



<http://dx.doi.org/10.11646/zootaxa.3964.1.8>

<http://zoobank.org/urn:lsid:zoobank.org:pub:6BF99E00-3617-466B-9D89-C9DB3583DD18>

## ***Cyrtodactylus rosichonariefi* sp. nov. (Squamata: Gekkonidae), a new swamp-dwelling bent-toed gecko from Bunguran Island (Great Natuna), Indonesia**

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### **Abstract**

*Cyrtodactylus rosichonariefi* sp. nov. is the second newly described species of Bent-toed gecko from Bunguran Island (Great Natuna), Indonesia. This species occurs in the Sekunyam Forest and is differentiated from all other species of the *C. semenanjungensis* species group of the Thai-Malay Peninsula by having the following unique combination of characteristics: intermediate size (SVL of adult male holotype 54.6 mm); enlarged femoral scales, femoral pores, no precloacal groove, enlarged precloacal scales, no precloacal pores; subcaudals not enlarged; and dorsal pattern blotched but lacking paired, dark, semilunar-shaped blotches on upper nape. The new species is the sister species of *C. majulah* Grismer, Wood & Lim.

**Key words:** new species, *Cyrtodactylus rosichonariefi* sp. nov., Sekunyam Forest, Bunguran Island, Indonesia

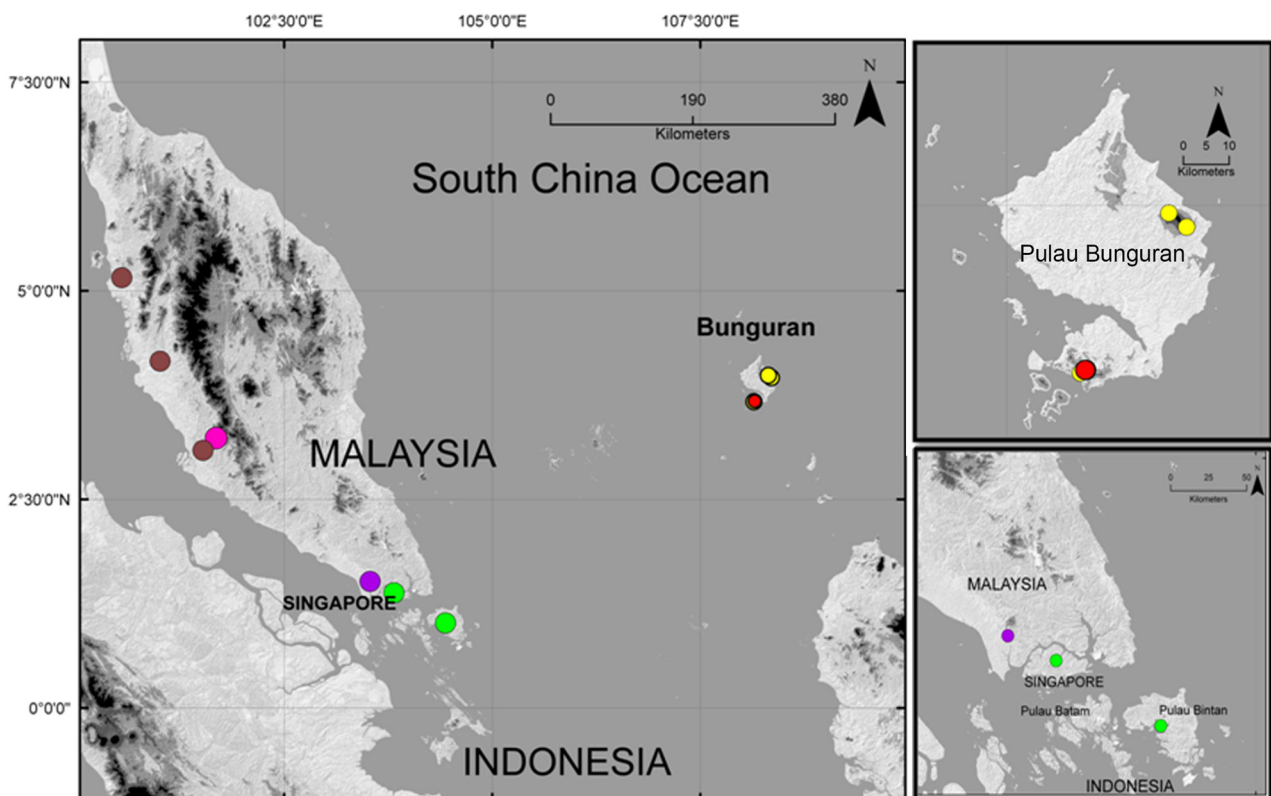
### **Introduction**

The Natuna and Anambas Archipelagoes lie between the Thai-Malay Peninsula and Borneo and serve as biogeographic stepping stones between Indochina and Sundaland (Whitten *et al.* 1987; Leong *et al.* 2003; Grismer *et al.* 2006; Grismer 2011). Even though the herpetofauna of the largest island of the Natuna Archipelago, Bunguran (Great Natuna) Island, has been studied for many years (Günther 1895; Smedley 1928, 1931a, b; Leong *et al.* 2003; Riyanto 2012) a number of new endemic species have recently been discovered, including *Cyrtodactylus hikidai* Riyanto, 2012, *Cnemaspis mumpuniae* Grismer, Wood, Anuar, Riyanto, Ahmad, Muin, Sumontha, Grismer, Chan, Quah, & Pauwels, 2014 and *C. sundainsula* Grismer, Wood, Anuar, Riyanto, Ahmad, Muin, Sumontha, Grismer, Chan, Quah, & Pauwels, 2014. During a survey of the Sekunyam Forest—a swampy area in the southern part of Bunguran Island (Fig. 1)—during August 2013 and April 2014, another new species of Bent-toed gecko (*Cyrtodactylus*) was discovered. Molecular and morphological analyses indicate that this population is part of the swamp-dwelling clade (Johnson *et al.* 2012) of the *C. semenanjungensis* species complex (Grismer *et al.* 2014b) of Peninsular Malaysia and Singapore, but it cannot be associated with any of known species in that complex. We here describe it as a new species.

### **Material and methods**

**Morphological analysis.** The following measurements were taken with Mitutoyo dial calipers to the nearest 0.1 mm under an AmScope microscope, following Grismer *et al.* (2014b): snout-vent length (SVL), taken from the tip of snout to the vent; tail length (TL), taken from the vent to the tip of the tail for both original or regenerated; tail

width (TW), taken at the base of the tail immediately posterior to the postcloacal swelling; forearm length (FL), taken on the dorsal surface from the posterior margin of the elbow while flexed 90° to the inflection of the flexed wrist; tibia length (TBL), taken on the ventral side from the posterior surface of the knee flexed at 90° to the base of the heel; trunk length (TrL), taken from the posterior margin of the forelimb at its insertion point on the body to the anterior margin of the hind limb at its insertion point on the body; head length (HL), the distance from the posterior edge of the retroarticular process of the lower jaw to the tip of the snout; head width (HW), measured at the angle of the jaws; head depth (HD), the maximum height of head from the occiput to the throat; eyeball diameter (ED), the greatest horizontal diameter of the eyeball; eye-to-ear distance (EE), measured from the anterior edge of the ear opening to the posterior edge of the eyeball; eye-to-snout distance (ES), measured from anterior most edge of the eyeball to the tip of the snout; eye-to-nostril distance (EN), measured between the anterior margin of the eyeball to the posterior margin of the external nares; interorbital distance (IO), measured across the head between the anterior edges of the orbit; ear length (EarL), the greatest horizontal distance of the ear opening; and internarial distance (IN), measured between the medial edges of the nares across the rostrum.



**FIGURE 1.** Location of Bunguran (Great Natuna) Island in the South China Sea. Closed red circle is type locality of *Cyrtodactylus rosichonariefi* sp. nov. Closed yellow circles are known localities of *C. hikidai*. Closed green circles are known localities of *C. majulah*. Closed brown circles are known localities of *C. payacola*. Closed pink circle is type locality of *C. metropolis*. Closed purple circle is type locality of *C. pantiensis*.

The following meristic characters were evaluated following Grismer (2005): precloacal pores (PP), enlarged precloacal scales (EPS), femoral pores (FP), enlarged femoral scales (EFS), longitudinal rows of tubercles on dorsum between ventrolateral folds (DT), paravertebral tubercles between midpoint of forelimb insertion and midpoint of hind limb insertion (PVT), and ventral scales across venter between ventrolateral folds (VS). Following Oliver *et al.* (2011), supralabial and infralabial scales were counted to both the midpoint of the eye and to the rictus (SuL) and infralabials (InL, including all enlarged scales from mental to rictus). Basal subdigital lamellae were counted from the most proximal lamella at least twice as large as adjacent palmar scales following Bauer *et al.* (2010). Measurements and scale counts were made on the right side of each specimen unless otherwise noted. To visualize some structures, such as subdigital keels, on very small specimens, we applied the reversible stain methylene blue in 70% alcohol. Some of the information on character states and their distribution in other species was obtained from Grismer *et al.* (2008, 2014b). Sex was determined by the presence or absence of

hemipenes, which were everted while injecting the specimen with ethanol. SVL, TL, and regenerated TL were measured both prior to and after fixation. Color notes were taken from digital images of living specimens prior to preservation. Latitude, longitude, and elevation of localities of specimens collected were recorded using a Garmin GPSmap 60CSx using WGS 84 map datum. Both specimens (holotype and paratype) were deposited in the Museum Zoologicum Bogoriense (MZB), Indonesian Institute of Sciences (LIPI), Cibinong, Bogor, Indonesia.

**Phylogenetic analysis.** We obtained sequence data from a 1502 bp fragment of the mitochondrial NADH dehydrogenase subunit 2 gene (*ND2*) including the flanking tRNAs (tRNA *WANCY*) from two ingroup samples. Outgroup taxa were based on Wood *et al.* (2012) and obtained from GenBank (see Grismer *et al.* 2014b; Table 1). Voucher specimens for the Bunguran Island population are MZB.Lace.12132–33, with corresponding GenBank numbers of KP256187 and KP256188, respectively. Genomic DNA was isolated from liver or skeletal muscle tissue stored in 95% ethanol using the Qiagen Dneasy™ tissue kit (Qiagen, Valencia, California, USA). *ND2* was amplified using double-stranded PCR under the following conditions: 1.0 µl genomic DNA, 1.0 µl light strand primer, 1.0 µl heavy strand primer, 1.0 µl dinucleotide pairs, 2.0 µl 5x buffer, MgCl 10x buffer, 0.1 µl Taq polymerase, and 7.56 µl ultra-pure H<sub>2</sub>O. PCR reactions were executed on an Eppendorf Mastercycler gradient thermocycler under the following conditions: initial denaturation at 95°C for 2 min, followed by a second denaturation at 95°C for 35 s, annealing at 48°C for 35 s, followed by a cycle extension at 72°C for 35 s, for 31 cycles. All PCR products were visualized on a 10 % agarose gel electrophoresis. Successful PCR products were vacuum purified using MANU 30 PCR plates (Millipore) and purified products were resuspended in ultra-pure water. Purified PCR products were sequenced using the ABI Big-Dye Terminator v3.1 Cycle Sequencing Kit in an ABI GeneAmp PCR 9700 thermal cycler. Cycle sequencing reactions were purified with Sephadex G-50 Fine (GE Healthcare) and sequence on an ABI 3730xl DNA analyzer at the Brigham Young University DNA Sequencing Center. Primers used for amplification and sequencing are those listed by Grismer *et al.* (2014b; Table 2).

For the phylogenetic analyses we applied two model-based methods, Maximum Likelihood (ML) and Bayesian Inference (BI). The Akaike Information Criterion (AIC) as implemented in Model test v3.7 (Posada & Crandall 1998), was used to calculate the best-fit model of evolution for each codon position (see Grismer *et al.* 2014b; Table 3). ML analysis was performed using RAxML HPC v7.5.4 (Stamatakis *et al.* 2008), and 1000 bootstrap pseudoreplicates were run via the rapid hill-climbing algorithm (Stamatakis *et al.* 2008). The BI analysis was carried out in MrBayes v3.2 (Ronquist *et al.* 2012) using default priors. Two simultaneous runs were performed with eight chains per run, seven hot and one cold, following default priors. The analysis was run for 5,000,000 generations and sampled every 500 generations according to Markov Chain Monte Carlo criteria. The analysis was halted after the average standard deviation split frequency was below 0.01. The program Tracer v1.5 (Drummond & Rambaut 2007) was employed to plot the log likelihood scores against the number of generations to assess convergence and to determine the appropriate number of burn in trees. We conservatively discarded the first 25% of the trees as burn-in. A consensus tree was then computed from the two parallel runs using Tree Annotator v1.6. Nodes that had posterior probabilities above 0.95 were considered to be significantly supported.

**TABLE 1.** A list of the sample used in the molecular analysis with Genbank accession number. Abbreviated voucher number are as follows: LSUHC, La Sierra University Herpetological Collection; FMNH, Field Museum of National History; MZB, Museum Zoologicum Bogoriense and ZRC, Zoological Reference Collection of Raffles Museum.

Voucher	Species	Locality	ND2 Genbank Accession Number
LSUHC 9513	<i>Cyrtodactylus intermedius</i> (Smith)	Thailand, Chantaburi Province	JQ889183
LSUHC 9514	<i>Cyrtodactylus intermedius</i> (Smith)	Thailand, Chantaburi Province	JQ889184
LSUHC 6471	<i>Cyrtodactylus elok</i> Grismer	West Malaysia, Pahang, Fraser's Hill, the Gap	JQ889180
FMNH 265806	<i>Cyrtodactylus</i> sp	Thailand, Loei, Phu Rua	JQ889188
FMNH 255454	<i>Cyrtodactylus interdigitalis</i> Ulber	Lao PDR, Khammouan Province, Nakai District	JQ889181

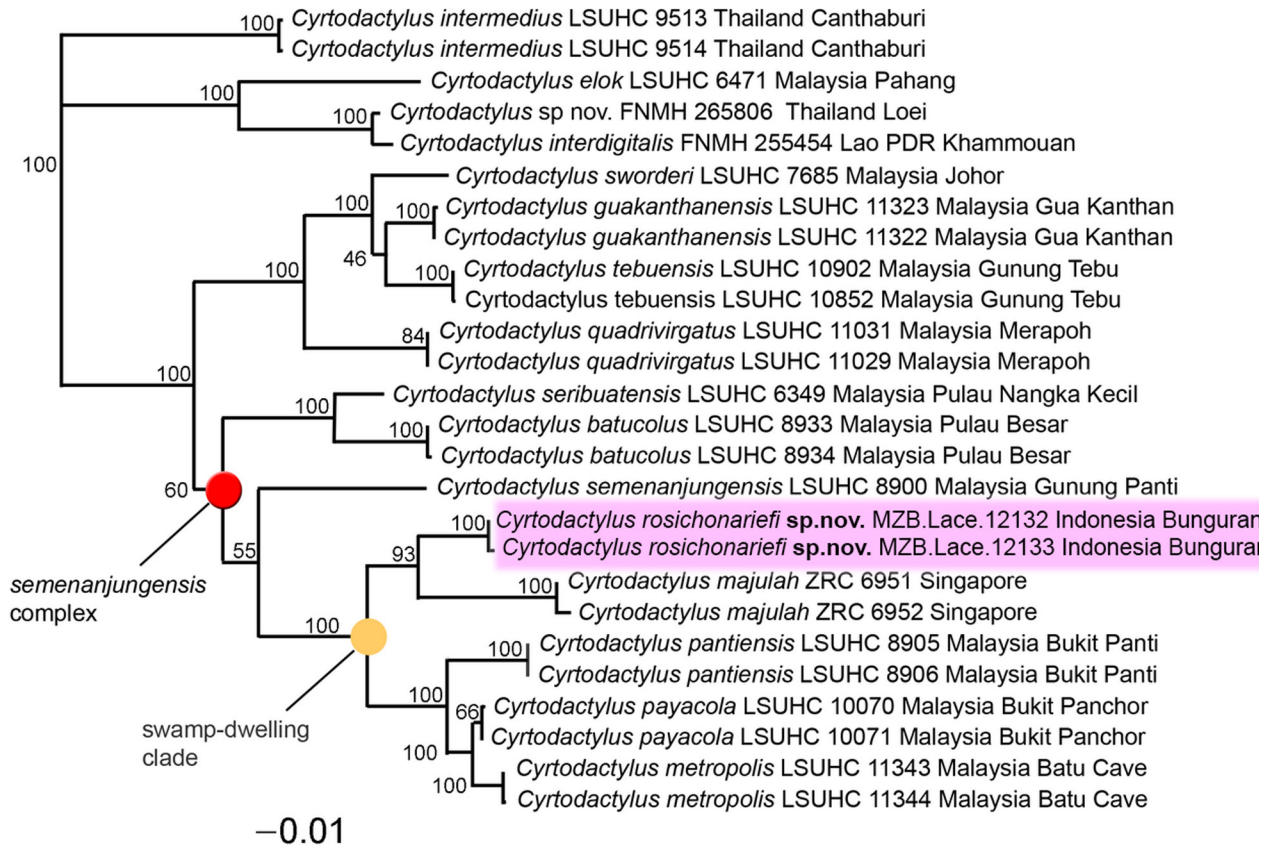
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**TABLE 1.** (Continued)

Voucher	Species	Locality	ND2 Genbank Accession Number
LSUHC 7685	<i>Cyrtodactylus sworderi</i> (Smith)	West Malaysia, Johor, Endau-Rompin, Peta, Sungai Kawal	JQ889189
LSUHC 11322	<i>Cyrtodactylus guakhantanensis</i> Grismer, Belabut, Quah, Chan, Wood & Hasim	Gua Khantan, Perak, Peninsula Malaysia	XX000000
LSUHC 11323	<i>Cyrtodactylus guakhantanensis</i> Grismer, Belabut, Quah, Chan, Wood & Hasim	Peninsula Malaysia, Gua Khantan, Perak	XX000000
LSUHC 10902	<i>Cyrtodactylus tebuensis</i> Grismer,, Anuar, Muin, Quah & Wood	West Malaysia, Terengganu, Gunung Tebu	JX988527
LSUHC 10852	<i>Cyrtodactylus tebuensis</i> Grismer,, Anuar, Muin, Quah & Wood	West Malaysia, Terengganu, Gunung Tebu	JX988525
LSUHC 11031	<i>Cyrtodactylus quadrivirgatus</i> Taylor	Malaysia, Merapoh	XX000000
LSUHC 11029	<i>Cyrtodactylus quadrivirgatus</i> Taylor	Malaysia, Merapoh	XX000000
LSUHC 6349	<i>Cyrtodactylus seribuatensis</i> Youmans & Grismer	West Malaysia, Johor, Pulau Nangka Kecil	JQ889187
LSUHC 8933	<i>Cyrtodactylus batucolus</i> Grismer, Chan, Brismer, Wood & Belabut	West Malaysia, Melaka, Pulau Besar	JQ889178
LSUHC 8934	<i>Cyrtodactylus batucolus</i> Grismer,, Anuar, Muin, Quah & Wood	West Malaysia, Melaka, Pulau Besar	JQ889179
LSUHC 8900	<i>Cyrtodactylus semenanjungensis</i> Grismer & Leong	West Malaysia, Johor, Gunung Pantí	JQ889177
MZB.Lace.	<i>Cyrtodactylus rosichonariefi</i> <b>sp. nov.</b>	Indonesia, Great Natuna (Bunguran)	KP256187
MZB.Lace.	<i>Cyrtodactylus rosichonariefi</i> <b>sp. nov.</b>	Indonesia, Grat Natuna (Bunguran)	KP256188
ZRC 2.6951	<i>Cyrtodactylus majulah</i> Grismer, Wood & Lim	Singapore, Nee Son Swamp	JX 988529
ZRC 2.6952	<i>Cyrtodactylus majulah</i> Grismer, Wood & Lim	Singapore, Nee Son Swamp	JX 988530
LSUHC 8905	<i>Cyrtodactylus pantiensis</i> Grismer, Chan, Brismer, Wood & Belabut	West Malaysia, Gunung Pantí	JQ889185
LSUHC 8906	<i>Cyrtodactylus pantiensis</i> Grismer, Chan, Brismer, Wood & Belabut	West Malaysia, Gunung Pantí	JQ889186
LSUHC 10070	<i>Cyrtodactylus payacola</i> Johson, Quah, Anuar, Muin, Wood, Grismer, Greer, Chan, Ahmad, Bauer & Grismer	West Malaysia, Bukit Panchor	JQ889190
LSUHC 10071	<i>Cyrtodactylus payacola</i> Johson, Quah, Anuar, Muin, Wood, Grismer, Greer, Chan, Ahmad, Bauer & Grismer	West Malaysia, Bukit Panchor	JQ889191
LSUHC 11343	<i>Cyrtodactylus metropolis</i> Grismer, Wood, Chan, Anuar & Muin	Peninsula Malaysia, Gombak, Batu Cave	XX000000
LSUHC 11344	<i>Cyrtodactylus metropolis</i> Grismer, Wood, Chan, Anuar & Muin	Peninsula Malaysia, Gombak, Batu Cave	XX000000

## Results

The phylogenetic analysis strongly indicates that the Bunguran Island population is embedded within the swamp-dwelling clade of the Thai-Malay Peninsula and, within this clade, it is the sister species to *Cyrtodactylus majulah* Grismer, Wood & Lim, 2012 from Singapore and Pulau Bintan (1.0 BPP/93 ML; Fig. 2). Additionally, based on comparisons with other species, these specimens can be differentiated from all other members of the swamp-dwelling clade and is therefore described below as a new species.



**FIGURE 2.** Phylogram of the relationships of the species within the *Cyrtodactylus semenanjungensis* complex. The tree is a Maximum Likelihood topology (-ln L 13709.785816) with Maximum Likelihood bootstrap values. Bayesian posterior probabilities are 1.0 at all nodes and not shown on the tree.

***Cyrtodactylus rosichonariefi* sp. nov.**

English common name: Rosichonariefi’s Bent-toed Gecko

Indonesian common name: Cicak Kecil Rosichonariefi

(Figs. 3, 4)

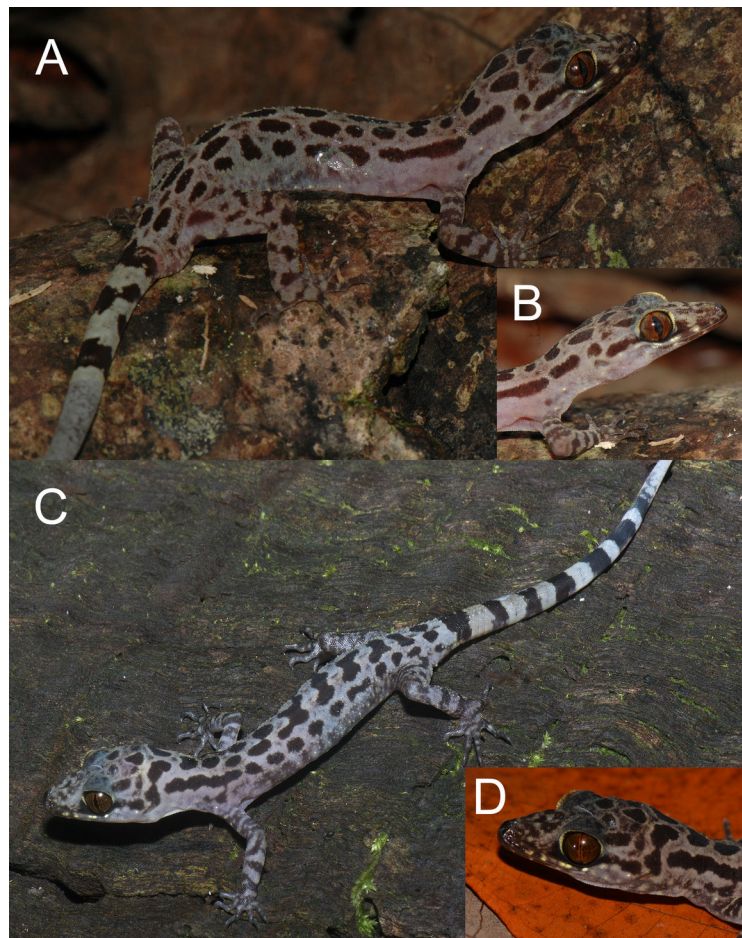
**Holotype.** MZB.Lace.12132, an adult male from the Sekunyam Forest, Bunguran Selatan Subdistrict, Natuna District, Kepulauan Riau Province, Bunguran Island (Great Natuna), Indonesia (3°40’29.4” N; 108°09’16.0” E; elevation 80 m), collected on 15 August 2013 at 20h25 by A. Riyanto and Zamri.

**Paratype.** MZB.Lace.12133, subadult male, Sekunyam Forest, Bunguran Selatan Subdistrict, Natuna District, Kepulauan Riau Province, Bunguran Island, Indonesia (03°40’30.1” N; 108°09’21.1” E; elevation 80 m), collected on 16 April 2014 at 19h30 by A. Riyanto and L.L. Grismer.

**Diagnosis.** SVL of only known adult male 54.6 mm; body relatively robust; limbs and digits short, relatively slender; 19 irregularly aligned rows of strongly keeled dorsal tubercles; 34 paravertebral tubercles; 46 ventral scales between ventrolateral folds; no preloacal groove; no preloacal pores; six slightly enlarged rows of femoral scales on the anterior portion of the thighs meet abruptly with postfemoral scales; enlarged preloacal scales; 12 or 13 subdigital lamellae on the first toe; 18 or 19 subdigital lamellae on the fourth toe; no enlarged subcaudal scales; reddish brown iris.

**Description of holotype** (Fig. 3A). Adult male, SVL 54.6 mm; head moderately long (HL/SVL 0.30), relatively narrow (HW/HL 0.58), depressed (HD/HL 0.39), distinct from neck; lores and interorbital regions concave; canthus rostralis prominent and rounded; frontonasal region concave; snout elongate (ES/HL 0.37), relatively pointed, longer than ED (ED/ES 0.60); scales on snout and forehead small, rounded, granular,

homogeneous; scales on snout larger than those on occipital region; eye large (ED/HL 0.22); pupil vertical with crenellated margins when constricted, and smooth margins when expanded; supraciliaries short, bearing small conical spines posteriorly; ear opening oval, large (EarL/HL 0.10);  $EE > ED$  ( $EE/ED 1.38$ ); rostral incompletely divided dorsally by a Y-shaped shallow groove; two enlarged supranasals separated from each other by three intersupranasals, two of them contact the smaller snout scales and one of them completely surrounded by the larger scales (Fig. 4C); naris oval, bordered by rostral anteriorly, first supralabial and supranasal dorsally, and two enlarged postnasals dorsally; orbit separated from supralabials by three rows of small scales; mental triangular, wider (2.1 mm) than deep (1.6 mm), bordered anterolaterally by first infralabials and posteriorly by paired elongate postmentals that contact medially for 40% of their posterior sections, followed by seven gular scales arranged in a row with two slightly enlarged scales at their lateral termini (Fig. 4B); both right and left sides consist of 10 supralabials to the rictus, 8 to midpoint the eye; nine infralabials scales to the rictus (Fig. 4A).

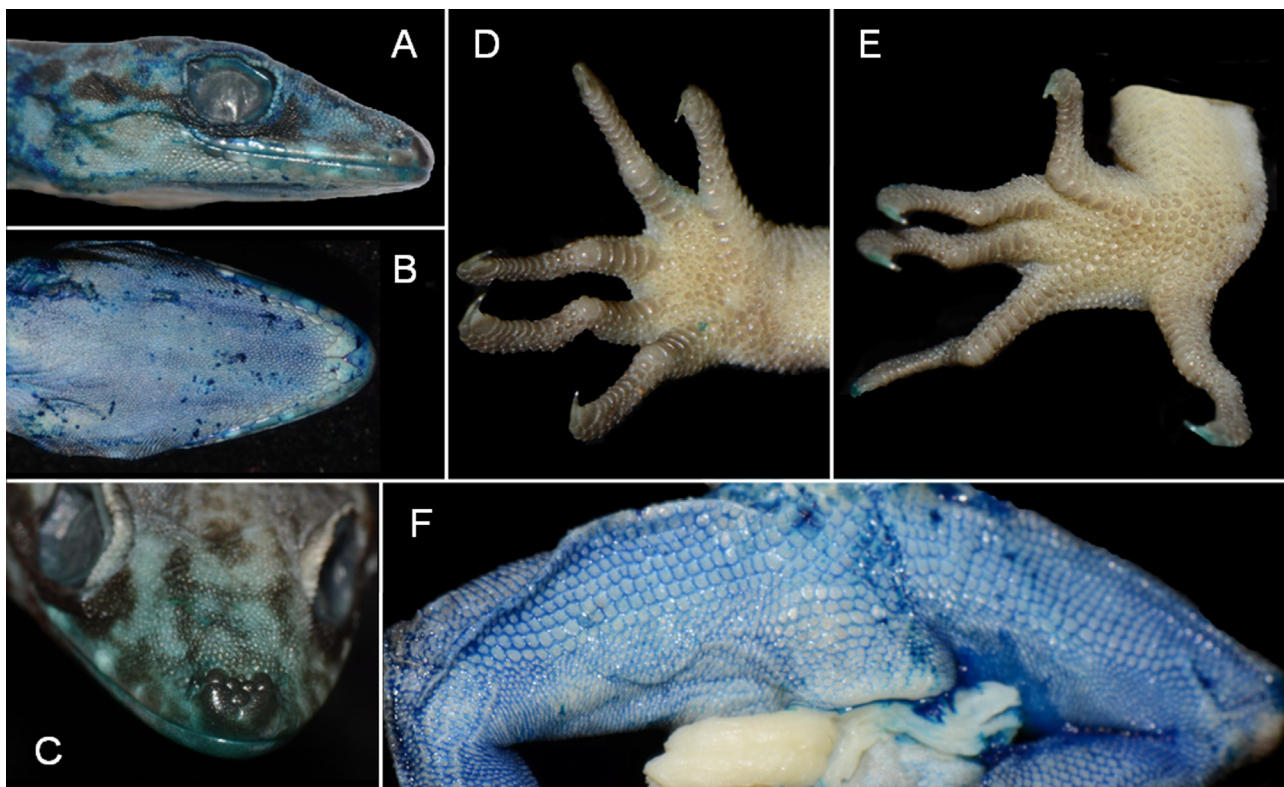


**FIGURE 3.** Specimens of *Cyrtodactylus rosichonariefi* sp. nov. (A) Holotype (MZB.Lace.12132), adult male, SVL 54.6mm. (B) Lateral view of head the holotype showing the eye, with a reddish brown iris and yellow supraciliaries. (C) Paratype (MZB.Lace.12133), subadult male, SVL 45.9 mm. (D) Lateral view of head the paratype.

Body relatively robust, elongate ( $TrL/SVL 0.46$ ) with ventrolateral folds; ventrolateral folds with bearing small, scattered tubercles; gular region bearing relatively homogeneous, smooth scales; dorsal scales granular to conical; 19 irregular rows of dorsal tubercles at midbody; smallest tubercles on flanks and in the frontal region; 34 paravertebral tubercles; ventral scales much larger than dorsals, smooth, round, subimbricate, largest posteriorly; 46 ventral scale rows at midbody between ventrolateral folds; precloacal groove absent; no precloacal pores; six slightly enlarged rows of femoral scales on the anterior portion of the thighs meet abruptly with postfemoral scales; (Fig. 4F); precloacal region has 6 rows of slightly enlarged scales (Fig. 4F); scales on palmar surfaces granular, juxtaposed (Fig. 4D); scales on plantar surfaces and hind limbs granular, juxtaposed (Fig. 4E).

Forelimbs and hind limbs relatively robust ( $FL/SVL 0.16$ ;  $TBL/SVL 0.16$ ); digits relatively short, strongly inflected at basal interphalangeal joints, all bearing slightly curved claws; basal subdigital lamellae nearly as broad

as digit; subdigital lamellae on manus 12–14–15–16–14, not including ventral claw sheath; count of subdigital lamellae on pes 12–15–17–19–18, not including ventral claw sheath; interdigital webbing present but weakly developed; relative length of fingers II>III>IV>I>V and of toes IV>V> III> II> I.



**FIGURE 4.** Detailed illustrations of the holotype of *Cyrtodactylus rosichonariefi* sp. nov (MZB.Lace.12132). (A) Lateral view of head. (B) Ventral view of the head, showing patterns of mental, postmental, and smooth scales on the throat. (C) Snout region, showing rostral and supranaries scales. (D) Ventral view of right palmar, showing scales on palmar surface. (E) Ventral view of right pes, showing scales on the plantar surface. (F) Cloacal region, showing the absence of precloacal pores, enlarged femoral scales, and femoral pores.

Tail regenerated (and broken during the preservation process), cylindrical, segmented, with each segment consisting of 7–8 scales in a row dorsally, tapering to the tip, no median enlarged subcaudal scales; one postcloacal tubercle on each side of tail base; medial row of subcaudals smooth, no enlarged scales; dorsal caudal scales flat, round, hexagonal, or pentagonal, and juxtaposed.

**Coloration in life** (Fig. 3A). Ground color of body, head, limbs, and tail pinkish grey; dark, irregularly shaped markings on rostrum and top of head; weak dark stripe extending from postnasal region through eye and continuing to ear opening; paired offset, paravertebral dark blotches extending onto base of tail to form irregularly shaped bands alternating with irregularly shaped white bands; some whitish tubercles on flanks; dorsal surfaces of limbs banded; ventral surfaces dull, generally immaculate, and lighter than dorsal surfaces; iris reddish brown with yellow supraciliary scales (Fig. 3B).

**Variation.** The coloration and pattern of the paratype closely matches that of the holotype (Fig.3A, C). The paratype has a blotched vertebral region that continues onto the caudal regions as irregularly shaped bands of which there are seven anterior to the regenerate. Measurement (in mm) of holotype (MZB.Lace.12132) is followed by sub adult male paratype in parentheses (MZB.Lace.12133): SVL 54.6 (45.9), TrL 23.8 (19.4), HL 16.6 (13.7), HW 9.7 (8.3), HD 6.4 (5.5), ED 3.7 (3.6), EE 5.1 (4.2), ES 6.2 (6.0), EN 4.5 (4.4), IO 4.9 (3.5), IN 2.0 (1.8), EarL 1.6 (0.9), FL 8.5 (6.8), TBL 8.8 (8.5), TL 58.3 regenerated (broken) and TW 5.0 (3.6).

**Etymology.** The specific epithet *rosichonariefi* combines the names of two Indonesian scientists. We would like to recognize the contributions made by Rosichon Ubaidillah, an entomologist and director of the Museum Zoologicum Bogoriense (MZB), and Ahmad Jauhar Arief, a former director of MZB. Both gentlemen are very supportive and provide opportunities and facilities for young researchers at the MZB to develop their skills. We felt that naming a species after them is a much-deserved honor.

**Species comparisons.** *Cyrtodactylus rosichonariefi* **sp. nov.** is distinguished from all congeners of the *C. semenanjungensis* species complex (Grismer *et al.* 2014b) of Peninsular Malaysia and Singapore except *C. majulah*, *C. pantiensis* Grismer, Chan, Grismer, Wood & Belabut, *C. metropolis* Grismer, Wood, Chan, Anuar & Muin, and *C. payacola* Johnson, Quah, Shahrul, Muin, Wood, Grismer, Greer, Chan, Ahmad, Bauer & Grismer, by having a reddish iris, absence of reticulated pattern on head, lack femoral pores and lack of enlarged median subcaudal. As enumerated in Table 2, *C. rosichonariefi* can be readily differentiated from *C. majulah*, *C. metropolis*, *C. pantiensis* and *C. payacola* by absence both of precloacal pores and tubercles on the forearm. It differs from *C. majulah* by absence of enlarged precloacal scales, fewer dorsal tubercles (19 *versus* 22), fewer paravertebral tubercles (34 *versus* 39–46) and fewer subdigital lamellae on the fourth toe (18–19 *versus* 20–23). It is further differentiated from *C. metropolis* by the absence of enlarged precloacal scales, fewer dorsal tubercles (16 *versus* 22), fewer subdigital lamellae on the fourth toe (18–19 *versus* 20–21) and by having a blotched as opposed to a banded dorsal pattern. The new species can be differentiated from *C. pantiensis* by fewer dorsal tubercles (19 *versus* 22) and subdigital lamellae on fourth toe (18–19 *versus* 22–23). It can be differentiated from *C. payacola* by absence of enlarged precloacal scales, fewer dorsal tubercles (19 *versus* 21) and fewer paravertebral tubercles (34 *versus* 37–39). These character states are scored across all species of the swamp-dwelling clade in Table 2.

**Natural history.** Sekunyam Forest surrounds a small swampy area where the type material collected (Fig. 5). The holotype was found while it was foraging 1 m above ground on the trunk of a small tree (trunk diameter approximately 30 cm). The paratype (and one additional specimen that was not vouchered) entered a burrow on the forest floor to escape. All lizards were found in the vicinity of a small swampy pond that is periodically flooded during rains. The natural history of this species is very similar to that of all the other swamp-dwelling species except for the secondarily karst-adapted species *C. metropolis* (Grismer *et al.* 2014b).

**TABLE 2.** Comparison of selected mensural and meristic characters of *Cyrtodactylus rosichonariefi* **sp. nov.** with other members of the swamp-dwelling clade. Data for *C. majulah*, *C. metropolis*, *C. pantiensis* and *C. payacola* were taken from the original descriptions. / = data unavailable. Abbreviations are listed in the text.

Species	<i>rosichonariefi</i> <b>sp. nov.</b>	<i>majulah</i>	<i>metropolis</i>	<i>pantiensis</i>	<i>payacola</i>
Number or source	2	Grismer <i>et al.</i> 2012	Grismer <i>et al.</i> 2014b	Grismer <i>et al.</i> 2008	Johnson <i>et al.</i> 2012
Maximum SVL (in mm)	54.6	68.0	82.2	77.2	67.7
Tuberculation on forearm	no	yes	yes	yes	yes
Tuberculation on hindlimb	yes	yes	yes	yes	yes
Tuberculation on occiput	yes	yes	yes	yes	yes
Tuberculation on lateral fold	yes	/	/	/	/
SuL (to the rictus)	10	8–9	9–10	10	10
InL	9	7–8	7–8	8	7–10
DT	19	22	22	22	21
PVT	34	39–46	32–44	35–37	37–39
VS	46	43–51	3–44	40–45	37–58
Lamellae under 4 <sup>th</sup> toe	18–19	20–23	20–21	22–23	18–21
EPS	no	yes	yes	no	yes
EFS	no	no	yes	no	no
PP	no	7–11	2	8–9	11–12
Precloacal groove	no	no	no	no	shallow





**FIGURE 5.** Microhabitat of *Cyrtodactylus rosichonareifi* sp. nov. within the Sekunyam Forest, Bunguran Island, Indonesia.

## Discussion

The discovery of a new species on a large island on the Sunda Shelf is not surprising, especially an island as remote as Bunguran. The description of *Cyrtodactylus rosichonareifi* sp. nov. brings the total number of endemic amphibians and reptiles on Bunguran Island to at least seven (Leong *et al.* 2003; Riyanto 2012; Grismer *et al.* 2014a) and underscores its growing importance to the biodiversity of Indonesia. The occurrence in the Natuna Archipelago of species more closely related to taxa on the Thai-Malay Peninsula as opposed to Borneo is a growing theme (e.g., Grismer *et al.* 2014a, 2015) that underscores the fact that the Sunda Shelf was land-positive as little as 20,000 years ago (Sathiamurthy & Voris 2006) and that the Natuna, Anambas, and Seribuat Archipelagos served as a semi-fragmented, hilly corridor between Borneo and the Thai-Malay Peninsula. Associated with this

corridor were lowland swampy areas which, based on the phylogenetic placement of *C. rosichonariefi* in the swamp-dwelling clade (Fig. 2), facilitated its dispersal eastward to the area that eventually became Bunguran Island.

We are certain that many more new species will be found on this underexplored and environmentally heterogeneous island, and we have several expeditions planned for this island and its surrounding satellite islands. Given the rich biodiversity of Bunguran Island, it is imperative that conservation measures be put into place to protect this portion of Indonesia's natural heritage.

## Acknowledgements

AR thanks the Government of Natuna c.q. Badan Lingkungan Hidup Daerah for the kind invitation to survey several sites on Bunguran island in 2013, and Bambang Sunarko (Head of Research Center for Biology—LIPI) and Rosichon Ubaidillah (Director of MZB-LIPI) for giving permission and the opportunity to be able to conduct surveys on the Natuna Islands, and to the amazing next generation of MZB scientists (Tri Haryoko, Cahyo Rachmadi, Anang Setiawan, Sigit Wiantoro, Darmawan, and Sofian Sauri) for the kind collaboration during fieldwork in 2013. We also thank to Ardi and Zamri, for assistance in obtaining the type series.

We thank Aaron M. Bauer (Department of Biology, Villanova University, Pennsylvania, USA) and Hinrich Kaiser (Department of Biology Victor Valley College, California, USA) for reviewing the manuscript. This research was made possible by a research grant from the College of Arts and Sciences at La Sierra University awarded to L. Lee Grismer.

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