




## A new species of *Lepidodactylus* (Squamata: Gekkonidae) from Umboi Island, Papua New Guinea

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### Abstract

We describe a new species of *Lepidodactylus* from Umboi Island, just to the west of New Britain. It is a member of the *Lepidodactylus guppyi* Group and can be distinguished from all other Melanesian *Lepidodactylus* by aspects of digital scalation, digital webbing, enlarged femoral/precloacal scales, and color pattern. It is genetically distinct from its closest congeners, and genetic and morphological data indicate that the new species is most similar among named species to *Lepidodactylus guppyi* from the Solomon Islands, but it diverged from this species and other close relatives approximately 8 MYA or longer at a time prior to the existence of the island that it now occupies. The new species is known from only three individuals collected on a single tree, and efforts to find more animals in what seemed good habitat nearby were unsuccessful. This duplicates the pattern of apparent rarity seen for many *Lepidodactylus* species. Sufficient habitat exists on Umboi Island for arboreal geckos, suggesting that the species is not actually endangered but is ecologically cryptic. However, lack of needed information leads us to assess this species' conservation status as Data Deficient.

**Key words:** Bismarck Arc, cryptic species, ecological crypsis, gecko, lizard

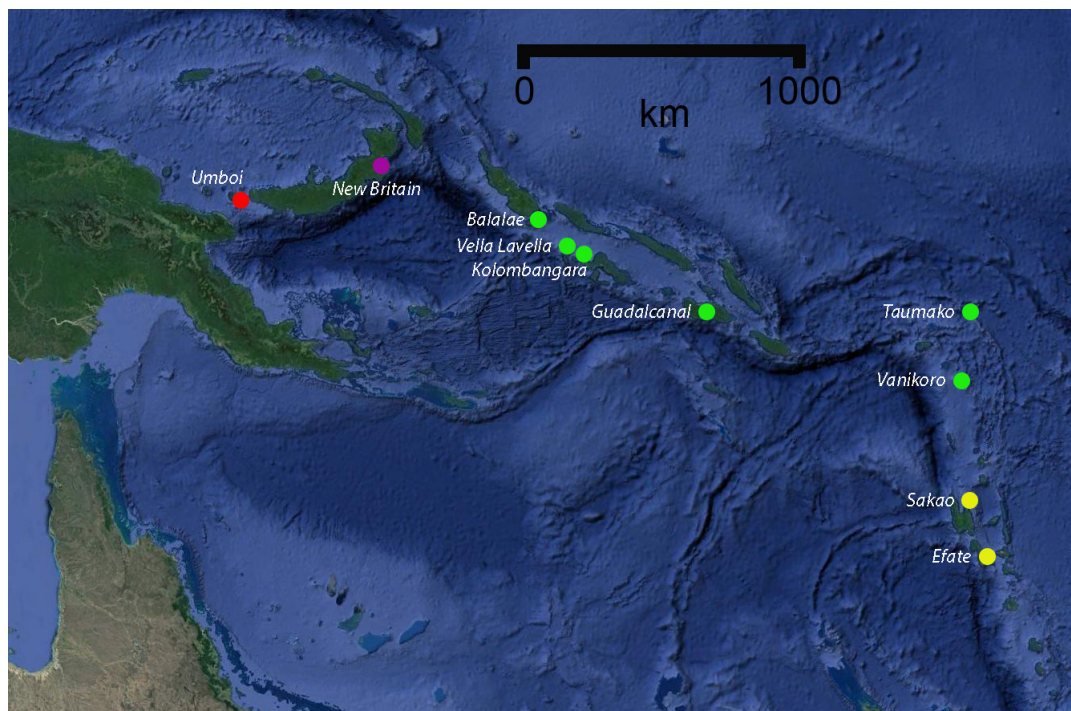
### Introduction

*Lepidodactylus* is, after *Cyrtodactylus*, the second-most-speciose genus of geckos inhabiting the western Pacific, with 44 currently recognized species (Uetz *et al.* 2022) and several additional candidate species identified (Oliver *et al.* 2018; McDonald *et al.* 2022). *Lepidodactylus* represents a paraphyletic genus, with the clade to which it belongs including *Luperosaurus* and *Ptychozoon* (Oliver *et al.* 2018). This entire clade (*Lepidodactylus sensu lato*) contains 61 named species and 32 candidate species (McDonald *et al.* 2022, with modifications in Eliades *et al.* 2021; Kraus *et al.* 2022), with most species found in the Philippines and western Melanesia. The Papuan region—that part of western Melanesia from the Solomon Islands in the east to Lydekker's Line in the west—holds 19 named *Lepidodactylus* (Kraus 2019; Kraus & Oliver 2020; Karkkainen *et al.* 2020), although the widespread *L. pantai* may prove to be a synonym of *L. woodfordi* (Karin *et al.* 2021), known with certainty only from its holotype. Brown & Parker (1977) reviewed *Lepidodactylus* from this region and assigned species to three informal groups based on the morphology of their toe pads. Oliver *et al.* (2018) showed that none of these three groups was monophyletic, yet these informal groups retain their heuristic usefulness for identifying and discriminating among the many species of the genus.

Few species of *Lepidodactylus* seem to be abundant (the unisexual-bisexual complex called *L. lugubris* is an exception), and most species in the Papuan region seem rarely encountered and rarely collected in even moderate numbers. Consequently, taxonomic understanding of these lizards has proceeded slowly—with four of the Papuan species described by Brown & Parker (1977) and another nine since that time—and some lineages remain taxonomically unresolved due to insufficient material available to make informed decisions. Furthermore, several of the Papuan species collected decades ago remain known only from one or two specimens. This paucity of study material stems in part from the cryptic ecologies of many of these species combined with the frequent failure by

biologists to identify and clearly target their microhabitats. In the Papuan region, species that inhabit coastal forests or open habitats, including villages, (see Oliver *et al.* 2018 for a discussion of habitat usage in this genus) can sometimes be found in some numbers, but inhabitants of lowland rainforests have proven more elusive, presumably because their arboreal microhabitats are more difficult to target and access.

In 2018, the first and last authors of this report conducted a set of herpetofaunal surveys on the four easternmost of the volcanic islands of the Western Bismarck Arc, excluding Long Island, which had previously been surveyed (Cook *et al.* 2001). This island arc is defined as those islands of the Bismarck Arc west of 148°E; it comprises entirely volcanic islands (all but two active or dormant) and extends for 600 km west of New Britain (Woodhead *et al.* 2010), lying off the northeastern coast of New Guinea. Among the lizards we found during our surveys was a new species of *Lepidodactylus* of the *L. guppyi* Group (cf. Oliver *et al.* 2018) from Umboi Island, the largest island (880 km<sup>2</sup>) of the Western Bismarck Arc. Umboi Island is comprised of several connected stratovolcanoes (Johnson *et al.* 1972), lies only 22 km W of the large island of New Britain (Fig. 1), and is largely covered with rainforest except in the vicinity of its many villages. We take this opportunity to describe this new *Lepidodactylus* here.



**FIGURE 1.** Map of Melanesia, showing the localities sampled for molecular analysis for members of the *Lepidodactylus guppyi* Group: *L. laticinctus* **sp. nov.** (red), *L. guppyi* (green), *L. vanuatuensis* (yellow), and *Lepidodactylus* sp. New Britain (purple).

## Materials and Methods

We collected animals under applicable national and provincial permits, removed liver tissues and fixed them in ethanol for later molecular analyses, fixed the specimens in 10% buffered formalin, and transferred them to 75% ethanol for storage. We measured snout-vent length using a ruler, tail length with either a ruler (on straight tails) or a non-elastic string laid along the tail and then placed along a ruler (for curled tails), and all other measurements using a binocular dissecting scope with an attached micrometer or with vernier calipers. We measured snout-vent length, tail length, and trunk length to the nearest 0.5 mm and all other measurements to the nearest 0.1 mm. Measurements include: snout-vent length (SVL), from tip of snout to vent; trunk length (TrL), from posterior edge of forearm insertion to anterior edge of hindleg insertion; tail length (TL), from vent to tip of tail; tail width (TW), measured at widest point of tail behind the cloacal sacs; head length (HL), from tip of snout to anterior margin of ear opening, taken in lateral view; head width (HW), maximum width of head; forearm length (FA), from central base of palm to elbow; crus length (CS), from central base of heel to knee; ear diameter (Ear), longest dimension of ear, typically on a diagonal axis; eye diameter (EY), greatest horizontal diameter of eye between the surrounding scales; eye-naris distance (EN), from anteriormost point of eye to center of naris; snout length (SN), from anteriormost point of eye

to tip of snout, taken in lateral view; internarial distance (IN), distance between centers of nares; ear-to-eye distance (EE), shortest straight-line distance between anterior edge of ear opening to posterior corner of eye; length of the fourth toe, from terminal scensor to the proximal base of the web between T3 and T4 (T4L); width of the fourth toe across its widest point (T4W); length of the series of complete lamellae on the fourth toe (T4lamellaeL); length of webbing between T3 and T4 from base of this webbing to its center of emargination (T3T4webL), and length of webbing between T4 and T5 from base of this webbing to its center of emargination (T4T5webL). We counted numbers of supralabials to mid-eye, infralabials (to angle of jaw), lamellae under T1 and T4, divided lamellae under T4, enlarged precloacal/femoral scales, number of precloacal/femoral pores (in males), and number of precloacal scales in a straight line between the apex of the precloacal pore-bearing series and the cloaca. For specimens we collected, we measured mass (g) with a 10-g Pesola spring scale following euthanasia.

As noted by Kraus (2019), Brown & Parker's (1977) treatment of the genus used toe width, degree of toe webbing, and extent of lamellae along the toe (referred to them as "scansors") as diagnostic features, but each of those was described in approximate terms (e.g., "toes one-third webbed") and not quantified. We follow Kraus (2019) in including the assorted toe, lamella, and webbing measures noted above so as to obtain more precise measures of differences in these features.

Specimens of the new species are deposited in the University of Michigan Museum of Zoology, Ann Arbor (UMMZ). We compared these to specimens of related Papuan species in the British Natural History Museum, London (BMNH); University of Kansas Biodiversity Institute, Lawrence (KU); and Museum of Comparative Zoology, Harvard University, Cambridge (MCZ) (Appendix I); or to data available from Brown & Tanner (1949), Brown (1964), Brown & Parker (1977), Kraus (2019), Karkkainen *et al.* (2020), Kraus & Oliver (2020), and Kraus *et al.* (2022).

We used a NucleoSpinTissue kit (Macherey-Nagel) to extract total DNA from liver tissue (fixed in 96% ethanol) of two specimens of the new species, followed the standard protocol for animal tissues, and incubated the samples for two h. We received DNA extracts of five *L. guppyi* samples included in this study from the University of Kansas. The rest of the sequences we obtained from GenBank accessions deposited from studies by Heinicke *et al.* (2012) and Oliver *et al.* (2018).

We amplified the mitochondrial NADH dehydrogenase subunit 2 (ND2) and the nuclear phosphoglycerate kinase (PDC) fragment using the same primers and protocols used in Kraus *et al.* (2022). We attempted as well to use RAG-1, following Oliver *et al.* (2018), but were unable to reliably obtain sequence data for that gene. Macrogen Europe performed the sequencing. We visualized and assembled chromatograms with Sequencher ver. 5 (Gene Codes Corporation, Ann Arbor, MI). All new sequences are deposited in GenBank (Appendix II).

We included 13 samples of the *L. guppyi* Group in our phylogenetic analysis, using 11 other lineages of *Lepidodactylus s.l.* together with *Gekko vittatus* (Appendix II) as outgroups (Oliver *et al.* 2018). We used MAFFT7 online (Kuraku *et al.* 2013; Katoh *et al.* 2019) to produce sequence alignments and trimmed the sequences in Mesquite v 3.10 (Maddison & Maddison 2019). There were a total of 888 (ND2) and 394 (PDC) base pairs in the final aligned dataset. We concatenated the two separate data sets with SequenceMatrix (Vaidya *et al.* 2011).

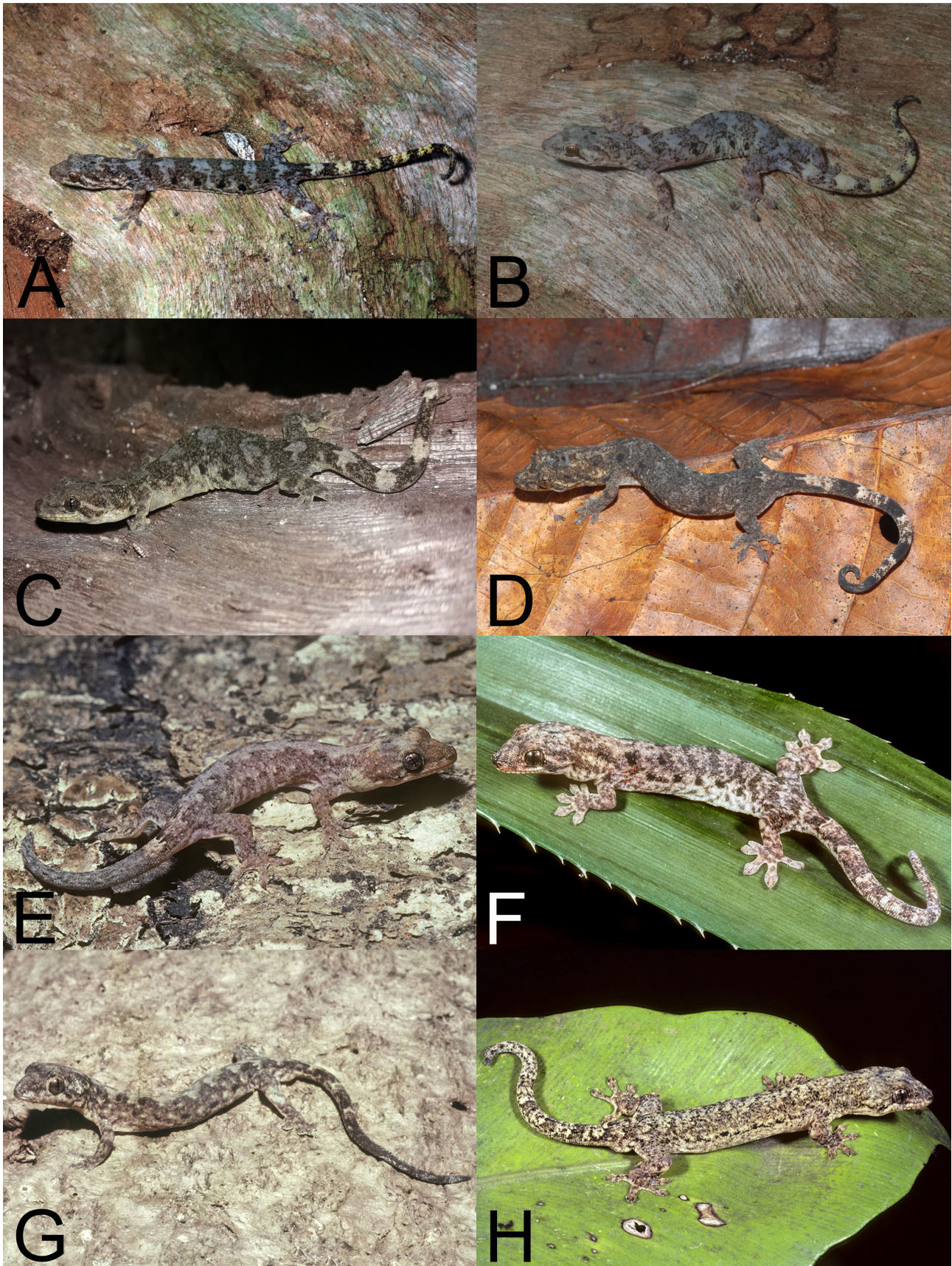
We conducted phylogenetic analyses using parsimony, maximum likelihood, and Bayesian inference as optimality criteria. We used TNT v. 1.5 (Goloboff & Catalano 2016) for the parsimony analysis. We chose to treat gaps as missing data and used a search strategy consisting of 100 replications and ten rounds of both ratchet and tree drifting followed by tree fusing (Goloboff 1999). We executed the command *xmult* until 50 independent hits of the shortest tree were found. To visualize the branch lengths of the resulting trees we applied the command 'blength'. A majority consensus of the most-parsimonious trees (MP) was produced at the end of the analysis. We calculated support for each node using jackknife resampling (Farris *et al.* 1996) with 1000 replicates and with a probability of a character removal being 0.36.

For the likelihood analysis we used RAxML v. 8 (Stamatakis 2014) via the CIPRES portal (Miller *et al.* 2010). We separated the two genes into different partitions and applied a unique general time-reversible (GTR) model of sequence evolution (RAxML implements only GTR-based models of nucleotide substitutions) with corrections for a discrete gamma distribution (GTR+  $\Gamma$ ). At the end we estimated nodal-support values using the rapid bootstrap algorithm with 1000 replicates together with the GTR-GAMMA model (Stamatakis *et al.* 2008).

For the Bayesian analysis we used a parallel version of MrBayes 3.2.7a via the CIPRES portal (Miller *et al.* 2010). The analysis included two independent runs with eight chains, both with one million generations, sampling every 100 generations, allowing both partitions to evolve under different rates.

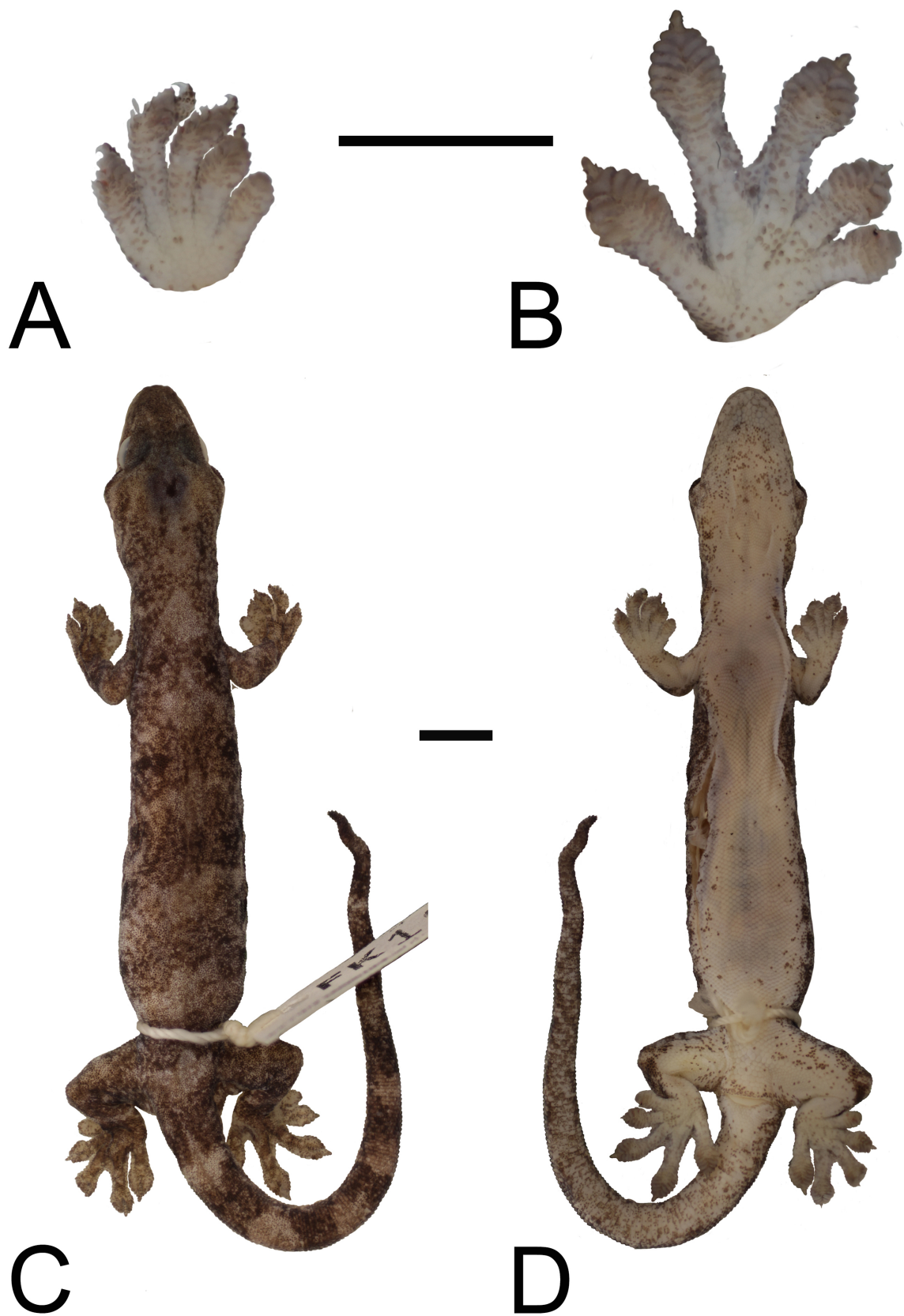
We estimated genetic divergences between the new and described species by calculating uncorrected p-distances of both data sets with MEGA v. 7.0.21 (Kumar *et al.* 2016; Stecher *et al.* 2020).





**FIGURE 2.** Portraits in life of (A) paratype of *Lepidodactylus laticinctus* **sp. nov.** (UMMZ 249263), Umboi Is., PNG; (B) holotype of *L. laticinctus* **sp. nov.** (UMMZ 249264), Umboi Is., PNG; (C) paratype of *L. laticinctus* **sp. nov.** (UMMZ 249265), Umboi Is., PNG; (D); *Lepidodactylus* sp. (SAMA R64666), New Britain, PNG; (E, F) *L. guppyi*, Guadalcanal Is., Solomon Islands, (G) *L. guppyi*, Malaupaina Is., Solomon Islands, and (H) *L. guppyi*, Ngela Is., Solomon Islands. Photos (A, B) F. Kraus, (C) V. Weijola, (D) S. Richards, and (E–H) M. McCoy.





**FIGURE 3.** (A) Palmar view of right hand, (B) plantar view of right foot, (C) dorsum, and (D) venter of holotype of *Lepidodactylus laticinctus* **sp. nov.** (UMMZ 249264), Umboi Is. Scale bars are 5 mm.

## Results

### *Lepidodactylus laticinctus* sp. nov.

Figs. 2, 3

*Holotype*.—UMMZ 249264 (field tag FK 18122), mature female, collected by V. Weijola at Lablab, 5.7207°S, 148.0668°E, sea level, Umboi Island, Morobe Province, Papua New Guinea, 2 April 2018.

*Paratypes*.—Same data as holotype (UMMZ 249263), and same data as holotype except collected 19 April 2018 (UMMZ 249265).

*Diagnosis*.—A fairly large (adult female SVL 49–49.5 mm) species of *Lepidodactylus* having a subcylindrical tail without a lateral fringe of enlarged scales, 38–41 enlarged scales of pore-bearing series extending to distal ends of thighs, 2 divided subterminal lamellae on T4, 9–12 T4 lamellae, 8–9 T1 lamellae, rather short toes ( $T4L/SVL = 0.086–0.088$ ), lamellae occupying slightly more than half of toes ( $T4\text{ lamellae}L/T4L = 0.53–0.60$ ), fairly wide toes ( $T4W/T4L = 0.36–0.40$ ) with moderate webbing ( $T3T4webL/T4L = 0.16–0.21$ ), dorsum in life pale gray with five wide darker gray-brown bands between axilla and tail base, and tail banded with yellow and brown or pale and darker brown.

*Comparisons with other species*.—The subcylindrical tail without a lateral fringe of enlarged scales and the two divided subterminal scansors under the toes place *Lepidodactylus laticinctus* sp. nov. in Brown and Parker's (1977) phenetic Group II. Hence, it is distinguished from Papuan species belonging to Group I (*L. aignanus*, *L. magnus*, *L. mutahi*, *L. pumilis*, *L. sacrolineatus*, and *L. zweifeli*) by having two divided subterminal lamellae (vs. none in members of Group I); and it is distinguished from Papuan species belonging to Group III (*L. lugubris*, *L. pantai*, and *L. woodfordi*) in having a subcylindrical (vs. flattened) tail lacking (vs. having) a lateral fringe of scales and in having the terminal scansors entire on all toes (vs. divided on T2–T5). From other Papuan members of Group II, *L. laticinctus* sp. nov. differs as follows: from *L. dialeukos*, *L. kwasnickae*, *L. mitchelli*, *L. novaeguineae*, *L. orientalis*, and *L. pulcher* in having 38–41 enlarged scales of the pore-bearing series (vs. 14 in *L. dialeukos*, 12–15 in *L. kwasnickae*, 12–14 in *L. mitchelli*, 12–17 in *L. novaeguineae*, 19–33 in *L. orientalis*, and 18–20 in *L. pulcher*) that extend to the knee (vs. being limited to the precloacal region in the other six species); and from *L. pollostos* and *L. shebae* in its larger size (SVL 49–49.5 mm vs. 35.5 mm in the sole specimen [adult male] of *L. pollostos* and 36 mm in the sole specimen [adult male] of *L. shebae*) and greater number of enlarged scales of the pore-bearing series (38–41 vs. 17 in *L. pollostos* and ~34 in *L. shebae*), and dorsal ground color pale gray (vs. reddish brown in *L. pollostos* and *L. shebae*).

Among Papuan Group II species, *L. laticinctus* sp. nov. is most similar to *L. guppyi*, from which it differs in having a lower number of divided T4 lamellae (uniformly 2 vs. 2–4, mean 2.8, mode 3 in *L. guppyi*), fewer average number of T1 and T4 lamellae, fewer enlarged femoral/precloacal scales, shorter toes, smaller eye, shorter snout, and shorter temporal region (Table 1). *Lepidodactylus laticinctus* sp. nov. is most distinctive from *L. guppyi* in its color pattern, differing in its dorsal pattern of five wide gray-brown bands between the axilla and tail base on a pale-gray ground color (vs. typically with six or more narrow and poorly defined brown bands on a brown ground color, or with no bands at all, in *L. guppyi*, Fig. 2) and in having a distinct, pale postocular stripe (vs. stripe absent or only vaguely developed in *L. guppyi*). It is also quite different genetically from *L. guppyi* (see below).

*Description of holotype*.—A mature female of medium size (SVL = 49.5 mm, TrL = 24.0 mm); cut anterolaterally on right trunk, liver removed. Head relatively long (HL/SVL = 0.21) and wide (HW/HL = 0.81), distinct from neck. Loreal region slightly inflated; no distinct canthus rostralis. Top of snout, area between nares, and area posterior to nares shallowly concave. Snout tapered and rounded at tip, relatively long (SN/HL = 0.43), significantly longer than eye diameter (SN/EY = 1.8). Eye of modest size (EY/HL = 0.24, EY/EN = 0.74); pupil vertical, constricted into series of four lobes; anterior supraciliaries slightly larger than adjacent granules, posterior ones subequal to adjacent granules. Ear opening small (Ear/HL = 0.078), compressed, oriented vertically; distance between ear and eye larger than eye diameter (EE/EY = 1.6). Rostral twice as wide (2.0 mm) as high (1.0 mm), highest just medial to nares, lower between these points; length 0.35 mm. Supranasals separated by three internasals. Rostral in contact with first supralabials, two supranasals, and three internasals. External nares circular; each bordered by rostral, two supranasals, first supralabial, and one (L) or two (R) postnasals. Mental virtually an equilateral triangle, 0.9 mm wide. Mental bordered posteriorly by two enlarged postmentals and in point contact with one genial; enlarged postmentals bordered posteriorly by subequal scales that progressively decrease in size posteriorly to join granular



chin scales. First five infralabials bordered below by somewhat enlarged scales, subequal in size to postmentals; remaining scales below infralabials of approximately same size as throat scales, which decrease in size medially. Supralabials to mid-orbital position eight on each side, to angle of jaw 11 (R) and 12 (L). Infralabials 11 on each side.

**TABLE 1.** Differences in mensural and meristic data between *Lepidodactylus laticinctus* **sp. nov.** and *L. guppyi*.

Character	<i>Lepidodactylus laticinctus</i> <b>sp. nov.</b>		<i>Lepidodactylus guppyi</i>	
	Mean	Range	Mean	Range
T4L/SVL	0.087	0.086–0.088	0.096	0.088–0.101
T4scansorL/T4L	0.56	0.53–0.60	0.63	0.54–0.79
EY/SVL	0.50	0.49–0.51	0.59	0.52–0.67
EN/SVL	0.69	0.63–0.71	0.79	0.71–0.85
IN/EN	0.63	0.62–0.65	0.60	0.55–0.63
EY/SN	0.55	0.53–0.57	0.62	0.56–0.71
EY/EE	0.61	0.60–0.61	0.70	0.52–0.75
#T4 lamellae	9.7	9–12	10.9	9–14
#T1 lamellae	8.2	8–9	9.7	8–11
#enlarged precloacal/ femoral scales	40	38–41	44	39–49

Body of rather narrow habitus ( $\text{TrL/SVL} = 0.48$ ), slightly depressed dorsoventrally. Dorsal scales on head, body, limbs, and throat tiny, juxtaposed granules, larger on sides and snout; tubercles absent. Ventral scales larger, flat and smooth, subimbricate, gradually decreasing in size laterally to become granular.

Enlarged precloacal/femoral scales in single series of 41 scales extending almost to knees; thigh scales anterior to this row larger than those posterior. Enlarged scales form a pubic patch between the precloacal series and vent; no tiny scales between the precloacal series and the pubic patch; eight scales in a row between apex of enlarged precloacal series and vent. Scales on palms and soles rounded, flattened, smooth, subimbricate.

Fore- and hindlimbs relatively small but well-developed ( $\text{FA/SVL} = 0.09$ ,  $\text{CS/SVL} = 0.11$ ). Digits well-developed (Fig. 3A, B), widely dilated throughout their length ( $\text{T4W/T4L} = 0.42$ ), all but first fingers and toes with recurved claws; clawed phalanges laterally compressed, free above and extending slightly beyond terminal lamellae. Subdigital lamellae narrow and smooth, all undivided except penultimate and antepenultimate lamellae divided on F2–F5 and T2–T5 (Fig. 3A, B), all lamellae undivided on F1 and T1; lamellae extend for only slightly more than half length of each toe ( $\text{T4 scansor L/T4L} = 0.56$ ). Lamellae of manus 7–9–10–10–9 on right, 8–9–10–9–8 on left; of pes 9–9–9–9–9 on right, 8–9–9–9–8 on left. Relative lengths of digits on manus and pes  $\text{I} < \text{II} < \text{V} < \text{III} < \text{IV}$ . Webbing present between all digits; toes approximately one-fifth webbed or less ( $\text{T3T4webL/T4L} = 0.21$ ,  $\text{T4T5webL/T4L} = 0.14$ ).

Tail complete, subcylindrical, almost as long as body ( $\text{TL/SVL} = 0.95$ ), relatively narrow ( $\text{TW/SVL} = 0.076$ ); lateral margins without skin flanges or spines (Fig. 3C). Scales of tail small, square, flat, smooth, subimbricate, larger ventrally than dorsally. Cloacal sacs not swollen (Fig. 3D), with small external orifices situated near lateral margins of vent; single slightly enlarged, blunt postcloacal spur on each side of tailbase; midventral scales of sac hexagonal, slightly larger than those ventrolaterally.

*Color in preservative:* Dorsal ground color brown with five wide, dark-brown bands between axilla and tail base (Fig. 3C), these darker laterally than medially, imparting impression of lateral dark-brown blotches; one more vaguely outlined dark-brown band on neck, and vague dark-brown mottling on nape; tail with pale-brown ground and eight dark-brown bands, the last covering tail tip. Head medium brown, darker on snout; labials stippled with brown on a dirty-white ground. Venter dirty white; chin and throat speckled with brown scales; chest, abdomen, and undersides of limbs with few brown scales joining to form flecks laterally (Fig. 3D). Palmar and plantar surfaces dirty white with few pale-brown scales forming scattered flecks. Iris chocolate brown.

*Measurements (in mm).*—SVL = 49.5, TrL = 24.0, TL = 47.0, TW = 3.9, FA = 4.4, CS = 5.5, HL = 10.3, HW = 8.3, Ear = 0.8, EE = 4.1, EY = 2.5, SN = 4.4, EN = 3.4, IN = 2.1, T4L = 4.3, T4W = 1.8, T4 scansor L = 2.4, T3T4webL = 0.9, T4T5webL = 0.6, mass = 1.85 g.

*Variation.*—The two paratypes are very similar to the holotype in most respects. UMMZ 249263 has two small, calcified endolymphatic sacs, six dark-brown tail bands, and a hint of a pale postocular stripe; UMMZ 249265 has two large, calcified endolymphatic sacs, eight dark-brown tail bands, and a hint of a pale postocular stripe. It further differs in having the central dark-brown band closer to, and not evenly spaced from, its neighboring dark-brown bands; the head and neck are darker than in the holotype; and the chin and throat are only finely and sparsely stippled with brown.

*Measurements of paratypes (in mm).*—(UMMZ 249263): SVL = 49.0, TrL = 24.0, TL = 41.0, TW = 3.7, FA = 5.1, CS = 5.6, HL = 10.8, HW = 8.5, Ear = 0.6, EE = 4.1, EY = 2.5, SN = 4.5, EN = 3.1, IN = 2.0, T4L = 4.3, T4W = 1.7, T4 scissor L = 2.3, T3T4webL = 0.7, T4T5webL = 0.6, mass = 1.80 g. (UMMZ 249265): SVL = 49.0, TrL = 24.5, TL = 39.0, TW = 3.5, FA = 4.7, CS = 5.7, HL = 10.6, HW = 8.3, Ear = 0.6, EE = 4.0, EY = 2.4, SN = 4.5, EN = 3.5, IN = 2.2, T4L = 4.2, T4W = 1.5, T4 scissor L = 2.5, T3T4webL = 0.9, T4T5webL = 0.7, mass = 2.05 g.

*Color in life.*—Field notes for UMMZ 249263 (Fig. 2A) state “Dorsum brown gray with brown bands; venter pale yellow; tail pale yellow with brown bands. Iris coppery brown.” The holotype was very similar (Fig. 2B) except that the venter was pale gray. UMMZ 249265 (Fig. 2C) differed somewhat more: “Pale brown with darker-brown mottling, vaguely arrayed in bands, which are clearer on the tail. Venter very pale yellow, almost white, unflecked. Iris brown.” Photos of all specimens clearly show a pale postocular stripe.

*Genetics.*—Pairwise distances (Table 2) between the samples of *Lepidodactylus laticinctus* **sp. nov.** and the *Lepidodactylus* sp. specimen from New Britain (SAMA R64666) are 16.2–16.4% for ND2 (Table 2) and 1% for PDC (Table 3); differences between the new species and the *L. guppyi*/*L. vanuatuensis* samples are 13.9–16.2% for ND2 and 0.8% for PDC.

**TABLE 2.** Pairwise distances among samples of the *L. guppyi* Group and their immediate sister taxon for ND2. Genera are *L* = *Lepidodactylus*, *Lup* = *Luperosaurus*.

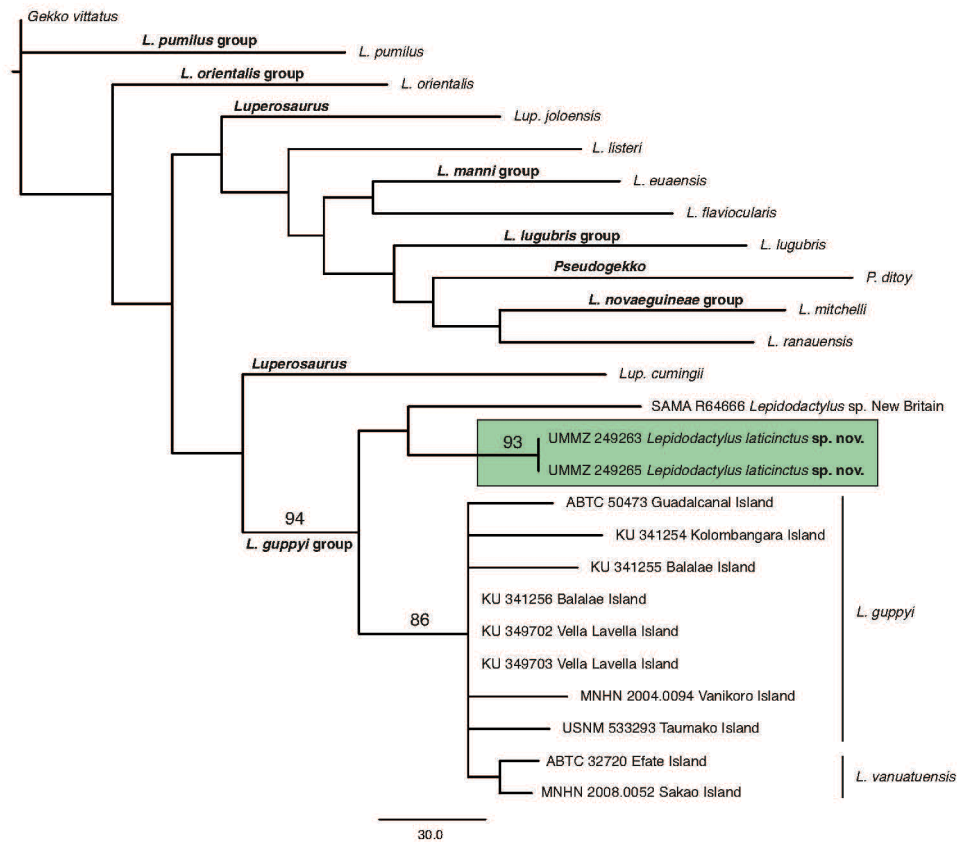
Sample	1	2	3	4	5	6	7	8	9	10
1 <i>L. vanuatuensis</i> ABTC32720										
2 <i>L. vanuatuensis</i> MNHN2008	0.0264									
3 <i>L. laticinctus</i> <b>sp. nov.</b> UMMZ 249263	0.1387	0.1431								
4 <i>L. laticinctus</i> <b>sp. nov.</b> UMMZ 249265	0.1395	0.1465	0.0000							
5 <i>Lepidodactylus</i> sp. SAMA R64666	0.1456	0.1610	0.1620	0.1644						
6 <i>L. guppyi</i> ABTC 50473	0.0508	0.0528	0.1401	0.1383	0.1524					
7 <i>L. guppyi</i> KU341254	0.0648	0.0635	0.1620	0.1554	0.1752	0.0603				
8 <i>L. guppyi</i> KU341255	0.0520	0.0579	0.1462	0.1453	0.1582	0.0520	0.0672			
9 <i>L. guppyi</i> MNHN2004	0.0508	0.0440	0.1474	0.1463	0.1637	0.0542	0.0705	0.0633		
10 <i>L. guppyi</i> USNM533293	0.0406	0.0465	0.1460	0.1485	0.1569	0.0530	0.0648	0.0576	0.0530	
11 <i>Lup. cumingii</i> TNHC 61910	0.2449	0.2516	0.2496	0.2460	0.2540	0.2381	0.2582	0.2418	0.2460	0.2517

TNT analysis resulted in 573 MP trees of length 2265 steps. In the majority consensus tree (Fig. 4), the sole specimen of *Lepidodactylus* sp. from New Britain is resolved as sister to *L. laticinctus* **sp. nov.** but with no branch support. Together they form the sister clade (JF = 94) to a polytomy including all *L. guppyi* and *L. vanuatuensis* specimens (JF = 86). Likelihood analysis (Fig. 5) and Bayesian analysis (not shown) produced a result largely congruent to that of parsimony with the difference that the New Britain specimen was resolved as sister (BS = 51, pp = 1) to all remaining representatives of the *L. guppyi* clade, being followed first by *L. laticinctus* **sp. nov.** (BS = 99, pp = 1) and then by the *L. guppyi*/*L. vanuatuensis* clade (BS = 97).



**TABLE 3.** Pairwise distances among samples of the *L. guppyi* Group and their immediate sister taxon for PDC. Genera are *L* = *Lepidodactylus*, *Lup* = *Luperosaurus*.

Sample	1	2	3	4	5	6	7	8	9
1 <i>L. laticinctus</i> sp. nov. UMMZ 249263									
2 <i>L. laticinctus</i> sp. nov. UMMZ 249265	0.0000								
3 <i>Lepidodactylus</i> sp. SAMA R64666	0.0102	0.0102							
4 <i>L. guppyi</i> KU341254	0.0077	0.0076	0.0178						
5 <i>L. guppyi</i> KU341255	0.0077	0.0076	0.0178	0.0000					
6 <i>L. guppyi</i> KU341256	0.0060	0.0060	0.0179	0.0000	0.0000				
7 <i>L. guppyi</i> KU349702	0.0077	0.0076	0.0178	0.0000	0.0000	0.0000			
8 <i>L. guppyi</i> KU349703	0.0077	0.0076	0.0178	0.0000	0.0000	0.0000	0.0000		
9 <i>L. guppyi</i> USNM533293	0.0077	0.0076	0.0178	0.0000	0.0000	0.0000	0.0000	0.0000	
10 <i>Lup. cumingii</i> TNHC 61910	0.0153	0.0153	0.0204	0.0229	0.0229	0.0179	0.0229	0.0229	0.0229



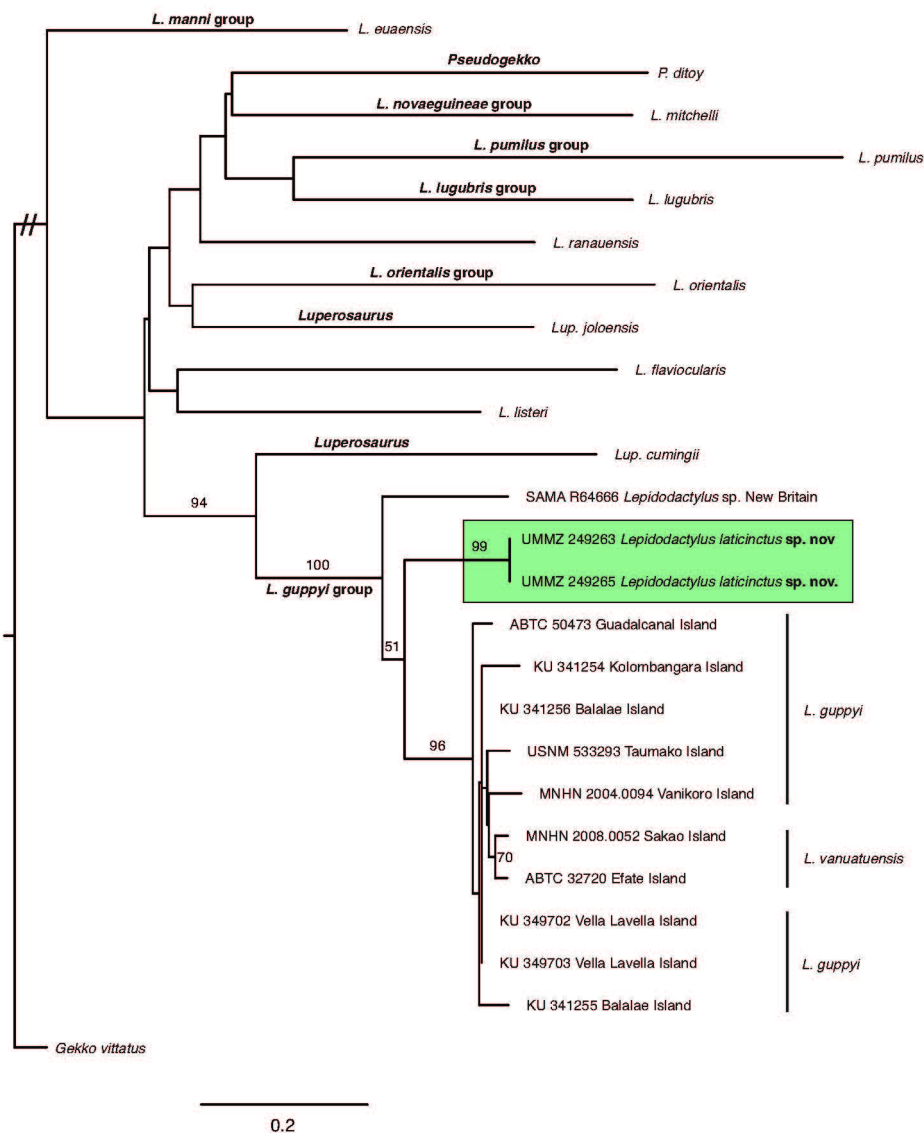
**FIGURE 4.** The majority consensus of 573 most-parsimonious trees of the *Lepidodactylus guppyi* Group for concatenated dataset with jackknife resampling values > 50% shown on the nodes. Branch lengths represent the number of optimized character-state changes.

**Etymology.**—The name is a masculine Latin combinatorial adjective from *latus*, meaning “broad”, and *cinctum*, meaning “band”, in recognition of the distinctive dorsal pattern of this species.

**Range.**—Known only from the type locality (Fig. 1), but likely to occur across the coastal areas of Umboi Island and possibly more widely throughout the lowlands of that island. We did not find this species on surveys of coastal and lowland forests of nearby Sakar and Tolokiwa islands.

**Ecology.**—All three animals were found active at night ~ 50–200 cm above ground on a single large, isolated *Casuarina* tree on a sandy beach only a few meters from the ocean in a village area of moderately high human use (walking trails, boat launch, nearby residences). There is considerable coastal and secondary forest all along the eastern shore of Umboi Island. We searched extensively throughout these forests for one week and failed to find

additional individuals, so the ecology of this species needs to be better delimited. All specimens have red mites lodged between the digital lamellae, with UMMZ 249265 being especially heavily infested in these regions.



**FIGURE 5.** Maximum-likelihood tree of the *Lepidodactylus guppyi* Group for concatenated dataset with bootstrap values >50% shown for each node rooted with *Gekko vittatus* as outgroup. Scale bar corresponds to the mean number of nucleotide substitutions per site.

## Discussion

*Lepidodactylus* is a speciose genus, yet it is morphologically conservative, with many candidate species suggested by phylogenetic relationships derived from molecular data (Oliver *et al.* 2018) yet poorly diagnosable using traditional characters (FK, unpubl. data). Consequently, diagnoses may rely on relatively small morphological differences (often character means or modes) to distinguish among species that are molecularly divergent. *Lepidodactylus laticinctus* **sp. nov.** is one such species. These lizards are molecularly distinct and geographically isolated from their closest relatives, yet morphological differences between it and its closest relative largely involve nuances of color pattern (Fig. 2) or trends in scalational or mensural features (Table 1). Nonetheless, the sum of morphological and molecular evidence presented here—as well as the geographical isolation of *L. laticinctus* **sp. nov.** from its closest relatives—suggests that these geckos are an independently evolving lineage that meets the unified species concept applicable to allopatric species (de Queiroz 2007).



Our molecular results indicate that both *L. laticinctus* **sp. nov.** and the undescribed population from eastern New Britain lie basal to *L. guppyi*+*L. vanuatuensis* within the *L. guppyi* Group though the parsimony analysis places those two as sister taxa and the likelihood and Bayesian analyses place them in series to *L. guppyi*+*L. vanuatuensis* (Figs. 4, 5). We planned to compare our specimens of *L. laticinctus* **sp. nov.** to this New Britain specimen, but the latter was unfortunately lost in the mail at the start of the covid lockdowns in April 2020. So, we were unable to assess whether morphometric or meristic differences exist between this taxon and *L. laticinctus* **sp. nov.**, but differences in color pattern seem evident (Fig. 2A–C vs. D). Better diagnosis of the New Britain lineage must await collection of new material. Nonetheless, it would appear at this time that the *L. guppyi* Group arose in western Melanesia and subsequently spread eastward to occupy the far-flung islands east of New Britain.

Oliver *et al.* (2018) did not have specimens of *L. laticinctus* **sp. nov.** in their extensive sampling of *Lepidodactylus* species inasmuch as we collected that species subsequent to publication of that study. Using their date estimates for nodes on their tree, the unnamed New Britain population diverged from *L. guppyi* and *L. vanuatuensis* at an estimated 8.8 MYA, and the radiation of *L. guppyi* and *L. vanuatuensis* populations diverged at an estimated 2 MYA. Given our placement of *L. laticinctus* **sp. nov.** with respect to these other lineages (Figs. 4, 5) and the similarly high genetic divergences of *L. laticinctus* **sp. nov.** and the New Britain lineage to the *L. guppyi* and *L. vanuatuensis* populations (Table 2), we presume *L. laticinctus* **sp. nov.** to have diverged soon after the divergence of the New Britain lineage. This is of interest because the Western Bismarck Arc is a series of Quaternary volcanoes resulting from the subduction of the Australian Plate beneath the South Bismarck Plate (Woodhead *et al.* 2009), and the eastern portion of that subduction process—the Finisterre Terrane—has collided with New Guinea only within the past 3.7 MYA (Abbott 1995) to <1 MYA (Gill *et al.* 1993), generating the eastern islands of this arc at that time. The importance of this is that *L. laticinctus* **sp. nov.** would appear to be much older than the island on which we found it to reside (a pattern also true for *L. sacrolineatus* in its montane habitat on New Guinea, cf. Kraus & Oliver 2020). Adjacent islands of the Western Bismarck Arc are of equivalent age and could also not serve as a point of origin of the species. Options for nearby land masses of sufficient age for *L. laticinctus* **sp. nov.** to have arisen on are the Huon Peninsula and New Britain. The latter seems more likely inasmuch as the Finisterre Terrane that comprises the Huon Peninsula too is of recent origin (Abbott 1995) and members of the *L. guppyi* Group are not known from New Guinea. In contrast, New Britain has existed for at least 30 MY (Hall 2002), and it is known to contain a member of the *L. guppyi* Group. If *L. laticinctus* **sp. nov.** arose on New Britain, we would expect surveys of its western end to reveal this species, but comprehensive herpetofaunal surveys in that area have not yet been done.

A further result of our molecular analyses is that the similar molecular divergences found by us between *L. guppyi* and *L. vanuatuensis* and within *L. guppyi* (Table 2), combined with the possible paraphyly of the former (Fig. 5), suggest that a comprehensive, quantitative assessment of character variation across that clade would be desirable to confirm that the two species truly are distinct. In its original description, *L. vanuatuensis* was discriminated from *L. guppyi* on the basis of having fewer rows of scales around the midbody and less-dilated toe pads (Ota *et al.* 1998). The former difference was quantified, but the latter was not (indeed, though widely used, toe-pad width in Melanesian *Lepidodactylus* was never quantified until the study of Kraus [2019], which found that qualitative claims for digital width were often not very useful). Ota *et al.* (1998) also found a genetic difference of 6.6% for *cytb* between a single individual of *L. guppyi* and one of *L. vanuatuensis*, which is slightly larger than what we find for ND2 (Table 2). It may be that these island populations represent a rapidly diverging complex of closely related species, or it may be that their geographic expansion has occurred sufficiently recently that these populations do not yet represent independently evolving lineages. Comprehensive examination of molecular and morphological variation across the entire large range of *L. guppyi* and *L. vanuatuensis* would be desirable to clarify these taxonomic questions.

Our three specimens of *L. laticinctus* **sp. nov.** were all found on a single large *Casuarina* tree along a village beach. Efforts to locate more individuals in nearby, more continuous forests proved unsuccessful for reasons that we could not determine. We met with the same lack of success in locating this species at another coastal village to the north that contained ample secondary forest and coastal forest and on nearby, well-wooded Sakar Island. Two possibilities that are not mutually exclusive suggest themselves for this apparent rarity. First, *L. laticinctus* **sp. nov.** may be ecologically cryptic, possibly primarily inhabiting the canopy of these forests and rarely descending to a level at which humans can readily encounter them. This would be consistent with the cryptic ecologies of many other *Lepidodactylus* species. Second, we found the geckos *Gehyra mutilata*, *G. oceanica*, *Gekko vittatus*, *Hemidactylus frenatus*, and *Lepidodactylus lugubris* in these same habitats on both Umboi and adjacent islands, and

it may be that *L. laticinctus* **sp. nov.** is generally rare due to competition and/or predation from these relatives. Both hypotheses could be true if *L. laticinctus* has been pushed to more interior and higher-elevation forests on Umboi, an interpretation consistent with the taxon-cycle hypothesis (Wilson 1961). It should be noted that Oliver *et al.* (2018) only found evidence for the taxon cycle operating in *Lepidodactylus* species inhabiting “continental” islands like New Guinea and Borneo, and that those species inhabiting oceanic islands like Umboi did not show evidence of this pattern. However, recent invasions of these islands by *H. frenatus* and *L. lugubris* may be displacing *L. laticinctus* in real time. Discriminating among these hypotheses requires considerably more extensive surveys than we were able to do.

The paucity of available ecological data for *Lepidodactylus laticinctus* leads us to classify its IUCN conservation status as Data Deficient, a classification that applies to more than one-third of species in this clade (McDonald *et al.* 2022). It may not be biologically threatened at this point because of the large amount of forested habitat on Umboi and nearby islands, much of it secondary but still acceptable to these and other geckos. However, it could also truly be rare due to competition or predation from other geckos, in particular competition from those introduced in the past century or so (*H. frenatus*, *L. lugubris*). This would be a graver concern than mere possession of a cryptic ecology inasmuch as a broad suite of geckos is widespread and common on the Bismarck Arc islands. *Lepidodactylus sensu lato* was recently identified as having a high number of threatened species, a large number of species deficient in sufficient data to evaluate conservation status, and a high risk of cryptic extinction (McDonald *et al.* 2022). The latter two clearly stem from the cryptic ecologies of these species and the effect this has had on collecting success and, hence, knowledge of diversity and ecology within this clade. *Lepidodactylus laticinctus* **sp. nov.** clearly fits with this common clade-wide pattern in being poorly known, difficult to detect despite repeated focused efforts, and currently known from only a restricted area. Consequently, a more precise understanding of this species’ ecological requirements would be desirable for understanding any potential conservation risk faced by it.

## Acknowledgements

We thank M. McCoy and S. Richards for providing photographs used in Figure 2; S. Myers for compiling Figure 3; P. Campbell (BMNH), R. Brown and A. Motta (KU), S. Kennedy-Gold and J. Martinez (MCZ), and G. Schneider (UMMZ) for loans of specimens and/or tissues; P. Oliver for helpful comments on the ms.; the PNG National Museum and Art Gallery for providing in-country collaborative assistance, and the PNG Department of Environment and Conservation, PNG National Research Institute, and Morobe Provincial Government for permission to work in Morobe Province. This research was supported by National Geographic Society grant 226R-17 to FK and VW and a grant from Dr. Erik Mattison to FK; laboratory costs were covered by a grant from the Turku University Foundation to VV and VW. VW’s work was covered by postdoctoral research grants 105541 and 158161 from Svenska Kulturfonden. Collections were made under University of Michigan IACUC protocol 00008137, PNG research visa 99902505541, and PNG export permit 018071 to FK, and USFWS import permit 388103 to the University of Michigan.

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## Appendix I

### Additional Specimens Examined

*Lepidodactylus guppyi* ( $n = 16$ ): Papua New Guinea: Bougainville Island (MCZ 65862, 67124, 68126, 74518–19); Solomon Islands: Faro Island (BMNH 84.3.2.54, holotype), Balalae Island (KU 341255), Kolombangara Island (BMNH 1973.217–20, KU 341254), Rendova Island (KU 351259), Savo Island (MCZ 115564), Tulagi Island (MCZ 67122), Vella Lavella Island (KU 349702).

## Appendix II

**Specimens used for molecular study and their GenBank accession numbers. Novel specimens sequenced in this study are in bold; the remainder are from Oliver *et al.* (2018).**

Genera are *L* = *Lepidodactylus*, *Lup* = *Luperosaurus*, *P* = *Pseudogekko*; localities are countries (PI = Philippine Islands, PNG = Papua New Guinea, SI = Solomon Islands), followed by island names.

Catalog number	Species	PDC	ND2	Locality
Ingroup				
UMMZ 249265	<i>L. laticinctus</i> <b>sp. nov.</b>	<b>OQ933853</b>	<b>OQ933849</b>	PNG: Umboi
UMMZ 249263	<i>L. laticinctus</i> <b>sp. nov.</b>	<b>OQ933852</b>	<b>OQ933848</b>	PNG: Umboi
SAMA R64666	<i>Lepidodactylus</i> sp.	MG780633	MG780809	PNG: New Britain
KU341254	<i>L. guppyi</i>	<b>OQ933854</b>	<b>OQ933850</b>	SI: Kolombangara
KU349702	<i>L. guppyi</i>	<b>OQ933858</b>	-	SI: Vella Lavella
KU349703	<i>L. guppyi</i>	<b>OQ933857</b>	-	SI: Vella Lavella
KU341255	<i>L. guppyi</i>	<b>OQ933856</b>	<b>OQ933851</b>	SI: Balalae
KU341256	<i>L. guppyi</i>	<b>OQ933855</b>	-	SI: Balalae
ABTC 50473	<i>L. guppyi</i>	-	MG780717	SI: Guadalcanal
MNHN 2004.0094	<i>L. guppyi</i>	-	JX515612	SI: Vanikoro
USNM 533293	<i>L. guppyi</i>	JX515647	JX515620	SI: Taumako
ABTC 32720	<i>L. vanuatuensis</i>	-	MG780827	Vanuatu: Efate
MNHN 2008.0052	<i>L. vanuatuensis</i>	-	JX515622	Vanuatu: Sakao
Outgroups				
USNM 322126	<i>L. euaensis</i>	JX515641	JX515611	Tonga: Eua
<u>KU 341207</u>	<i>L. flaviocularis</i>	-	MG780716	SI: Guadalcanal
SAMA R32507	<i>L. listeri</i>	-	MG780722	Christmas
BPBM 19795	<i>L. lugubris</i>	-	MG780735	PNG: Misima
ID 7174	<i>L. ranauensis</i>	-	MG780776	Malaysia: Sabah
BPBM 15845	<i>L. mitchelli</i>	MG780624	MG780797	PNG: Boiaboiawaga
UMMZ 247929	<i>L. orientalis</i>	MW525371	MW525365	PNG: New Guinea
LSUMZ 97472	<i>L. pumilus</i>	-	MG780774	PNG: Daru
TNHC 61910	<i>Lup. cumingii</i>	JX515650	JX515623	PI: Luzon
KU 314947	<i>Lup. joloensis</i>	-	JQ437900	PI: Mindanao
KU 326437	<i>P. ditoy</i>	JX515652	JX515625	PI: Leyte
BPBM 19780	<i>Gekko vittatus</i>	JN019102	JN019069	PNG: Rossel