup – Nui Ba National Park, Lam Dong, Lang Bian plateau, southern Vietnam) from altitudes around 1000–1200 m a.s.l. and corresponds to typical *C. irregularis* s. str.

c) The third lineage includes *Cyrtodactylus* from Ba Ho cascade near Nha Trang in Khanh Hoa Province, collected from an altitude of about 500 m a.s.l. regarded here as *Cyrtodactylus*. sp.1.

d) The fourth lineage encompasses populations of *Cyrtodactylus* from Bu Gia Map National Park, collected from primary forests in hilly areas at altitudes of 350–700 m a.s.l. (border of Binh Phuoc and Dak Nong provinces) described here as *Cyrtodactylus bugiamapensis* **sp. nov.**

e) The fifth lineage corresponds to populations from the northern outcrop of the Lang Bian plateau – the Chu Yang Sin mountain (Chu Yang Sin National Park, Dak Lak Province) from altitudes around 1000 m a.s.l., recently described as *C. ziegleri* (Nazarov *et al.* 2008).

f) The sixth lineage includes a *Cyrtodactylus* specimen from Nui Chua mountain (Nui Chua National Park, Ninh Thuan Province) from an altitude of around 200 m a.s.l., regarded here as *Cyrtodactylus*. sp. 2.

g) The seventh lineage encompasses populations of *Cyrtodactylus* from lowland tropical monsoon forests (elevation less than 400 m a.s.l.) in Dong Nai, Binh Thuan and Ba Ria – Vung Tau provinces, recently described as *C. cattienensis* (Geissler *et al.*, 2009).

6) The phylogenetic relationships between these seven lineages are resolved with high support values. All species lineages are grouped into two major subclades: the first one joins *C. cattienensis* and *Cyrtodactylus*. sp. 2 – two species found at low elevations in lowland tropical monsoon forests of southern Vietnam; the monophyly of this group is well-supported (ML BS = 83%). The second group joins all other species of the *C. irregularis* complex mostly from mountains of Lang Bian plateau and adjacent foothill areas; monophyly of this group is moderately supported (NJ BS = 80%, but this topology is not supported by ML analysis).

7) Within the group of “mountainous” *Cyrtodactylus* species two subclades are revealed: one joins the mountainous species *C. ziegleri* from Chu Yang Sin National Park and population from hilly areas of Binh Phuoc and

Dak Nong provinces (*Cyrtodactylus bugiamapensis* **sp. nov.**), the second one joins the species from Lang Bian plateau and its eastern foothills in Lam Dong and Khanh Hoa provinces. Sister species relationships between *C. ziegleri* and *Cyrtodactylus bugiamapensis* **sp. nov.** are well-supported (ML BS = 94%).

8) Typical *C. irregularis* s. str. from Nui Ba mountain and environs of Da Lat form a sister group towards populations from the eastern edge of the Lang Bian plateau (*Cyrtodactylus bidoupimontis* **sp. nov.**). Despite geographical proximity and morphological similarities, these two lineages are clearly genetically separated (uncorrected *p*-distance = 9.78%), what assumes species status of *Cyrtodactylus bidoupimontis* **sp. nov.** The population of Ba Ho cascade (*Cyrtodactylus* sp. 1) from Khanh Hoa Province forms a sister group to the clade joining *C. irregularis* and *Cyrtodactylus bidoupimontis* **sp. nov.** (ML BS = 74%), though is genetically quite distant from both species (p-distance = 12.75% and 12.91% respectively).

Due to the aforementioned, consistent genetic differences of the *Cyrtodactylus* from Bu Gia Map on the one hand, and of the *Cyrtodactylus* from Bidoup – Nui Ba, together with distinct morphological differences (see below), we regard them as representing two new species, which we herein describe as:

Cyrtodactylus bugiamapensis sp. nov.

Holotype. Adult male ZMMU R-13366 collected by Nikolay Poyarkov in June 2011 within Bu Gia Map National Park, Dak Ka stream valley (12°12'N; 107°12' E), Bu Gia Map commune, Bu Gia Map District, Binh Phuoc Province, southern Vietnam, at an altitude of ca. 354 m a.s.l. (Fig. 3).

Paratypes. One adult male ZMMU R-13367-1, three adult females ZISP 26323; ZMMU R-13367-2; ZMMU R-13367-3, and one juvenile ZMMU R-13367-4 collected by Nikolay Poyarkov during 2009-2011, the same collection data as for the holotype; two adult females (IEBR A.2011.3 [field number Tao 993], VNMN 994, and a subadult male (ZFMK 92323 [field number Tao 995]), collected by Trung My Phung in May 2010 in Bu Gia Map commune, Bu Gia Map District, Binh Phuoc Province, southern Vietnam.

Diagnosis. A medium sized *Cyrtodactylus*, SVL 58.6–76.8 mm, TailL 65.3–83.0 mm; body slender, limbs and digits moderately long, original tail relatively thin, longer than the body; two pairs of postmental scales, first pair in broad contact with one another, size of the second pair about half of first pair; nostrils surrounded by supranasal, rostral, first supralabial, and three (rarely four) small postnasal scales; dorsal tubercles enlarged, conical, and with keels, in 20–24 irregular longitudinal rows; lateral folds weakly developed; 36–46 ventral scales between lateral folds; 164–205 ventral scales between postmental scales and cloaca; males with 7–11 precloacal pores in single ^-shaped series; precloacal groove and femoral pores absent; 6–8 implicit enlarged femoral scales on each side; midventral subcaudal scales uniform, larger than the scales on the caudal flanks, without transversely enlarged plates; only tail base with tail segments, tail-base whorls without prominent spurs; average number of subdigital lamellae on the fourth finger is 15.9 and on the fourth toe 18.3; ground coloration of back light yellow to light brown (light beige to brown in preservative); dorsal pattern consisting of unclear transversal bands formed by irregular roundish to oblong, dark brown spots; dark neck band, which can be medially divided, narrow, U-shaped, extending towards ear and orbit; dorsal head surface with few irregular dark spots; all dark dorsal pattern with distinct white bordering; tail with 8–11 dark transversal bands, which fade on the ventral side.

Description of Holotype. Medium sized (SVL 64.8 mm, TailL 66.0 mm), HeadL 17.7 mm, HeadW 12.0 mm, HeadH 7.3 mm , SnEye 7.0 mm, OrbD 3.8 mm, EarL 1.1 mm, EyeEar 5.2 mm; proportions are as follows: SVL/HeadL 3.66, HeadL/HeadW 1.47, HeadL/HeadH 2.42, SnEye/EyeEar 1.34.

Rostral is large, somewhat wider than high (RW 2.8 mm, RH 1.9 mm, RW/RH 1.4) with an inverse Y-shaped median suture (Fig. 4c); supralabials 11/10; scales between orbit and the seventh supralabial 3/4, small; infralabials 10/9; nares surrounded by rostral anteriorly, first supralabial laterally, supranasal and 4 nasals posteriorly; rostral about 5–6 times larger than supranasal; supranasals separated from each other by intersupranasal (two times smaller than supranasals); snout scales medially granular, those in contact with the supralabials are flattened and about 2–3 times larger than the medial ones; upper anterior ciliaries two times larger than posterior ones; head scales granular, some smaller than the median snout scales; dorsum of head and temporal region with rounded, keeled tubercles, that are three times larger than the surrounding scales; mental pentagonal, as wide as rostral (Fig. 4b); three pairs of enlarged postmentals, longer than wide, first pair in broad contact; dorsal scales granular, 3–4 times smaller than the ventral scales; dorsal tubercles round, conical, keeled, surrounded by 9–12 granular scales, tubercles forming about 20 irregular longitudinal rows at midbody; ventral scales smooth, 39 longitudinal rows at midbody; lateral folds weakly developed, marked by small light spots; dorsal surface of fore and hind limbs with granular scales and strongly keeled conical tubercles; fingers and toes without web, basal lamellae more rounded than on distal surface of digits, numbering 9 under first finger, 16/15 under fourth finger, 10 under first toe, and 18 (8 basal and 10 distal lamellae) under fourth toe; V – shaped row of precloacal scales with 8 pores, and three additional precloacal pores on enlarged scales below (Fig. 4d); enlarged femoral scales (without pores) are present; three pairs of enlarged postcloacal tubercles; first tail third with whorls, dorsally covered by convex keeled tubercles; posterior part of tail covered by flattened and rounded scales; subcaudals without enlarged plate row, flat, smooth, imbricate, about two times larger than dorsal scales on tail.

TABLE 3. Measurements and selected morphological characters of the type series of *Cyrtodactylus bugiamapensis* **sp. nov.**; f = female, j = juvenile, m= male.

	HOLOTYPE	PARATYPES							
	ZMMU R-13366	ZMMU R-13367-1	ZISP 26323	ZFMK 92323	VNMN 944	IEBR A.2011.3	ZMMU R-13367-2	ZMMU R-13367-3	ZMMU R-13367-4
Sex	M	M	F*	M	F	F	F	F	JUV
SVL	64.8	64.9	73.1	58.6	72.3	76.5	76.8	61.2	39.5
TailL	66	65*	49*	65.3	73	55*	83	71.5	45
TrunkL	27.6	28	33.3	24.3	30.7	32	34.7	26.7	16.2
HeadL	17.7	17.6	20	16.7	20.8	21.4	21	18.3	12.5
HeadW	12	12.6	13.1	10.7	12.6	13.7	13.9	11.4	7.3
HeadH	7.3	7.7	8	6.7	8	8.9	8.6	7	4.5
SnEye	7	7.2	8	6.5	7.8	8.1	8	6.8	4.3
OrbD	3.8	4.2	4.5	3.2	3.8	3.8	4.8	3.8	2.4
EarL	1.1	0.9	1.2	1	1.1	1.4	1.4	0.8	0.7
EyeEar	5.2	5.5	6.4	4.3	6	6.5	6.8	5.4	3.6
LS	9.7	10	10.8	9.7	11.7	11.7	11.6	8.3	6.4
ForeaL	9.1	9	10	8.2	10	10.8	10.6	8.2	5.5
FemurL	11.8	12.2	13.3	11.3	13.6	13	13.4	11.3	7.3
Crus L	9.3	9.2	11	9.2	11.3	11	11.8	9.1	6.7
LD4A	5.6	5.9	5.3	5.3	6.5	6.2	5.6	5.8	3.3
LD4P	7.1	7.2	7.2	6.2	8.6	7.6	7.9	7.0	4.5
V	39	42	38	46	36	42	40		43
SLB	178	188	164	201	189	205	189		181
TubL/TubW	20/46	23/46	22/42	20/43	20/45	22/44	24/46	22/46	20/42
SLH/SAH	108/86	99/89	96/76	106/88	102/82	95/82	96/80	101/78	110/95
LF4	15	16	16	16	15	16	16	17	16
LT4	18	17	17	18	19	19	20	20	17
PP	8(+3)***	7	7*	8	0	0	7*	**	0
SL	11/10	10/10	10/9	10	10	9	9/10	10/10	10/9
IL	10/9	9/8	8/8	9	9	8	8/8	8/9	9/9

* - perforated enlarged precloacal scales
**- damaged precloacal region
*** - see description of holotype

Coloration: Dorsal head surface brown with three roundish dark brown spots with contrasted white edge in the occipital region and two irregular patches on the tympanum region; nuchal band not broadened posteriorly, dark brown with a distinct white margin, extending from the neck to the posterior margins of eyes; labials brownish grey with white dots. Dorsum brownish grey with seven irregular, dark transverse bands, with light margins; flanks greyish white. Venter white, the lower side of toes and fingers grey; dorsal surface of limbs and digits brownish with irregular bands. Tail dorsum with 11 dark brown bands which are wider than the light grey bands in-between. Ventral side of tail dark grey with light spots that are becoming more distinct posteriorly.

For coloration in life see Fig. 3. During daytime, the colour is darker, making the colour pattern more indistinct.

Variation of paratypes. For the variation of the type series see Table 4 and Fig. 4a. The dorsal pattern is somewhat variable and two paratypes did not show additional pores below the V-shaped row of precloacal pores. Sexual dimorphism is well developed, males are smaller then females, precloacal pores are present in males only and males have more developed postcloacal spurs.

FIGURE 3. Holotype of *Cyrtodactylus bugiamapensis* **sp. nov.** from Bu Gia Map National Park, southern Vietnam.

Comparisons with Vietnamese species. *Cyrtodactylus bugiamapensis* **sp. nov.** differs from *C. badenensis* Nguyen, Orlov & Darevsky, *C. bichnganae* Ngo, *C. caovansungi* Orlov, Nguyen, Nazarov, Ananjeva & Nguyen, *C. chauquangensis* Hoang, Orlov, Ananjeva, Johns, Hoang & Dau, *C. condorensis* (Smith), *C. cucphuongensis* Ngo & Chan, *C. eisenmanae* Ngo, *C. grismeri* Ngo, *C. hontreensis* Ngo, Grismer & Grismer, *C. huongsonensis* Luu, Nguyen, Do & Ziegler, *C. intermedius* (Smith), *C. martini* Ngo, C. *nigriocularis* Nguyen, *C. paradoxus* (Darevsky & Szczerbak), *C. phongnhakebangensis* Ziegler, Rösler, Herrmann & Vu, *C. phuquocensis* Ngo, Grismer & Grismer, C. *takouensis* Ngo & Bauer, *C. roesleri* Ziegler, Nazarov, Orlov, Nguyen, Vu, Dang, Dinh & Schmitz, and *C. yangbayensis* Ngo & Chan, by the absence of transversally enlarged subcaudals. From the Vietnamese *Cyrtodactylus* species, which equally lack transversally enlarged subcaudals (*C. cattienensis* Geissler, Nazarov, Orlov, Böhme, Phung, Nguyen & Ziegler, *C. cryptus* Heidrich, Rösler, Vu, Böhme & Ziegler, *C. huynhi* Ngo & Bauer, *C. irregularis* Smith, *C. pseudoquadrivirgatus* Rösler, Nguyen, Vu, Ngo & Ziegler, and *C. ziegleri* Nazarov, Orlov, Nguyen & Ho), the new species differs as follows. From *C. huynhi* the new species differs by lacking femoral pores (3–8 pores present in *C. huynhi*). *Cyrtodactylus bugiamapensis* **sp. nov.** differs from *C. cryptus* and *C. pseudoquadrivirgatus* by enlarged femoral scales (absent in both species versus 6–8 in *Cyrtodactylus bugiamapensis* **sp. nov.**) and the dorsal pattern (blotched in the new species versus banded in *C. cryptus*).

Cyrtodactylus bugiamapensis **sp. nov.** is most similar to the members of the *C. irregularis* complex. *Cyrtodactylus bugiamapensis* **sp. nov.** differs from *C. pseudoquadrivirgatus* by the presence of enlarged femoral scales and by a continuous dark neck-band with distinct white borders, which is absent in *C. pseudoquadrivirgatus*. *Cyrtodactylus bugiamapensis* **sp. nov.** differs from *C. irregularis* s. str. by the absence of large spurs on the tail-base whorls (which are present in *C. irregularis*), by a thin tail which is longer than the body (index SVL/TailL = 0.91, n=6) versus a comparatively thick tail in *C. irregularis* which is shorter than the body (index SVL/Lcd = 1.1, n=3) and by its smaller maximum size (SVL 76.8 mm versus 86 mm in *C. irregularis*). From the likewise phenetically similar *C. cattienensis*, *Cyrtodactylus bugiamapensis* **sp. nov.** differs by the dorsal pattern (which consists of separate roundish dark-brown spots with yellowish-white borders in the new species versus dark-brown pattern without light borders in *C. cattienensis*), and by its larger size (SVL 58.6–76.8 mm versus 49.9–70.0 mm in *C. cattienensis*). From *C. ziegleri*, the new species can be distinguished by its different dorsal pattern (blotched in the new species versus predominantly banded in *C. ziegleri*) and by its smaller size (SVL 74–76.8 mm versus 84.6–93 mm in *C. ziegleri*). In addition, the average number of subdigital lamellae on the fourth finger and toe in *Cyrtodactylus bugiamapensis* **sp. nov.** is 15.9 and 18.3, versus 17.1 and 22.1 in *C. ziegleri*. Moreover, *Cyrtodactylus bugiamapensis* **sp. nov.** has shorter limbs (index SVL / fore limbs 2.65 and SVL/ hind limbs 2.26, n=9) versus relatively elongated limbs in *C. ziegleri* (index SVL / fore limbs 2.51 and SVL/ hind limbs 2.17, n=8). For more detailed comparisons see Table 6.

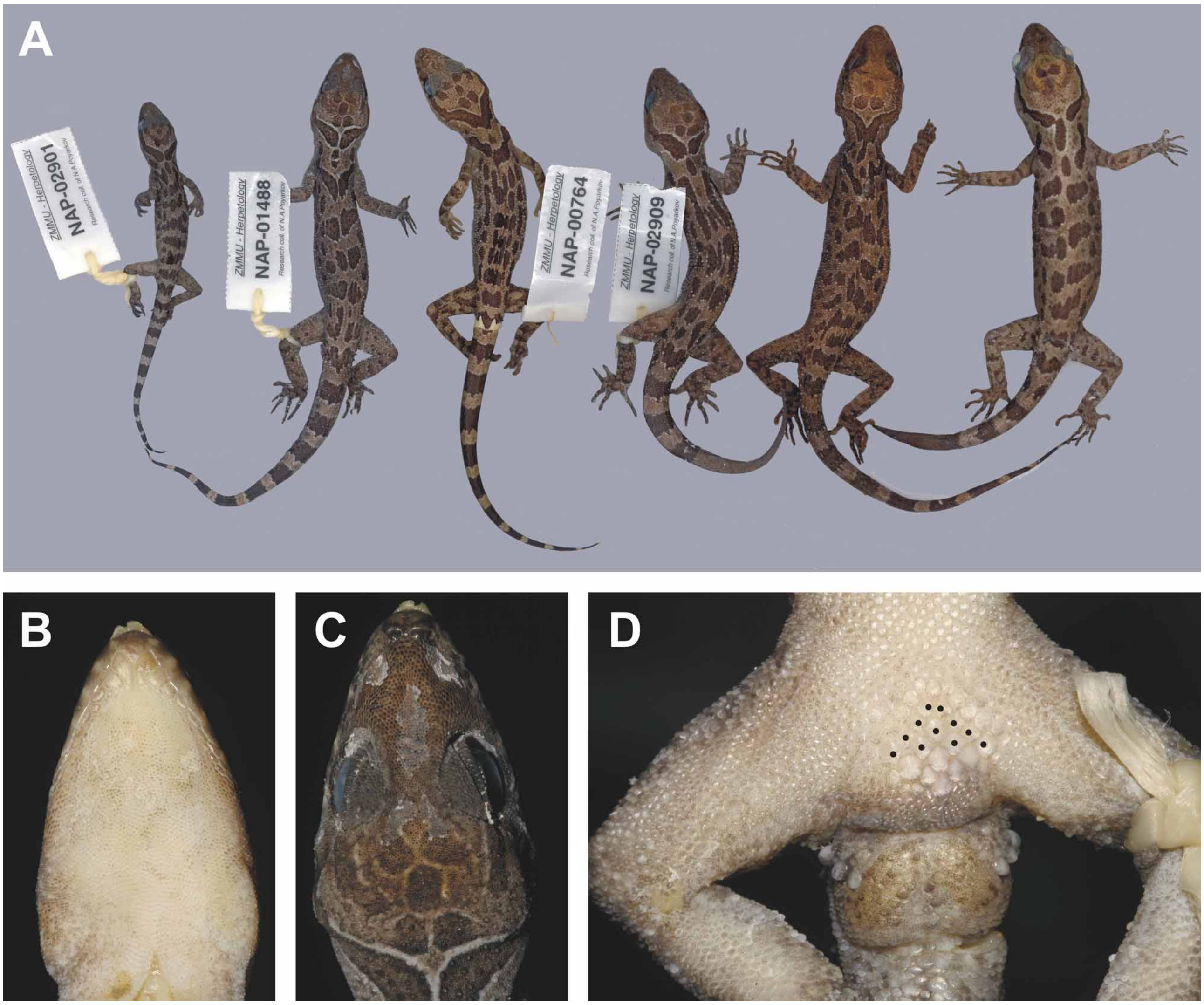

FIGURE 4. Part of the type series of *Cyrtodactylus bugiamapensis* **sp. nov.** from Bu Gia Map National Park, southern Vietnam, showing variation in dorsal colour pattern (A). Holotype of *Cyrtodactylus bugiamapensis* **sp. nov.**: mental scalation (B), rostral scalation (C) and precloacal region (D).

Comparisons with congeners from Southeast Asia. *Cyrtodactylus bugiamapensis* sp. nov. differs from other mainland congeners by the following characters. By the absence of transversely enlarged subcaudal plates the new species may be distinguished from: *C. aequalis* Bauer, *C. annandalei* Bauer, *C. aurensis* Grismer, *C. baluensis* (Mocquard), *C. chanhomeae* Bauer, Sumontha & Pauwels, *C. consobrinus* (Peters), *C. feae* (Boulenger), *C. ingeri* Hikida, *C. jarujini* Ulber, *C. lomyenensis* Ngo & Pauwels, *C. malayanus* (de Rooij), *C. oldhami* (Theobald), *C. pageli* Schneider, Nguyen, Schmitz, Kingsada, Auer & Ziegler, *C. peguensis* (Boulenger), *C. russelli* Bauer, *C. sumonthai* Bauer, Pauwels & Chanhome, and *C. teyniei* David, Nguyen, Schneider & Ziegler. By the absence of a precloacal groove, *Cyrtodactylus bugiamapensis* sp. nov. differs from the following Southeast Asian mainland species: *C. marmoratus* (Gray), *C. pulchellus* Gray, and *C. rubidus* (Blyth). The new species can be distinguished from the following species by the presence of enlarged femoral scales: *C. brevidactylus* Bauer, *C. buchardi* David, Teynie & Ohler, *C. chrysopylos* Bauer, *C. gansi* Bauer, and *C. elok* Dring.

FIGURE 5. Type locality of *Cyrtodactylus bugiamapensis* **sp. nov.**: Dak Ka stream valley, environs of the second forest station in Bu Gia Map National Park, Bu Gia Map community, Bu Gia Map District, Binh Phuoc Province, southern Vietnam.

Etymology. The specific epithet is a Latinized toponymic adjective and commemorates the type locality of the new species, the tropical monsoon forest of Bu Gia Map National Park. As common names we propose Bu Gia Map Bent–toed Gecko (in English), and Thach sung ngón bu gia map (in Vietnamese).

Habitat description. Specimens were collected in lowland tropical forest in the valley of Dac Ka stream (Fig. 5). The forest condition varies from medium disturbed parts along the road and around the ranger station surrounded with non-disturbed parts of primary tropical forest. This area is quite hilly, with Dac Ka river tributaries forming numerous gorges. The forest floor is covered with numerous rocks of volcanic tuff; the canopy is closed for large parts. The forest composition is dominated by Dipterocarpaceae, Fabaceae, Poaceae and Magnoliaceae trees. Disturbed forest areas house bamboo and rattan palm bushes. The geckos were found at day time under tree logs or pieces of volcanic tuff, and at night on the tree trunks on approximately 1–2 m above the ground. One specimen was caught in the ruins of a brick building under ceramic tiles.

Distribution. So far, *Cyrtodactylus bugiamapensis* **sp. nov.** is known only from Bu Gia Map National Park (Bu Gia Map Commune, Bu Gia Map District, Binh Phuoc Province) and from the neighboring areas of Dak Nong Province (Quang Truc Commune, Tuy Duc District) (see Fig.1), southern Vietnam. Considering the geographic position of this area, records of *Cyrtodactylus bugiamapensis* **sp. nov.** from the adjacent Cambodia (Mondolkiri Province) are anticipated.

Phylogenetic position. According to mtDNA data, *Cyrtodactylus bugiamapensis* **sp. nov.** belongs to a mountain species group of the *Cyrtodactylus irregularis* complex and is sister species to *C. ziegleri* (*p*-distance between the two species is 7.39% of substitutions based on COI partial sequences).

Cyrtodactylus bidoupimontis sp. nov.

Holotype. Adult male ZMMU R-13368 collected from the northern slope of Bidoup Mountain, environment of Klong Klanh (= Long La[1]nh) village, Bidoup – Nui Ba National Park, Da Chais commune, Lac Duong District, Lam Dong Province, Vietnam (12° 10´ N, 108° 40´ E), 1700 m elevation, coll. 04-12.04.2004 by Nikolai Orlov (Fig. 6).

Paratypes. Adult male ZISP 26325 (field number NLO 36041), the same collection data as for the holotype; two adult males ZMMU R-13369-1, ZMMU R-13369-2, three adult females ZMMU R-13369-4, ZISP 26326, VNMN 3100 and two subadult females ZMMU R-13369-3 R-13369-5; collected by Nikolay Poyarkov between 6-10.05.2009 at an altitude of ca. 1600 m a.s.l. along the road to Nha Trang (723 road), 6–7 km from Klong Klanh, Da Nhim river valley in Bidoup – Nui Ba National Park, Lam Dong Province, Vietnam**.**

Diagnosis. A medium-sized *Cyrtodactylus* with a maximum SVL of 86.3 mm; body slender, limbs and digits moderately long, original tail thin and somewhat longer than body; two pairs of postmental scales, first pair in broad contact with one another, size of the second pair are about half of first pair (Fig. 7b); nostrils round, each surrounded by supranasal, rostral, first supralabial, and 2–3 small postnasals; dorsal tubercles enlarged, flattened roundish, smooth to weakly keeled, in 18–24 irregular longitudinal rows; lateral folds weakly developed, with enlarged tubercles; 38–43 ventral scales between lateral folds; 166–198 ventral scales between postmental scales and cloaca; subdigital lamellae below fourth finger 15–20 (mean 17.6), and below fourth toe 18–23 (mean 21.0); males with 4–6 precloacal pores in single ^-shaped series; precloacal groove absent; 8–10 enlarged femoral scales are present but femoral pores are lacking; enlarged subcaudals lacking; basal tail with segments; tail-base without large spurs; dorsal ground coloration light yellow with pattern consisting of 4–5 dark irregular transversal dorsal bands, usually with light borders; limbs with irregular transversal dark bands dorsally; neck band well developed, widened posteriorly; dorsal head surface light, without pattern or sometimes with pallid dark spots; tail with 7–9 dark transversal bands which fade on the ventral side.

Description of Holotype. SVL 77 mm, TailL 86 mm, HeadL 23.2, HeadW 15.9 mm, HeadH 8.6 mm , SnEye 9.0 mm, EyeEar 6.8 mm; proportions are as follows: SVL/HeadL 3.32, HeadL/HeadW 1.46, HeadL/HeadH 2.7, SnEye/EyeEar 1.32.

Rostral wider than high (RW 3.4 mm, RH 2.1 mm, RW/RH 1.48) with an inverse Y-shaped median suture (Fig. 7c); supralabials 8/9; small scales between orbit and the seventh supralabial 2/2; infralabials 8; left nostril surrounded by rostral anteriorly, first supralabial laterally and two nasals posteriorly; right nostril surrounded by rostral, first supralabial and two postnasals, supranasal not in contact with nostril; rostral about 8 times larger than supranasal; supranasals separated from each other by one intersupranasal, the same size or larger than supranasals; head scales granular, half as large as median snout scales; centre of dorsal head surface and temporal region with rounded, unkeeled tubercles, that are three times larger than the surrounding scales; mental triangular, showing the same width as rostral (Fig. 7b); two pairs of enlarged postmentals, trapezoidal, longer than wide, bordering mental; dorsal scales granular; dorsal tubercles round, smooth, weakly keeled, surrounded by 9–10 granular scales, tubercles forming 23 longitudinal irregular rows at midbody; ventral scales smooth, medial scales three times larger than the dorsal granules, 41 longitudinal rows at midbody; lateral folds weakly developed; dorsal limb surface with granular scales and smooth tubercles; five precloacal pores in an angle series; ten enlarged femoral scales on each side located in continuous series without gap between precloacal and femoral scales (Fig. 7d); femoral pores lacking; precloacal region with a patch of 8 enlarged scales; 1/2 enlarged postcloacal tubercles; tail base whorls covered by convex scales on dorsal surface, posterior part of tail with flattened and rounded scales; subcaudals not enlarged, flat, smooth, imbricate, about two times larger than scales on tail dorsum.

Coloration in alcohol: Dorsal head surface light grey with 9 irregular dark brown patches; nuchal band broadened posteriorly, dark brown, extending from the neck to the posterior corners of eyes; labials darker with light

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[1] The name of this village is written as “Long Lanh” in the Vietnam Administrative Atlas (Le, The, 2009).

spots; back light brownish with five irregular, dark brown transverse bands, consisting of separate spots; flanks greyish white; venter cream, the lower sides of toes and fingers grey; dorsal limbs and digits light with dark transversal spots; upper side of tail with 8 dark brown bands which are wider than the light bands in-between; ventral side of tail dark grey with white spots that are becoming darker posteriorly.

Variation of paratypes. For the variation of paratypes see Table 4 and Fig.7a. Sexual dimorphism is present, males are slightly smaller then females, precloacal pores are present in males only and males have more developed postcloacal spurs.

FIGURE 6. Paratype of *Cyrtodactylus bidoupimontis* **sp. nov.** (ZMMU R-13367-2) in life from Bidoup – Nui Ba National Park, southern Vietnam.

Comparisons with Vietnamese species. *Cyrtodactylus bidoupimontis* **sp. nov.** differs from *C. badenensis* Nguyen, Orlov & Darevsky, *C. bichnganae* Ngo, *C. caovansungi* Orlov, Nguyen, Nazarov, Ananjeva & Nguyen, *C. chauquangensis* Hoang, Orlov, Ananjeva, Johns, Hoang & Dau, *C. condorensis* (Smith), *C. cucphuongensis* Ngo & Chan, *C. eisenmanae* Ngo, *C. grismeri* Ngo, *C. hontreensis* Ngo, Grismer & Grismer, *C. huongsonensis* Luu, Nguyen, Do & Ziegler, *C. intermedius* (Smith), *C. martini* Ngo, *C. nigriocularis* Nguyen, *C. paradoxus* (Darevsky & Szczerbak), *C. phongnhakebangensis* Ziegler, Rösler, Herrmann & Vu, *C. phuquocensis* Ngo, Grismer & Grismer, C. *takouensis* Ngo & Bauer, *C. roesleri* Ziegler, Nazarov, Orlov, Nguyen, Vu, Dang, Dinh & Schmitz, and *C. yangbayensis* Ngo & Chan, by the absence of transversally enlarged subcaudals. *Cyrtodactylus bidoupimontis* **sp. nov.** differs from *C. cryptus* Heidrich, Rösler, Vu, Böhme & Ziegler by having enlarged femoral scales and lower number of ventral scales (38–43 versus 47–50 in *C. cryptus*). *Cyrtodactylus bidoupimontis* **sp. nov.** differs from *C. huynhi* Ngo & Bauer by having a higher number of enlarged femoral scales (8–10 versus 3–5 in *C. huynhi*), and by lacking femoral pores (3–8 present in *C. huynhi*). The new species is most similar to the members of the *C. irregularis* complex (*Cyrtodactylus bugiamapensis* **sp. nov.**, *C. cattienensis* Geissler, Nazarov, Orlov, Böhme, Phung, Nguyen & Ziegler, *C. cryptus* Heidrich, Rösler, Vu, Böhme & Ziegler, *C. huynhi* Ngo & Bauer, *C. irregularis* Smith, *C. pseudoquadrivirgatus* Rösler, Nguyen, Vu, Ngo & Ziegler, and *C. ziegleri* Nazarov, Orlov, Nguyen & Ho). *Cyrtodactylus bidoupimontis* **sp. nov.** differs from *Cyrtodactylus bugiamapensis* **sp. nov.** in the dorsal pattern (posteriorly distinctly widened nuchal band versus thinner and sometimes medially divided nuchal band in *Cyrtodactylus bugiamapensis* **sp. nov.**); as well *Cyrtodactylus bidoupimontis* **sp. nov.** has banded dorsal pattern versus blotched in *Cyrtodactylus bugiamapensis* **sp. nov.** *Cyrtodactylus bidoupimontis* **sp. nov.** has elongate limbs (index SVL / fore and hind limbs 2.05 and 2.44, n=6) compared to *Cyrtodactylus bugiamapensis* **sp. nov.** (2.26 and 2.65, n=9). *Cyrtodactylus bidoupimontis* **sp. nov.** has a higher number of subdigital lamellae on fourth finger and toe (average value 17.6 and 21) compared with *Cyrtodactylus bugiamapensis* **sp. nov.** (15.9 and 18.3). *Cyrtodactylus bidoupimontis* **sp. nov.** has a relatively larger and more massive head (index SVL / Head L and SVL / Head W for *C. bidoupimontis* is 3.46 and 5.2, n=6) than *Cyrtodactylus bugiamapensis* **sp. nov.** (3.55 and 5.48, n=8). In addition, the maximum known SVL in *Cyrtodactylus bidoupimontis* **sp. nov.** slightly exceeds that of *Cyrtodactylus bugiamapensis* **sp. nov.** (80 mm versus 76.8 mm). *Cyrtodactylus bidoupimontis* **sp. nov.** differs from *C. cattienensis* by its larger maximal body size (SVL 60.5–86.3 mm versus 49.9–70.0 mm) and a different dorsal pattern (*Cyrtodactylus bidoupimontis* **sp. nov.** usually has dorsal bands with light bordering, but *C. cattienensis* never has light edge on dorsal pattern). *Cyrtodactylus bidoupimontis* **sp. nov.** has higher mean number of subdigital lamellae in the fourth toe and finger (17.6 and 21 versus 14.5 and 17 accordingly for *C. cattienensis*). *Cyrtodactylus bidoupimontis* **sp. nov.** also has a higher mean number of ventral scales (40.6 versus 37.4 in *C. cattienensis*).

TABLE 4. Measurements and selected morphological characters of the type series of *Cyrtodactylus bidoupimontis* **sp. nov.**; f = female, m = male; sub = subadult.

	Holotype	Paratypes							
	ZMMU R-13368	ZISP 26325	ZMMU R-13369-1	ZMMU R-13369-2	ZMMU R-13369-3	ZMMU R-13369-4	ZISP 26326	VNMH 3100	ZMMU R-13369-5
Sex	m	m	m	m	f sub	f	f	f	f sub
SVL	77.0	74.0	78.2	79.0	60.5	80.0	86.3	80.5	59.7
TailL	86.0	75.0	*	*	52.0	82.0	*	49.3*	43.7*
TrunkL	34.7	29.5	32.6	35.5	25.5	36.5	36.8	36.1	26.2
HeadL	23.2	21.2	22.7	22.0	18.5	22	25.4	22.7	18.3
HeadW	15.9	15.3	14.3	15.0	11.3	14.5	16.5	16.3	11.3
HeadH	8.6	8.3	8.7	8.5	7.2	8.6	10.3	10.3	6.5
SnEye	9.0	8.3	8.8	8.4	7.0	8.8	9.8	9.0	7
OrbD	4.0	3.8	4.6	4.4	3.6	4.6	4.7	4.3	3.3
EarL	1.2	1.4	1.8	1.6	1.2	1.6	1.8	1.8	1.3
EyeEar	6.8	6.0	6.8	6.5	5.7	6.2	8.2	7.2	6.0
LS	11.4	12.0	11.8	13.5	10.0	12.0	14.1	13.0	9.8
ForeaL	11.2	11.1	11.0	11.8	8.5	11.4	12.8	11.8	8.6
FemurL	14.6	15.0	14.7	16.2	11.8	14.2	16.6	16.0	11.8
Crus L	12.1	12.6	12.4	12.7	9.3	12.0	13.8	14.2	9.5
LD4A	8.0	8.4	8.5	8.2	7.0	8.6	9.7	8.6	6.0
LD4P	10.8	11.2	10.6	9.6	8.7	10.0	11.2	10.8	7.6
V	41	43	40	38	42	40	43	39	42
SLB	166	174	197	198	192	183	195	180	178
TubL/TubW	23/40	22/36	22/40	18/41	20/44	24/42	22/46	20/40	20/37
SLH/SAH	85/76	81/73	99/79	104/89	94/90	91/74	82/78	96/90	104/90
LF4	20	18	18	17	18	15	17	18	18
LT4	22	22	23	20	21	18	20	21	20
PP	5	6	4	6	0	0	0	0	0
SL	9/8	11/11	9/8	8/10	10/10	9/10	10/10	10/10	9/10
IL	8/8	11/11	10/10	7/10	11/11	10/10	9/9	9/10	8/9

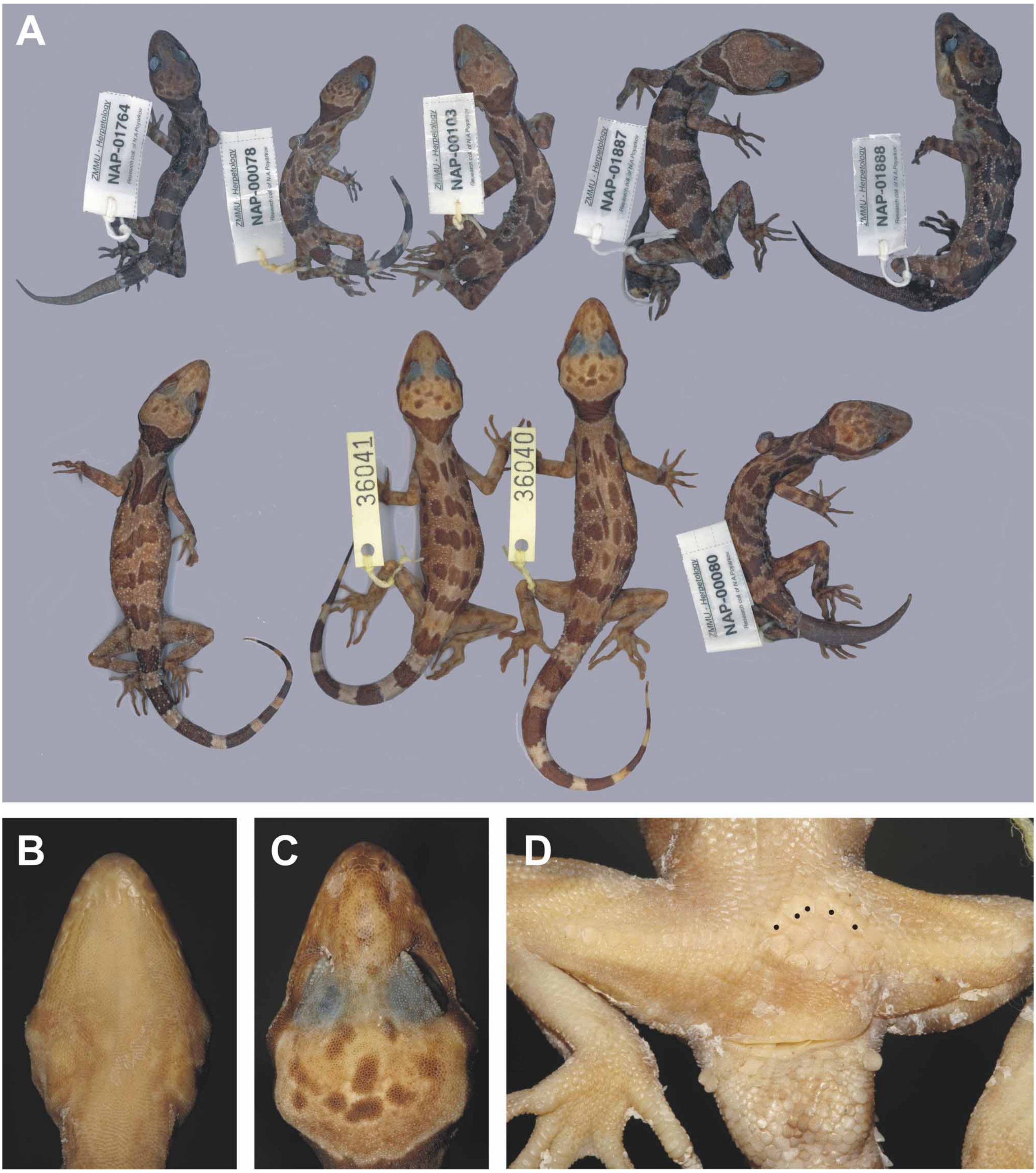

FIGURE 7. The type series of *Cyrtodactylus bidoupimontis* **sp. nov.** from Bidoup – Nui Ba National Park, southern Vietnam, showing variation in dorsal colour pattern (A). Holotype of *Cyrtodactylus bidoupimontis* **sp. nov.**: mental scalation (B), rostral scalation (C) and precloacal region (D).

Cyrtodactylus bidoupimontis **sp. nov.** differs from *C. pseudoquadrivirgatus* by having enlarged femoral scales and continuous neck-band, the presence of enlarged femoral scales, and by its slightly smaller maximal size (SVL 60.5–86.3 mm versus 84.6–93 mm in *C. pseudoquadrivirgatus*). *Cyrtodactylus bidoupimontis* **sp. nov.** differs from *C. ziegleri* by its slightly smaller maximal body size (SVL 60.5–86.3 versus 84.0–93.0 mm), by the absence of femoral pores (1–3 on each side in *C. ziegleri*). *Cyrtodactylus bidoupimontis* **sp. nov.** is most closely related to *C. irregularis* s.str., from which it morphologically differs by the absence of large spurs on the tail-base (versus big, strongly keeled conical spurs in *C. irregularis*), by flattened roundish, smooth to weakly keeled dorsal tubercles versus triangular pyramidal keeled tubercles in *C. irregularis*. *Cyrtodactylus bidoupimontis* **sp. nov.** in addition has a pallid, unclear pattern on the dorsal head surface (versus distinct dark-brown irregular spots with light edging in *C. irregularis*), and more elongate limbs: index SVL / fore and hind limbs is 2.05 and 2.44 (n=6) versus 2.24 and 2.55 (n=7) in *C. irregularis*.

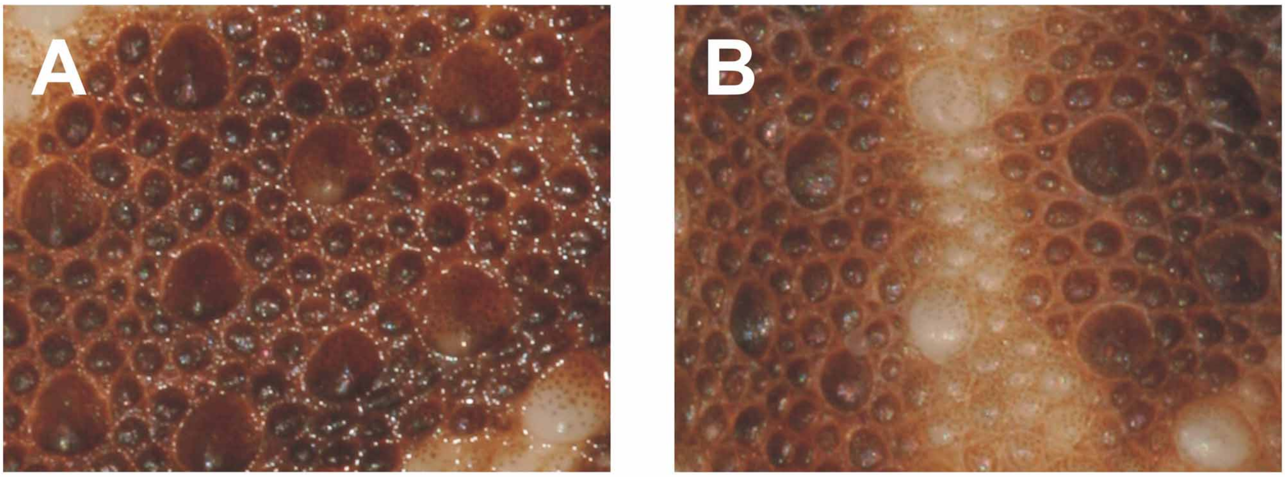

FIGURE 8. Dorsal tubercles in *C. irregularis* s. str. NLO 36031 (A) and holotype of *Cyrtodactylus bidoupimontis* **sp. nov.** (B).

Comparisons with congeners from surrounding countries of Southeast Asia. *Cyrtodactylus bidoupimontis* **sp. nov.** differs from other congeners from surrounding countries of Southeast Asia by the following characters. By the absence of transversely enlarged subcaudal plates the new species may be distinguished from: *C. aequalis* Bauer, *C. annandalei* Bauer, *C. aurensis* Grismer, *C. baluensis* (Mocquard), *C. chanhomeae* Bauer, Sumontha & Pauwels, *C. consobrinus* (Peters), *C. feae* (Boulenger), *C. intermedius* (Smith), *C. ingeri* Hikida, *C. interdigitalis* Ulber, *C. jarujini* Ulber, *C. lomyenensis* Ngo & Pauwels, *C. malayanus* (de Rooij), *C. oldhami* (Theobald, 1876), *C. pageli* Schneider, Nguyen, Schmitz, Kingsada, Auer & Ziegler, *C. peguensis* (Boulenger), *C. pulchellus* Gray, *C. russelli* Bauer, *C. slowinskii* Bauer, *C. sumonthai* Bauer, Pauwels & Chanhome, and *C. teyniei* David, Nguyen, Schneider & Ziegler. By the absence of a precloacal groove *Cyrtodactylus bidoupimontis* sp. nov differs from the following Southeast Asian species: *C. annulatus* (Taylor), *C. aurensis* Grismer, *C. cavernicolus* Inger & King, *C. fumosus* (Müller), *C. marmoratus* (Gray), *C. papuensis* (Brongersma), *C. philippinicus* Steindachner, *C. pubisulcus* Inger, *C. pulchellus* Gray, *C. rubidus* (Blyth), *C. sadleiri* (Wells & Wellington), *C. semenanjungensis* Grismer & Leong, and *C. tiomanensis* Das & Lim. From *C. agusanensis* (Taylor), *C. brevidactylus* Bauer, *C. buchardi* David, Teynié & Ohler, *C. chrysopylos* Bauer, *C. gansi* Bauer, *C. elok* Dring, *C. matsuii* Hikida, *C. sworderi* (Smith), and *C. yoshii* Hikida, the new species can be distinguished by the presence of enlarged femoral scales.

Etymology. The specific epithet is an adjective derived from the Vietnamese name of the type locality of the new species, Mount Bidoup and Latin root “mons” (nom.), “montis” (gen.) (“mountain”) commemorating the preference of the new species for higher altitudes and the evergreen forest of Bidoup – Nui Ba National Park. As common name we suggest Bidoup Bent–toed Gecko (in English), and Thach sung ngon bi dup (in Vietnamese).

Habitat description. Specimens were collected in primary mountainous subtropical forest in the valley of Da Nhim River at altitudes of ca. 1550–1920 m above sea level (Fig.8). The geckos were mostly found in areas of mixed subtropical forests with predominance of deciduous trees (Fagaceae, Lauraceae). The canopy is mostly formed by *Castanopsis*, *Lithocarpus*, *Quercus*, *Cinnamonum* and *Litsea* trees with dense undergrowth and various herbaceous vegetation including many species of ferns. Animals were found during day time under the bark on dead standing tree trunks or at night on the trees approximately 1–4 m above the ground. The species seems to be quite abundant in this area.

Distribution. *Cyrtodactylus bidoupimontis* **sp. nov.** inhabits mountainous evergreen tropical forests in the north-eastern part of the Langbian plateau at altitudes between 1500 to 1920 m a.s.l. (see Fig.1) So far, this species is reported from the Bidoup sector of Bidoup – Nui Ba National Park (Bidoup, Gia Rich and Hon Giao mountain systems; Da Chais and Da Nhim communes, Lac Duong District, Lam Dong Province, southern Vietnam). The new species is also found in adjacent areas of Khan Hoa Province: Khanh Thuong, Giang Ly and Son Thai Communes, Khanh Vinh District, southern Vietnam.

TABLE 5. Morphological characters of *Cyrtodactylus bugiamapensis* **sp. nov.** and *Cyrtodactylus bidoupimontis* **sp. nov.** compared with its Laotian and Vietnamese congeners (after David *et al.* 2011, complemented by data from Ngo 2011, Ngo & Chan 2011, Luu *et al.* 2011, Schneider *et al.* 2011; ordered by characters). Abbreviations are as follows: SVL: snout-vent length; TailL: tail length; V: ventral scales in longitudinal rows at midbody; EFS: enlarged femoral scales (unilateral value only); FP: femoral pores (in total, i.e., on both sides); PP: precloacal pores; LF4: subdigital lamellae under the fourth digit; LT4: subdigital lamellae under the fourth toe; m: male; f: female; –: characters unobtainable from literature.

Taxa	SVL (mm)	TailL (mm)	V	EFS	FP	PP (in males)	PP (in females)	LF4	LT4	Color pattern of dorsum	Enlarged subcaudals
***Cyrtodactylus. bugiamapensis* sp. nov.**	58.6-76.8 (adults)	65.3-83 (adults)	36-46	6-10	absent	7-8	0-7	15-17	17-20	blotched	Absent
***Cyrtodactylus bidoupimontis* sp. nov.**	74-86.3 (adults)	75-86.0 (adults)	38-43	6-8	absent	4-6	0	15-20	18-23	banded	Absent
C. badenensis	59.3–74.1	58.6–82.4	25–28	absent	absent	0	0	-	18–22	banded	Present
C. bichnganae	95.3–99.9	96.3–115.6	30–31	11–13	18	10	8	18–20	16–20	banded	Present
C. buchardi	60–65	46–54	30	absent	absent	9	0	14	12	blotched	Absent
C. caovansungi	90.4–94	120	38–44	8	6	9	0	22	23–25	banded	Present
C. cattienensis	43.5– 69	51–64.7	28–42	3–8	absent	6–8	0	12–16	14–19	banded	Absent
C. chauquangensis	90.9–99.3	97–108.3	36–38	absent	absent	6–7	7	16–18	19–23	banded	Present
C. condorensis	80	100	35–40	present	-	4–7	?	-	-	blotched	Present
C. cryptus	62.5–90.8	63.5–88.4	47–50	absent	absent	9–11	0	18–19	20–23	banded	Absent
C. cucphuongensis	96.0	79.3	42	14	absent	0	–	21	24	banded	present
C. eisenmanae	76.8–89.2	91–103.8	44–45	4–6	absent	0	0	18–20	17–18	banded	Present
C. grismeri	68.3–95	111.3–115.1	33–38	0	-	0	0	16–18	16–19	banded	Present
C. hontreensis	72.4–88.9	84.2–106.5	40–42	2–5	absent	7–8	0	16	17–19	banded	Present
C. huongsonensis	73.4–89.8	90.5	41–48	7–9	15–17	6	8	17–19	20–23	banded	present
C. huynhi	54.8–79.8	61.5–78.6	43–46	3–5	3-8	7–9	0-8	15–17	17–20	banded	Absent

continued on next page.

TABLE 5. (continued)

Taxa	SVL (mm)	TailL (mm)	V	EFS	FP	PP (in males)	PP (in females)	LF4	LT4	Color pattern of dorsum	Enlarged subcaudals
C. interdigitalis	59–80	71–90	37–42	present	16-18	14	0	17–22	16–20	banded	Present
C. intermedius	61–85	80–110	40–50	6–10	-	8–10	?	20	22	banded	Present
C. irregularis	72–86	66–74	38–45	7–8	-	5–7	0-6	15–16	18–19	blotched	Absent
C. jarujini	85–90	105–116	32–38	present	13–24	15	0	15–17	18–19	blotched	Absent
C. lomyenensis	68.2–71.2	72.2–86.1	35–36	17–18	present	39–40 (PP + FP)	20–32 (PP + FP)	16–19	19–23	banded	Present
C. martini	64.4–96.2	76.0–101.2	39–43	14–18	absent	4	0	19-23	22-24	banded	Absent
C. nigriocularis	82.7–107.5	70.6–121	42–49	absent	absent	0–2	0	-	17–21	uniformly brown	Present
C. pageli	65.8-81.8	76.8-113.2	41-44	absent	absent	4	0	19-23	19-23	blotched	Present
C. paradoxus	52–84	80.8–111	32–40	present	absent	0–4	0	15–18	17–23	banded	Present
C. phongnhakebangensis	52–96.3	83–110	32–42	present	present	32–42 (PP + FP)	0-41 (PP + FP)	17–19	17–26	banded	Present
C. phuquocensis	62.2–85.8	92.0-103.1	42–46	10–11	absent	7–9	0-8	18	15–18	banded	Present
C. pseudoquadrivirgatus	48.6–83.3	55.7–82.3	41–57	absent	absent	5–9	5-10	15–21	16–25	blotched	Absent
C. roesleri	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
C. takouensis	74.7–81.1	77.7–91	39–40	3–5	0-2	3–4	0	16–17	18–20	banded	Present
C. teyniei	89.9	ca 110	38	23	absent	unknown	13	17–18	19–20	blotched	Present
C. wayakonei	72.0–86.8	76.8–89.0	31–35	absent	absent	6–8	7	17–18	19–20	banded	Present
C. yangbayensis	78.5–92.3	91.3–109.1	39–46	5–16	0–2	6–8	0	16–19	15–17	banded	Present
C. ziegleri	84.6–93	95–107	33–39	8–10	0–6	5–8	0-8	16–19	18–21	banded	Absent

Phylogenetic position. According to mtDNA data (COI partial sequence), *C. bidoupimontis* belongs to a mountain species group of the *C. irregularis* complex and is sister species to *C. irregularis* sensu stricto (*p*-distance between the two species is 9.78% of substitutions according to COI partial sequences).

FIGURE 9. Habitat of *Cyrtodactylus bidoupimontis* **sp. nov.**: Da Nhim river valley, between Bidoup and Hon Giao mountains, Giang Ly forest of Bidoup—Nui Ba National Park, Da Chais community, Lac Duong District, Lam Dong Province, southern Vietnam.

Discussion

In the present paper fragments of the COI mtDNA gene were for the first time applied for barcoding and the evaluation of potential cryptic diversity within the diverse and in part taxonomically complicated gecko genus *Cyrtodactylus*. Low inter- and intrapopulational variation as well as not overlapping values of genetic distances for inter- and intraspecific comparisons make COI a promising genetic marker for barcoding, genetic species identification and evaluation of phylogenetic relationships among groups of closely related species and species complexes. However due to possible effects of fragment saturation, COI cannot successfully resolve evolutionary relationships between distantly related taxa even within the same genus which constrains phylogenetic application of this marker. In the face of complicated morphological species diagnoses and only recently revealed complex diversity of *Cyrtodactylus*, COI-barcoding appears to be a useful tool for the recognition of species delimitation and taxonomic studies in this gecko genus.

Our analysis supports pronounced phylogenetic structuring within the southern cluster of the *C. irregularis* complex which assumes following taxonomic considerations:

Our data confirm the proposed species status of *C. ziegleri* (Nazarov *et al.*, 2008) and *C. cattienensis* (Geissler *et al.*, 2009), which are both based on morphology and also from mtDNA sequences quite distinct from *C. irregularis* s. str.

The taxonomic diversity within the *C. irregularis* complex appears to be clearly underestimated. Due to distinct genetic differences, although in part only supported by slight morphological differences, we herein propose species status for *Cyrtodactylus* populations from Bu Gia Map and Bidoup – Nui Ba National Parks. These populations are herein described as *Cyrtodactylus bugiamapensis* **sp. nov.** and *Cyrtodactylus bidoupimontis* **sp. nov.**

Populations of the *C. irregularis* complex from Nui Chua Mountain in Ninh Thuan Province and from Ba Ho cascade in Khanh Hoa Province also clearly represent separate lineages which might deserve species status, however, which will be dealt with separately and published elsewhere.

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