

A new potentially endangered limestone-associated Bent-toed Gecko of the *Cyrtodactylus pulchellus* (Squamata: Gekkonidae) complex from northern Peninsular Malaysia

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Abstract

A survey of a limestone forest at Gunung Baling, Kedah, West Malaysia lead to the discovery of an undescribed species of Bent-toed Gecko from the *Cyrtodactylus pulchellus* complex. *Cyrtodactylus evanquahi* sp. nov. can be distinguished from all other species in the *C. pulchellus* complex by a suite of morphological and color pattern characteristics: prominent tuberculation, higher number of dark body bands, and a smaller maximum SVL. It is further differentiated from all other species as follows; no tubercles on the ventral surface of the forelimbs, gular region, or in the ventrolateral folds; 31–34 paravertebral dorsal tubercles; 18–23 longitudinal rows of tubercles; 29–33 ventral scales; 22–23 subdigital lamellae on the fourth toe; 32–36 femoroprecloacal pores; a shallow precloacal groove in males; body bands and nuchal loop edged with a thin white line bearing tubercles; no scattered white spots on the dorsum; six or seven dark body bands much thinner than interspaces; 9–11 dark caudal bands on original tail; bands on the original tail separated by immaculate white caudal bands. It is further differentiated by an uncorrected pairwise genetic divergence of 6.50–15.67% from all other congeners in the *C. pulchellus* complex. It is most closely related to *C. pulchellus* from Penang Island ~76 km to the southwest. In addition to the new samples from Gunung Baling, we added four samples of *C. bintangrendah* from the new locality of Belukar Semang, Perak. The discovery of yet another new species of the *C. pulchellus* complex from a limestone habitat continues to underscore the high degree of endemism and the importance of these unique habitats for biodiversity, and the continued need for their conservation.

Key words: Conservation, Gunung Baling, Karst, Kedah, ND2, new species, Southeast Asia

Introduction

Dispersed throughout Southeast Asia are thousands of isolated limestone/karst formations and their associated forests, which have been known to harbor high biotic diversity and a multitude of endemic vertebrate and invertebrate species (e.g., Chin 1977; Kiew 1998; Clements *et al.* 2006, and references therein; Latinne *et al.* 2011). However, these formations are also targets for limestone quarrying for commercial use that pose a serious threat for biodiversity conservation and the discovery of new species. There have been numerous species discoveries of *Cyrtodactylus* (Gray) in Peninsular Malaysia and its adjacent islands (for a complete summary see Grismer & Quah 2019), with

eight of the thirty-one species being associated with karst and limestone forests (Grismer *et al.* 2016a, d, and references therein). Recent field explorations of karst formations in the Salween Basin and the Shan Plateau of Myanmar, have led to the discovery of 28 of new species of geckos—with most of them belonging to the genus *Cyrtodactylus* (Connette *et al.* 2017; Grismer *et al.* 2017, 2018a,b,c,d,e,f,g).

One particular clade that has received considerable attention is the *Cyrtodactylus pulchellus* complex of Peninsular Malaysia and southern Thailand. This complex currently contains 16 species (Grismer & Ahmad 2008; Grismer *et al.* 2012, 2014d, 2016b; Sumontha *et al.* 2012; Quah *et al.* 2019) that are distributed from Surat Thani, Thailand, in the north, south to Gunung Angsi, Negeri Sembilan, Malaysia, and a few offshore islands (Fig. 1). Throughout this distribution there are numerous karst formations that have yet to be surveyed. One unsurveyed isolated karst formation is the popular hiking destination, Gunung Baling, Kedah, Peninsular Malaysia, which is under threat from cement quarries on adjacent sides of the hiking trail head.

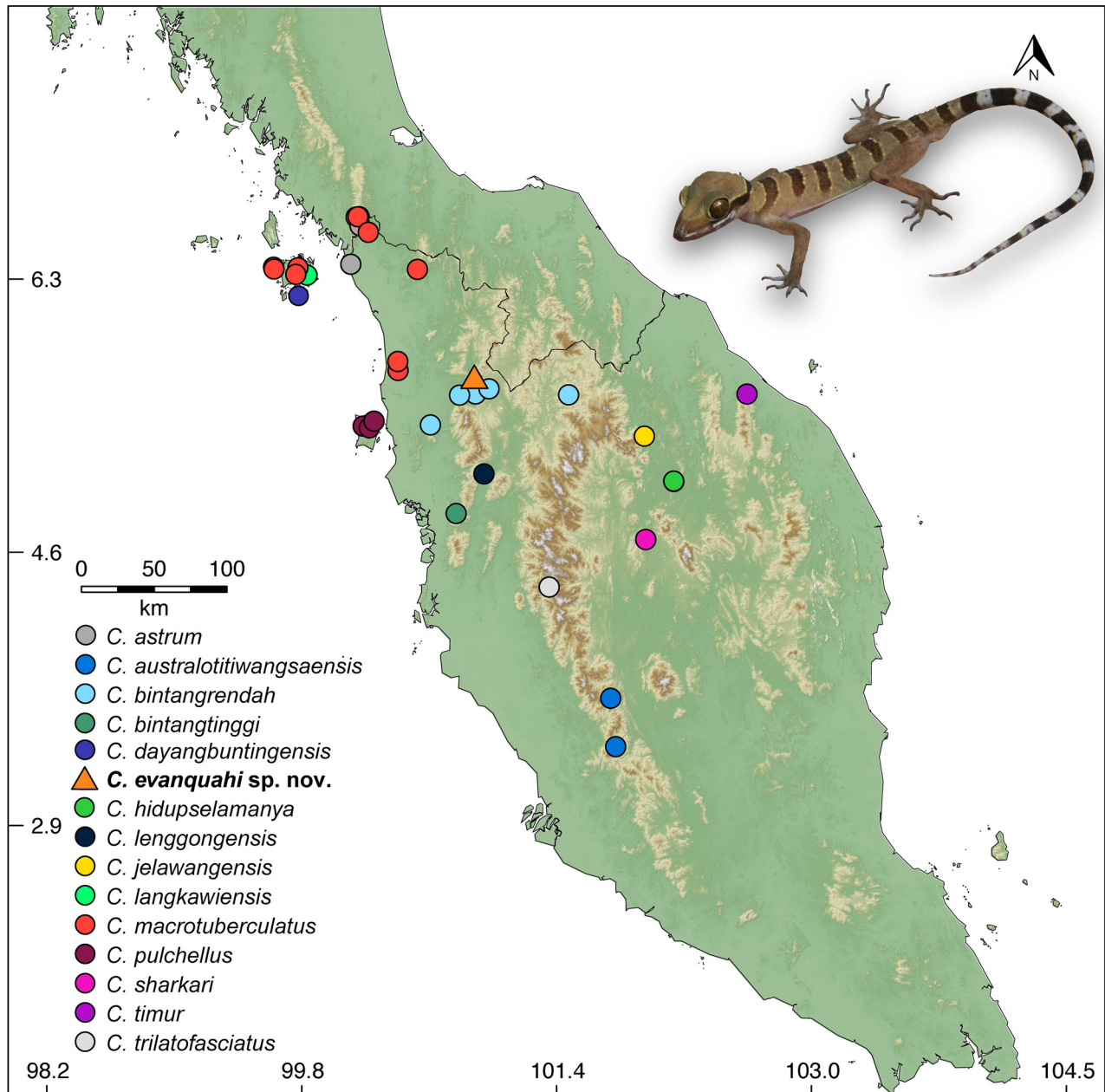


FIGURE 1. Taxon sampling for the *Cyrtodactylus pulchellus* complex used in this study (excludes *C. lekaguli* Grismer, Wood, Quah, Anuar, Muin, Sumontha, Ahmad, Bauer, Wangkulangkul, Grismer & Pauwels from the map).

Recently we conducted a survey of this formation and its associated forest at Gunung Baling, Kedah, West Malaysia, and discovered a new population of *Cyrtodactylus* (Fig. 1). We collected three individuals and sequenced

the mitochondrial NADH dehydrogenase subunit two gene (ND2) and its flanking tRNAs, and phylogenetically resolved this new population as the sister species to *C. pulchellus* from Pulau Pinang, Penang, West Malaysia. Morphological and color pattern characters indicate that this new population differs from all currently recognized species in the *C. pulchellus* complex, and it is described here as a new species.

Materials and Methods

Species concept. Here we employ the General Lineage Concept (GLC; De Queiroz 2007), which states that a species is independently evolving from other populations due to lack of gene flow between the individuals of the populations. We take an integrative taxonomic approach using the mitochondrial lineages of the phylogenetic tree with a suite of morphological characters to develop a species hypothesis for the new population from Gunung Bal-ing, Kedah, West Malaysia.

Taxon sampling and outgroup selection. The goal of this study was to reconstruct the phylogenetic relationships in the *Cyrtodactylus pulchellus* complex with additional genetic material from recently collected samples of *C. bintangrendah* Grismer, Wood, Quah, Anuar, Muin, Sumontha, Ahmad, Bauer, Wangkulangkul, Grismer & Pauwels ($n=4$) from Belukar Semang, Perak and the three individuals from the new population described above (Table 1). We used the distantly related *Hemidactylus frenatus* (Duméril & Bibron), *Tropiocolotes steudneri* (Peters) and *Agamura persica* (Duméril), and five species of *Cyrtodactylus* (Gray) as outgroups, based on Wood, *et al.* (2012), see Table 1 for accession numbers.

TABLE 1. Taxon sampling for ingroup and outgroup, locality data, and GenBank accession numbers from specimens used in this study. Voucher number abbreviations are as follows: BYU, Monte L. Bean Life Science Museum at Brigham Young University; FMNH, Field Museum of Natural History; USMHC, Herpetological Collection of the Universiti Sains Malaysia, Minden, Penang; JB, Jon Boone captive collection; LSUHC, La Sierra University Herpetological Collection; MAM, Mohd Abdul Muin field series; ZMKU, Zoological Museum Kasetsart University, Thailand. LA = Laos, TH= Thailand, WM = West Malaysia, N/A = Not applicable.

Voucher	Species	Locality	Latitude	Longitude	GenBank
N/A	<i>Hemidactylus frenatus</i>	unknown	N/A	N/A	JX519468
FMNH 247474	<i>Agamura persica</i>	Pakistan, Baluchistan Province, Makran District, Gwadar	N/A	N/A	JX440515
JB 28	<i>Tropiocolotes steudneri</i>	unknown	N/A	N/A	JX440520
LSUHC 6471	<i>C. elok</i>	WM, Pahang, Fraser's Hill, The Gap	N/A	N/A	JQ889180
LSUHC 9513	<i>C. intermedius</i>	TH, Chantaburi Province, Khao Khitchakut	N/A	N/A	JX519469
LSUHC 9514	<i>C. intermedius</i>	TH, Chantaburi Province, Khao Khitchakut	N/A	N/A	JX519470
FMNH 255454	<i>C. interdigitalis</i>	LA, Khammouan Province, Nakai District	N/A	N/A	JQ889181
FMNH 265806	<i>C. sp.</i>	TH, Loei, Phu Rua	N/A	N/A	JX519471
LSUHC 10024	<i>C. astrum</i>	WM, Perlis, Wang Kelian	6.69675	100.179183	JX519472
LSUHC 10023	<i>C. astrum</i>	WM, Perlis, Wang Kelian	6.69675	100.179183	JX519474
LSUHC 9215	<i>C. astrum</i>	WM, Perlis, Perlis State Park	6.698324	100.191407	JX519473
LSUHC 9962	<i>C. astrum</i>	WM, Perlis, Perlis State Park, Gua Wang Burma	6.700083	100.197967	JX519475
LSUHC 9986	<i>C. astrum</i>	WM, Perlis, Perlis State Park, Gua Wang Burma	6.700083	100.197967	JX519476
LSUHC 9987	<i>C. astrum</i>	WM, Perlis, Perlis State Park, Gua Wang Burma	6.700083	100.197967	JX519477
LSUHC 8807	<i>C. astrum</i>	WM, Perlis, Gua Kelam	6.644147	100.203899	JX519478

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TABLE 1. (Continued)

Voucher	Species	Locality	Latitude	Longitude	GenBank
LSUHC 8808	<i>C. astrum</i>	WM, Perlis, Gua Kelam	6.644147	100.203899	JX519479
LSUHC 8809	<i>C. astrum</i>	WM, Perlis, Gua Kelam	6.644147	100.203899	JX519480
LSUHC 8806	<i>C. astrum</i>	WM, Perlis, Gua Kelam	6.644147	100.203899	JX519481
LSUHC 8815	<i>C. astrum</i>	WM, Perlis, Kuala Perlis	6.405368	100.146534	JX519482
LSUHC 8816	<i>C. astrum</i>	WM, Perlis, Kuala Perlis	6.405368	100.146534	JX519483
LSUHC 6637	<i>C. australotitiwangsaensis</i>	WM, Pahang Genting Highlands	3.420644	101.788834	JX519484
LSUHC 8087	<i>C. australotitiwangsaensis</i>	WM, Pahang, Fraser's Hill	3.719498	101.757982	JX519485
LSUHC 8086	<i>C. australotitiwangsaensis</i>	WM, Pahang, Fraser's Hill	3.719498	101.757982	JX519486
LSUHC 9983	<i>C. bintangrendah</i>	WM, Kedah, Bukit Palong	5.602333	100.919833	JX519492
LSUHC 9984	<i>C. bintangrendah</i>	WM, Kedah, Bukit Palong	5.602333	100.919833	JX519487
MAM 00071	<i>C. bintangrendah</i>	WM, Perak, Belukar Semang	5.634289	101.003388	MN586885
MAM 00072	<i>C. bintangrendah</i>	WM, Perak, Belukar Semang	5.634289	101.003388	MN586886
MAM 00073	<i>C. bintangrendah</i>	WM, Perak, Belukar Semang	5.634289	101.003388	MN586887
MAM 00074	<i>C. bintangrendah</i>	WM, Perak, Belukar Semang	5.634289	101.003388	MN586888
USMHC 1351	<i>C. bintangrendah</i>	WM, Perak, Temengor	5.597118	101.49684	MN125079
USMHC 1352	<i>C. bintangrendah</i>	WM, Perak, Temengor	5.597118	101.49684	MN125080
USMHC 1353	<i>C. bintangrendah</i>	WM, Perak, Temengor	5.597118	101.49684	MN125081
LSUHC 10331	<i>C. bintangrendah</i>	WM, Kedah, Ulu Paip	5.4105	100.640317	MN125076
LSUHC 10519	<i>C. bintangrendah</i>	WM, Penang, Bukit Mertajam	5.594967	100.820883	MN125077
LSUHC 10520	<i>C. bintangrendah</i>	WM, Penang, Bukit Mertajam	5.594967	100.820883	MN125078
LSUHC 8862	<i>C. bintangtinggi</i>	WM, Perak, Bukit Larut	4.861917	100.799883	JX519493
LSUHC 9006	<i>C. bintangtinggi</i>	WM, Perak, Bukit Larut	4.861917	100.799883	JX519494
LSUHC 14353	<i>C. dayangbuntingensis</i>	WM, Kedah, Dayang Bunting Island	6.207804	99.784112	MN125090
LSUHC 14354	<i>C. dayangbuntingensis</i>	WM, Kedah, Dayang Bunting Island	6.207804	99.784112	MN125091
LSUHC 14355	<i>C. dayangbuntingensis</i>	WM, Kedah, Dayang Bunting Island	6.207804	99.784112	MN125092
BYU 53435	<i>C. evanquahi</i> sp. nov.	WM, Kedah, Gunung Baling	5.684989	100.912590	MN586889
BYU 53436	<i>C. evanquahi</i> sp. nov.	WM, Kedah, Gunung Baling	5.684989	100.912590	MN586890
BYU 53437	<i>C. evanquahi</i> sp. nov.	WM, Kedah, Gunung Baling	5.684989	100.912590	MN586891
LSUHC 12158	<i>C. hidupselamanya</i>	WM, Kelantan, Felda Chiku 7	5.060187	102.149277	KX011412
LSUHC 12159	<i>C. hidupselamanya</i>	WM, Kelantan, Felda Chiku 7	5.060187	102.149277	KX011413
LSUHC 12160	<i>C. hidupselamanya</i>	WM, Kelantan, Felda Chiku 7	5.060187	102.149277	KX011414
LSUHC 12161	<i>C. hidupselamanya</i>	WM, Kelantan, Felda Chiku 7	5.061443	102.149218	KX011415
LSUHC 12162	<i>C. hidupselamanya</i>	WM, Kelantan, Felda Chiku 7	5.061443	102.149218	KX011416
LSUHC 12163	<i>C. hidupselamanya</i>	WM, Kelantan, Felda Chiku 7	5.061443	102.149218	KX011417
LSUHC 12164	<i>C. hidupselamanya</i>	WM, Kelantan, Felda Chiku 7	5.061443	102.149218	KX011418
LSUHC 12165	<i>C. hidupselamanya</i>	WM, Kelantan, Felda Chiku 7	5.062775	102.148795	KX011419
LSUHC 12173	<i>C. hidupselamanya</i>	WM, Kelantan, Felda Chiku 7	5.062775	102.148795	KX011420
LSUHC 12174	<i>C. hidupselamanya</i>	WM, Kelantan, Felda Chiku 7	5.062775	102.148795	KX011421
LSUHC 12175	<i>C. hidupselamanya</i>	WM, Kelantan, Felda Chiku 7	5.062775	102.148795	KX011422
LSUHC 12176	<i>C. hidupselamanya</i>	WM, Kelantan, Felda Chiku 7	5.062775	102.148795	KX011423
LSUHC 12177	<i>C. hidupselamanya</i>	WM, Kelantan, Felda Chiku 7	5.062775	102.148795	KX011424

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TABLE 1. (Continued)

Voucher	Species	Locality	Latitude	Longitude	GenBank
LSUHC 11060	<i>C. jelawangensis</i>	WM, Kelantan, Gunung Stong	5.341083	101.966683	KJ659850
LSUHC 11061	<i>C. jelawangensis</i>	WM, Kelantan, Gunung Stong	5.341083	101.966683	KJ659851
LSUHC 11062	<i>C. jelawangensis</i>	WM, Kelantan, Gunung Stong	5.341083	101.966683	KJ659852
LSUHC 9435	<i>C. langkawiensis</i>	WM, Kedah, Pulau Langkawi, Wat Wanaram	6.337917	99.875117	JX519495
LSUHC 9125	<i>C. langkawiensis</i>	WM, Kedah, Pulau Langkawi, Wat Wanaram	6.337917	99.875117	JX519496
LSUHC 9437	<i>C. langkawiensis</i>	WM, Kedah, Pulau Langkawi, Wat Wanaram	6.337917	99.875117	JX519497
LSUHC 9434	<i>C. langkawiensis</i>	WM, Kedah, Pulau Langkawi, Wat Wanaram	6.337917	99.875117	JX519498
LSUHC 9124	<i>C. langkawiensis</i>	WM, Kedah, Pulau Langkawi, Wat Wanaram	6.337917	99.875117	JX519499
LSUHC 9123	<i>C. langkawiensis</i>	WM, Kedah, Pulau Langkawi, Wat Wanaram	6.337917	99.875117	JX519500
LSUHC 9122	<i>C. langkawiensis</i>	WM, Kedah, Pulau Langkawi, Wat Wanaram	6.337917	99.875117	JX519501
LSUHC 9120	<i>C. langkawiensis</i>	WM, Kedah, Pulau Langkawi, Wat Wanaram	6.337917	99.875117	JX519502
LSUHC 14347	<i>C. langkawiensis</i>	WM, Kedah, Pulau Langkawi, Wat Wanaram	6.337917	99.875117	MN125093
LSUHC 14348	<i>C. langkawiensis</i>	WM, Kedah, Pulau Langkawi, Wat Wanaram	6.337917	99.875117	MN125094
ZMKU 00720	R <i>C. lekaguli</i>	TH, Changwat Province, Takua Pa District	8.442344	98.514869	KX011425
ZMKU 00721	R <i>C. lekaguli</i>	TH, Changwat Province, Takua Pa District	8.442344	98.514869	KX011426
ZMKU 00722	R <i>C. lekaguli</i>	TH, Changwat Province, Takua Pa District	8.442344	98.514869	KX011427
ZMKU 00723	R <i>C. lekaguli</i>	TH, Changwat Province, Takua Pa District	8.442344	98.514869	KX011428
LSUHC 9975	<i>C. lenggongensis</i>	WM, Perak, Lenggong Valley	5.107183	100.972033	JX519488
LSUHC 9976	<i>C. lenggongensis</i>	WM, Perak, Lenggong Valley	5.107183	100.972033	JX519489
LSUHC 9974	<i>C. lenggongensis</i>	WM, Perak, Lenggong Valley	5.107183	100.972033	JX519490
LSUHC 9977	<i>C. lenggongensis</i>	WM, Perak, Lenggong Valley	5.107183	100.972033	JX519491
LSUHC 10329	<i>C. macrotuberculatus</i>	WM, Kedah, Bukit Wang	6.316667	100.483333	MN125088
LSUHC 10330	<i>C. macrotuberculatus</i>	WM, Kedah, Bukit Wang	6.316667	100.483333	MN125087
LSUHC 7560	<i>C. macrotuberculatus</i>	WM, Kedah, Pulau Langkawi, Gunung Machinchang	6.38657	99.667773	JX519503
LSUHC 9448	<i>C. macrotuberculatus</i>	WM, Kedah, Pulau Langkawi, Gunung Machinchang	6.38657	99.667773	JX519507
LSUHC 9449	<i>C. macrotuberculatus</i>	WM, Kedah, Pulau Langkawi, Gunung Machinchang	6.38657	99.667773	JX519509
LSUHC 9429	<i>C. macrotuberculatus</i>	WM, Kedah, Pulau Langkawi, Gunung Raya	6.383717	99.818767	JX519504
LSUHC 9428	<i>C. macrotuberculatus</i>	WM, Kedah, Pulau Langkawi, Gunung Raya	6.383717	99.818767	JX519506
LSUHC 6829	<i>C. macrotuberculatus</i>	WM, Kedah, Pulau Langkawi, Lubuk Semilang	6.342517	99.8057	JX519505

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TABLE 1. (Continued)

Voucher	Species	Locality	Latitude	Longitude	GenBank
LSUHC 7173	<i>C. macrotuberculatus</i>	WM, Kedah, Pulau Langkawi, Telaga Tujuh	6.375367	99.6706	JX519508
LSUHC 9671	<i>C. macrotuberculatus</i>	WM, Kedah, Hutan Lipur Sungai Tupah	5.748047	100.439729	JX519510
LSUHC 9672	<i>C. macrotuberculatus</i>	WM, Kedah, Hutan Lipur Sungai Tupah	5.748047	100.439729	JX519511
LSUHC 9693	<i>C. macrotuberculatus</i>	WM, Kedah, Hutan Lipur Sungai Tupah	5.748047	100.439729	JX519517
BYU 51869	<i>C. macrotuberculatus</i>	WM, Kedah, Kuala Nerang	6.373392	100.559541	MN125085
BYU 51870	<i>C. macrotuberculatus</i>	WM, Kedah, Kuala Nerang	6.373392	100.559541	MN125086
LSUHC 5999	<i>C. macrotuberculatus</i>	WM, Kedah, Gunung Jerai	5.803078	100.438029	JX519512
LSUHC 5939	<i>C. macrotuberculatus</i>	WM, Kedah, Gunung Jerai	5.803078	100.438029	JX519513
LSUHC 6000	<i>C. macrotuberculatus</i>	WM, Kedah, Gunung Jerai	5.803078	100.438029	JX519514
LSUHC 9980	<i>C. macrotuberculatus</i>	WM, Perlis, Perlis State Park	6.699476	100.190669	JX519515
LSUHC 9981	<i>C. macrotuberculatus</i>	WM, Perlis, Perlis State Park	6.699476	100.190669	JX519516
LSUHC 10038	<i>C. macrotuberculatus</i>	WM, Perlis, Bukit Chabang	6.603333	100.255278	JX519518
LSUHC 10037	<i>C. macrotuberculatus</i>	WM, Perlis, Bukit Chabang	6.603333	100.255278	JX519519
LSUHC 9667	<i>C. pulchellus</i>	WM, Penang, Pulau Pinang, Titi Kerawang	5.403394	100.223245	JX519520
LSUHC 9668	<i>C. pulchellus</i>	WM, Penang, Pulau Pinang, Titi Kerawang	5.403394	100.223245	JX519521
LSUHC 10022	<i>C. pulchellus</i>	WM, Penang, Pulau Pinang, Titi Kerawang	5.403394	100.223245	JX519522
LSUHC 6668	<i>C. pulchellus</i>	WM, Penang, Pulau Pinang, Empangan Air Itam	5.392577	100.261947	JX519523
LSUHC 6785	<i>C. pulchellus</i>	WM, Penang, Pulau Pinang, Moongate Trail	5.433774	100.290361	JX519524
LSUHC 6728	<i>C. pulchellus</i>	WM, Penang, Pulau Pinang, Moongate Trail	5.433774	100.290361	JX519525
LSUHC 6727	<i>C. pulchellus</i>	WM, Penang, Pulau Pinang, Moongate Trail	5.433774	100.290361	JX519526
LSUHC 6726	<i>C. pulchellus</i>	WM, Penang, Pulau Pinang, Moongate Trail	5.433774	100.290361	JX519527
LSUHC 6729	<i>C. pulchellus</i>	WM, Penang, Pulau Pinang, Moongate Trail	5.433774	100.290361	JX440552
LSUHC 11022	<i>C. sharkari</i>	WM, Gua Gunting, Merapoh, Pahang	4.70115	101.9752	KJ659853
LSUHC 10886	<i>C. timur</i>	WM, Terengganu, Gunung Tebu	5.601833	102.603167	KJ659854
LSUHC 11183	<i>C. timur</i>	WM, Terengganu, Gunung Tebu	5.601833	102.603167	KJ659855
LSUHC 11184	<i>C. timur</i>	WM, Terengganu, Gunung Tebu	5.601833	102.603167	KJ659856
LSUHC 11185	<i>C. timur</i>	WM, Terengganu, Gunung Tebu	5.601833	102.603167	KJ659857
LSUHC 10064	<i>C. trilatofasciatus</i>	WM, Pahang, Cameron Highlands	4.4086	100.376517	JX519529
LSUHC 10065	<i>C. trilatofasciatus</i>	WM, Pahang, Cameron Highlands	4.4086	100.376517	JX519530
LSUHC 10066	<i>C. trilatofasciatus</i>	WM, Pahang, Cameron Highlands	4.4086	100.376517	JX519531

Molecular analyses. From liver or muscle tissues stored in 95% ethanol, genomic DNA was isolated using the animal tissue protocol in the Qiagen DNeasyTM tissue kit (Valencia, CA, USA). The mitochondrial ND2 and the flanking tRNAs (~1335 bp) were amplified using a double-stranded Polymerase Chain Reaction (PCR) under

the following conditions: 1.0 μ l (~10–33 μ g) genomic DNA, 1.0 μ l (10 μ M) forward primer L4437b, 1.0 μ l (10 μ M) reverse primer L5002, 1.0 μ l deoxynucleotide triphosphates (dNTPs; 1.5 μ M), 2.0 μ l 5x buffer (1.5 μ M), 1.0 MgCl 10x buffer (1.5 μ M), 0.18 μ l Promega Taq polymerase (5u/ μ l), and 7.5 μ l H₂O, primers are from Macey *et al.* (1997) (Table 2). All PCR reactions were executed in 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 52°C for 35 s, followed by a cycle extension at 72°C for 35s, for 33 cycles. All PCR products were visualized on a 1.0% agarose gel electrophoresis. Successful amplified PCR products were vacuum purified using MANU 30 Millipore plates and purified products were resuspended in DNA grade water. Purified PCR products were sequenced in an ABI GeneAmp PCR 9700 thermal cycler using the primers presented in Table 2 and the ABI Big-Dye Terminator v3.1 Cycle Sequencing Kit. Cycle sequencing reactions were purified with Sephadex G-50 Fine (GE Healthcare) and sequenced on an ABI 3730xl DNA Analyzer at the BYU DNA Sequencing Center (DNASC). All new sequences produced from this study are deposited in GenBank (Table 1). All sequences were edited and aligned in Geneious v6.1.8 (Drummond *et al.* 2012), the alignment was constructed using the MAFFT v7.017 plugin (Katoh & Standley 2013) with an auto detect algorithm applied. Mesquite v3.02 (Maddison & Maddison 2015) was used to translate the reading frame of the coding portion of the gene.

TABLE 2. Primer sequences used for amplification and sequencing in this study for the ND2 gene and the flanking tRNAs.

Primer name	Primer reference		Sequence
L4437a	(Macey <i>et al.</i> 1997)	External	5'–AAGCAGTTGGGCCCATACC–3'
CyrtintF1	(Siler <i>et al.</i> 2010)	Internal	5'–TAGCCYTCTCYTCYATYGCCC–3'
CyrtintR1	(Siler <i>et al.</i> 2010)	Internal	5'–ATTGTKAGDGRGTCYAGGSTKGG–3'
H5934	(Macey <i>et al.</i> 1997)	External	5'–AGRGTGCCAATGTCTTTGTGRTT–3'

We partitioned the alignment based on codon positions (1st, 2nd and 3rd) and treated the tRNAs as a separate partition (four partitions in total). We used maximum likelihood (ML) and Bayesian Inference (BI) algorithms to estimate the phylogeny of the *Cyrtodactylus pulchellus* complex. The ML program available on the web server version of IQ-TREE (Nguyen *et al.* 2015; Trifinopoulos *et al.* 2016), was used to implement ModelFinder (Kalyaanamoorthy *et al.* 2017) to estimate models of nucleotide evolution for each codon position and the tRNAs (using the Bayesian Information Criterion [BIC]; Schwarz 1978). We assessed nodal support using 1000 bootstrap pseudoreplicates via the ultrafast approximation (UFB) algorithm (Hoang *et al.* 2018; Minh *et al.* 2013). All nodes having UFB values > 95 were considered significantly supported (Minh *et al.* 2013). The BI analysis was implemented in BEAST v2.5.1 (Bouckaert *et al.* 2014) using bModelTest (Bouckaert & Drummond 2017) to numerically integrate over uncertainty in models of substitution, while estimating the phylogeny using Markov chain Monte Carlo (MCMC). We ran the MCMC chain for 50 million generations while sampling every 5000 generations. We used Tracer v1.7 (Rambaut *et al.* 2018) to ensure that all parameters had an effective sample size (ESS) greater than 200 and showed a pattern consistent with stationarity. We then used TreeAnnotator v2.5.1 (Bouckaert *et al.* 2014) to summarize a maximum clade credibility tree using mean node heights and a 25% burnin. We considered all UFB $\geq$ 95 and PP $\geq$ 0.95 as strongly supported (Huelsenbeck *et al.* 2001; Erixon *et al.* 2003; Huelsenbeck & Rannala 2004; Nguyen *et al.* 2015; Wilcox *et al.* 2002). We calculated pairwise sequence divergences using the dist.dna function in the package APE (Paradis & Schliep 2018) implemented in R v3.5.2 (R Core Team 2018) with pairwise deletion on sites with missing data.

Morphological analysis. Color notes and digital images were collected from living specimens of both sexes and of all possible age classes prior to preservation. The following measurements were taken by PLW on the type series using Mitutoyo dial calipers to the nearest 0.1 mm, under a Nikon SMZ 1500 dissecting microscope on the left side of the body when possible: 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, 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 surface from the posterior surface of the knee while flexed 90° to the base of the heel; axilla to groin length (AG), 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 margin 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 measured from the occiput to the throat; eye diameter (ED), the greatest horizontal diameter of the eye-ball; eye to ear distance (EE), measured from the anterior edge of the ear opening to the posterior edge of the eye-ball; eye to snout distance (ES), measured from anteriormost margin of the eye-ball to the tip of snout; eye to nostril distance (EN), measured from the anterior margin of the eye ball to the posterior margin of the external nares; inner orbital distance (IO), measured between the anterior edges of the orbit; ear diameter (EL), the greatest vertical distance of the ear opening; and internarial distance (IN), measured between the nares across the rostrum.

Additional character states evaluated on the type series and comparative material (Appendix) included: number of supralabial and infralabial scales, counted from the largest scale immediately posterior to the dorsal inflection of the posterior portion of the upper jaw to the rostral and mental scales, respectively; the degree of body tuberculation — weak tuberculation referring to dorsal body tubercles that are low and rounded whereas prominent tuberculation refers to tubercles that are raised and keeled; the presence or absence of tubercles on the dorsal and ventral margins of the forearm; the number of paravertebral tubercles between limb insertions counted in a straight line immediately left of the vertebral column; the number of longitudinal rows of body tubercles counted transversely across the center of the dorsum from one ventrolateral fold to the other; the presence or absence of tubercles in the gular region, throat, and ventrolateral body folds; the number of longitudinal rows of ventral scales counted transversely across the center of the abdomen from one ventrolateral fold to the other; the shape of the subdigital lamellae proximal to the digital inflection; the number of subdigital lamellae beneath the fourth toe counted from the base of the first phalanx to the claw; the total number of femoroprecloacal pores (i.e., the contiguous rows of femoral and precloacal scales bearing pores combined as a single meristic referred to as the femoroprecloacal pores); the degree and arrangement of body tuberculation; the relative size and shape of the subcaudal scales; the number of dark body bands between the nuchal loop (Grismer 1988) and the caudal constriction; the width of the dark body bands relative to the width of the interspace between the bands; the presence or absence of a band outlined in white on the thigh; number of dark caudal bands on the original tail; the presence or absence of dark pigmentation infused in the white caudal bands of adults; and whether or not the posterior portion of the original tail in hatchlings and juveniles less than 50 mm SVL was white or whitish and faintly banded or boldly banded. Additional morphological data was obtained from the literature (Grismer & Ahmad 2008; Grismer *et al.* 2012, 2014d, 2016b; Sumontha *et al.* 2012; Quah *et al.* 2019). The type series was preserved with 10% formalin and later transferred to 70% ethanol for permanent storage. All type specimens are deposited in the Monte L. Bean Life Science Museum, Brigham Young University, Provo, Utah, USA (BYU), the museum abbreviations follow Sabaj (2016) and LSUHC refers to the La Sierra University Herpetological Collection, La Sierra University, Riverside, California, USA; USMHC refers to the Universiti Sains Malaysia Herpetological Collection in the School of Biological Sciences at the Universiti Sains Malaysia, Penang, Malaysia; MAM, refers to Mohd Abdul Muin field tag series.

Statistical analyses. All statistical analyses were implemented in R v3.5.2 (R Core Team 2018). Principal component analysis (PCA) and discriminant analysis of principal components (DAPC) were used to determine if the *Cyrtodactylus* from Gunung Baling population occupied unique positions in morphospace and the degree to which their variation in morphospace coincided with the putative species boundaries estimated by the molecular phylogenetic analyses (Fig. 2) relative to its closest relatives (see below) *C. pulchellus* Gray and *C. macrotuberculatus* Grismer & Ahmad. PCA was implemented by the `prcomp` command in R, is an indiscriminate analysis plotting the overall variation among individuals (i.e., data points) while treating each independently (i.e., not coercing data points into pre-defined groups). The number of supralabials, infralabials, paravertebral tubercles, longitudinal tubercles, ventral scales, lamellae on fourth toe, body bands, and ratio of body band to interspaces were compared for that of the new population from Gunung Baling with the type series of *C. pulchellus* and *C. macrotuberculatus* reported in Grismer *et al.* (2012). We removed femoroprecloacal pore counts from the PCA due to their presence in only males. For all other characters, both sexes and all size classes were used. All characters for PCA were log-transformed and scaled to their standard deviation prior to analysis in order to normalize their distribution so as to ensure characters with very large and very low values did not over-leverage the results owing to inter-variable nonlinearity and to insure the data were analyzed on the basis of correlation not covariance.

Based on a PCA, a DAPC was performed in the R package ADEGENET (Jombart *et al.* 2010) which places the individuals of each predefined population (inferred from the phylogeny and DFA) into separate clusters (i.e., plots of points) bearing the smallest within-group variance that produce linear combinations of centroids having the greatest between-group variance (i.e. linear distance; Jombart *et al.* 2010). DAPC relies on log transformed and standardized data from a PCA as a prior step to ensure that variables analyzed are not correlated and number fewer

than the data sample size. DAPC principal components with eigenvalues accounting for 80–90% of the variation in the data set were retained for the DAPC analysis according to the criterion of Jombart *et al.* (2010).

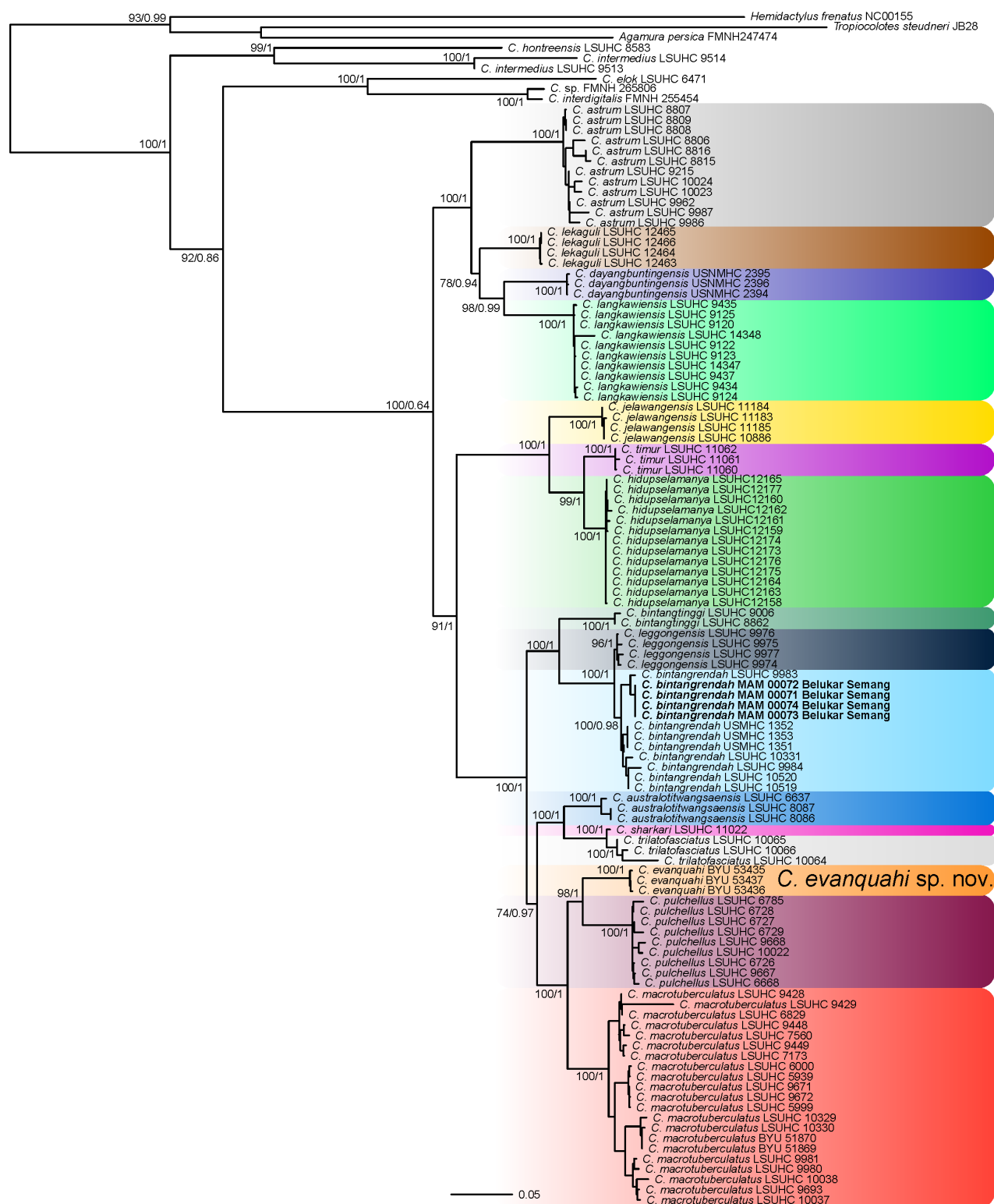


FIGURE 2. Reconstructed phylogenetic relationships of the *Cyrtodactylus pulchellus* complex based 1437 bp of ND2 and flanking tRNAs. The phylogenetic tree is a ML tree with ultrafast bootstrap support values and Bayesian posterior probabilities respectively. All new genetic samples are presented in bold.

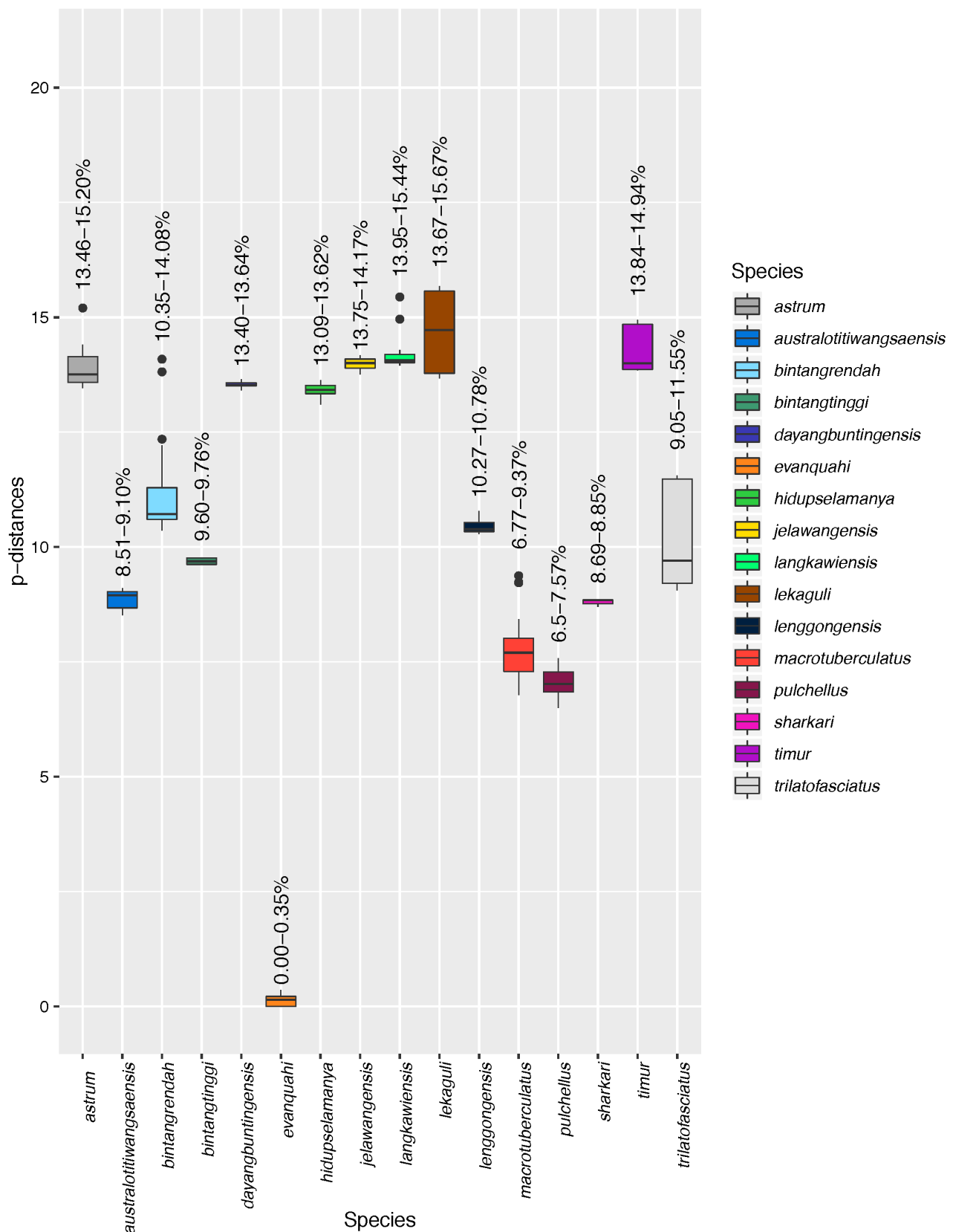


FIGURE 3. Box and whisker plots highlighting the uncorrected pairwise sequence divergences in the *Cyrtodactylus pulchellus* complex compared to *C. evanquahi* **sp. nov.** The comparison of *C. evanquahi* **sp. nov.** is the within species uncorrected pairwise divergences.

Results

Phylogenetic relationships. The final alignment of ND2 and the tRNAs was composed of 1437 base pairs with 504 parsimony-informative sites for the ingroup samples. The BIC selected HKY+F+G4 for the 1st codon position, TIM3+F+G4 for the 2nd position, TPM3u+F+I+G4 for the 3rd, and TN+F+G4 for the tRNAs, as the best fit models of molecular evolution. The models selected from bModelTest were similar to the ML models (Table 3): 121123 for the 1st (0.4255 posterior probability), 123324 for the 2nd (0.311 posterior probability), 123345 for the 3rd (0.3021 posterior probability), and 121131 for the tRNAs (0.2139 posterior probability). Both the estimated ML and MCC trees produced comparable topologies with only one node not recovered by both analyses (Fig. 2).

TABLE 3. Selected models of molecular evolution estimated by the BIC implemented in W-IQ-TREE (Nguyen *et al.* 2015; Trifinopoulos *et al.* 2016) using ModelFinder (Kalyaanamoorthy *et al.* 2017) and models selected and applied from bModelTest (Bouckaert & Drummond 2017).

Gene	Model selected/applied	Model selected/applied
ND2	(IQ-TREE)	(bModelTest)
1 st pos	HKY+F+G4	121123
2 nd pos	TIM3+F+G4	123324
3 rd pos	TPM3u+F+I+G4	123345
tRNAs	TN+F+G4	121131

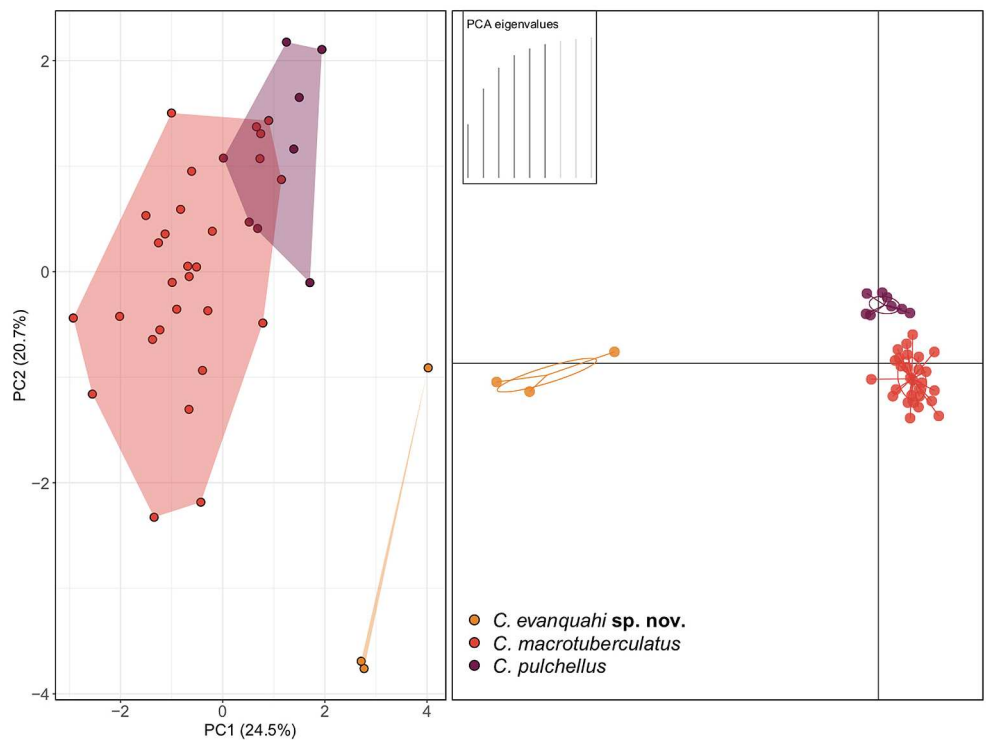


FIGURE 4. PCA (left) with convex hull polygons and DAPC (right) illustrating the morphospatial relationships of *C. evanquahi* sp. nov., *C. macrotuberculatus*, and *Cyrtodactylus pulchellus*.

The analyses recovered the new population from Gunung Baling, Kedah, deeply nested within the *C. pulchellus* complex, and is strongly supported (UFB 98 and PP 1.0) as the sister clade to *C. pulchellus* from Pulau Pinang, Penang (Fig. 2). The pairwise sequence divergences indicate that the Gunung Baling population is well differentiated (6.50–15.67%) from all other species in the *C. pulchellus* complex, it has a relatively low (0.35%) within population pairwise sequence divergence (Fig. 3) and is described as new below. The phylogenetic analyses recovered the four samples of *C. bintangrendah* from Belukar Semang, Perak nested within *C. bintangrendah*, and sister to LSUHC

9983 from Bukit Palong, Kedah (100 UFB and PP 1.0; Fig. 2). The morphology of the additional population of *C. bintangrendah* matched the genetic results (Figs. 2 and 3).

Morphological analysis. The results of the PCA and DAPC corroborate the phylogenetic hypothesis by indicating that the Gunung Baling population occupies a unique position in morphospace along the ordination of the first two principal components (PC; Fig. 4). The first PC accounts for 24.5% of the variation in the data set and loads most heavily for ventral scales and body bands, and the second PC accounts for an additional 20.7% of the variation, loading most heavily for the number of longitudinal tubercles and SVL (Table 4). Additional morphological and color pattern comparisons are presented in Table 5.

TABLE 4. Summary statistics and principal component analysis scores for *C. evanquahi* **sp. nov.**, *C. macrotuberculatus*, and *C. pulchellus*.

	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8
Standard deviation	1.4865	1.3650	1.0989	0.9908	0.9446	0.7937	0.7419	0.6829
Proportion of Variance	0.2455	0.2070	0.1342	0.1091	0.0992	0.0700	0.0612	0.0518
Cumulative Proportion	0.2455	0.4526	0.5867	0.6958	0.7949	0.8649	0.9261	0.9779
Eigenvalue	2.2098	1.8631	1.2076	0.9816	0.8923	0.6300	0.5503	0.4664
Supralabials	-0.0694	0.0886	-0.7310	0.0380	-0.4647	0.3083	-0.3648	-0.0515
Infralabials	0.3952	0.1932	-0.2941	-0.2581	-0.2786	-0.6530	0.3661	-0.0530
Paravertebral tubercles	-0.4785	0.2851	0.1052	-0.1293	0.0142	-0.1898	-0.1129	-0.7757
Longitudinal tubercles	0.1847	0.5971	0.0009	0.0119	0.2382	0.4187	0.2592	0.0436
Ventral Scales	0.4958	0.1107	0.0316	-0.4995	0.1285	0.3354	-0.1152	-0.3094
4th toe lamellae	0.2830	0.1058	0.3248	0.5947	-0.5291	0.1473	0.1896	-0.2875
Body Bands	0.4032	-0.4622	0.2031	-0.0904	-0.0651	-0.0156	-0.3878	-0.2345
Band/Interspace with	-0.2955	-0.1834	0.2585	-0.5324	-0.5236	0.3014	0.3667	0.1188
SVL	0.0066	0.4963	0.3918	-0.1426	-0.2732	-0.2049	-0.5647	0.3788

Taxonomy

Cyrtodactylus evanquahi **sp. nov.**

English: Evan Quah's banded Bent-toed Gecko

Malay: *Cicak Jari-bengkok Evan Quah*
(Figs. 5 and 6)

Holotype. Adult male, BYU 53435 collected on 13 August 2016 by Perry L. Wood, Jr. and Evan S. H. Quah from Gunung Baling, Kedah, Peninsular Malaysia (5.684989 N, 100.912590 E; 226 m).

Paratypes. Adult female, BYU 53436 and juvenile BYU 53437 collected on 14 August 2016 by Evan S. H. Quah and Perry L. Wood, Jr. both specimens bear the same collection data as the holotype.

Diagnosis. *Cyrtodactylus evanquahi* **sp. nov.** can be differentiated from all other species of *Cyrtodactylus* by having a combination of the following characters: maximum SVL of approximately 96 mm; nine or 10 supralabials; nine or 10 infralabials; prominent tuberculation on body; no tubercles on ventral surface of forelimbs, gular region, in ventrolateral body folds, or anterior one-third of tail; 31–34 paravertebral tubercles; 18–23 longitudinal tubercle rows; 29–33 ventral scales; 22 or 23 subdigital lamellae on fourth toe; 32–36 femoro-precloacal pores; shallow precloacal groove in males; six or seven dark dorsal body bands; body bands much narrower than interspaces; faint rostral chevron; body bands and nuchal loop edged with a thin white, tubercle-bearing line; dorsum lacking scattered pattern of white tubercles; no banding on base of thigh; 9–11 dark caudal bands on original tail; white caudal bands generally not immaculate; hatchlings and juveniles bearing white tail tips; and adult posterior caudal region white. All these characters are scored across all species of the *C. pulchellus* complex in Table 5.

TABLE 5. Diagnostic characters differentiating the 17 species of the *Cyrtodactylus pulchellus* complex. W=weak; M=moderate; S=strong; /=data unavailable. Some information was collected from the following literature (Grismer & Ahmad 2008; Grismer *et al.* 2012, 2014d, 2016b; Sumontha *et al.* 2012; Quah *et al.* 2019).

	<i>astrum</i>	<i>australotitiwangsaensis</i>	<i>bintangtinggi</i>	<i>bintangrendah</i>	<i>dayangbuntingensis</i>	<i>langkawensis</i>	<i>lekaguli</i>	<i>macrotuberculatus</i>	<i>phuketensis</i>
Supralabials	10–12	9–12	9–13	8–12	12–14	9–12	10–12	9–12	11–13
Infralabials	9–12	9–13	8–11	8 or 9	10–11	8–10	9–11	7–10	9 or 10
Tuberculation	W–M	W–M+	W–M	M+	W	W–M	W–M	S	S
Tubercles on ventral surface of forelimbs	No	No	No	No	No	No	No	Yes	Yes
Tubercles in gular region	No	No	No	No	No	No	No	Yes	Yes
Ventrolateral fold tuberculate	No	No	No	Yes	No	No	No	Yes	Yes
Paravertebral tubercles	45–57	37–45	31–42	36–44	35–36	38–44	30–50	34–44	41–43
Longitudinal rows of tubercles	22–29	23–30	21–26	22–25	20–22	22–25	20–24	19–27	23,24
Ventral scales	31–46	32–40	36–40	31–39	36–39	31–36	31–43	17–28	22–24
4th toe lamellae	20–24	21–27	21–25	21–24	21–23	19–21	20–25	20–24	19
Femoroprecloacal pores	31–38	39–45	37–41	41–46	26–29	30	33–36	28–41	33–36
Precloacal groove in males	Deep	Deep	Deep	Deep	Deep	Deep	Deep	Deep	Shallow
Body bands	4	3(1) or 4	3(1) or 4	4	4	4 or 5	4 or 5	4	3
Body band/ interspace ratio	1.00–2.00	1.00–2.00	1.00–1.25	1.00–1.25	0.75	0.75–1.00	1.00–2.00	1.00–1.50	1
Dorsum bearing scattered pattern of white tubercles	Yes	No	No	No	Yes	No	No	No	No
Hatchlings/ juveniles with white tail tip	Yes	No	No	No	Yes	Yes	/	No	No
Adult posterior caudal region white	No	No	No	No	No	No	No	No	No
Dark caudal bands on original tail	12–14	7–8	8–10	8 or 9	>7	11–16	12–14	7–10	8,9
White caudal bands in adults immaculate	No	Yes	Yes	Yes	No	No	No	No	Usually
Maximum SVL	108.1	119.8	111.4	114.4	99	99.1	103.5	118	114.7
Sample size	11	13	13	10	3	10	11	29	3

TABLE 5. (Continued)

	<i>pulchellus</i>	<i>trilatofasciatus</i>	<i>sharkari</i>	<i>jelawangensis</i>	<i>timur</i>	<i>hidupselamanya</i>	<i>lenggongensis</i>	<i>evanquahi</i> sp. n.
Supralabials	9–11	10–12	11	9–12	10–12	9–12	10 or 11	9 or 10
Infralabials	8–10	8–11	10	9–11	8–10	8–11	8–10	9 or 10
Tuberculation	M–M+	M	M	M–S	W	W	M	P
Tubercles on ventral surface of forelimbs	No	No	No	Yes	No	No	No	No
Tubercles in gular region	No	No	No	No	No	No	No	No
Ventrolateral fold tuberculate	No	No	No	No	No	No	No	No
Paravertebral tubercles	33–43	34–38	31	36–42	38–43	39–48	36–41	31–34
Longitudinal rows of tubercles	22–26	23–27	24	23–25	21–24	19–23	22–25	18–23
Ventral scales	29–34	33–36	41	31–36	31–40	26–33	32 or 33	29–33
4th toe lamellae	21–26	22–27	24	21–24	21–25	19–24	20–23	22–23
Femoro-precloacal pores	34–39	41–46	46	36	21 or 22	17–22	39–41	32–36
Precloacal groove in males	Deep	Deep	Shallow	Deep	Deep	Deep	Deep	Shallow
Body bands	4	3	4	4	4	4	4 or 5	6 or 7
Body band/interspace ratio	0.75–1.25	2.00–2.75	1.75	1.25–1.50	1.00–1.25	1.00–1.25	0.50–1.25	0.82–1.1
Dorsum bearing scattered pattern of white tubercles	No	No	No	No	No	No	No	No
Hatchlings/juveniles with white tail tip	No	/	/	Yes	No	Yes	/	Yes
Adult posterior caudal region white	No	No	No	No	No	Yes	No	Yes
Dark caudal bands on original tail	8–10	6	7	10	8–10	8–10	14	9–11
White caudal bands in adults immaculate	Yes	Yes	Yes	No	Yes	Yes	Yes	No
Maximum SVL	114.6	122.2	100.1	119.8	120.5	102.7	103.1	96
Sample size	13	6	1	4	5	14	4	3

Description of the Holotype. Adult male, 85 mm SVL; head large, moderate in length (HL/SVL 0.29), wide (HW/HL 0.65), slightly flattened (HD/HL 0.39), distinct from neck, triangular in dorsal profile; lores concave anteriorly, inflated posteriorly; frontal and prefrontal regions deeply concave; canthus rostralis rounded anteriorly; snout elongate (ES/HL 0.43), rounded in dorsal profile, laterally constricted; eye large (ED/HL 0.21); ear opening elliptical, taller than wide, moderate in size (EL/HL 0.03), obliquely oriented; eye to ear distance greater than diameter of eye; rostral rectangular, divided dorsally by an inverted Y-shaped furrow, bordered posteriorly by left and right supranasals, and one medial postrostrals (=internasals), bordered laterally by first supralabials; external nares bordered anteriorly by rostral, dorsally by large supranasal and smaller postrostral, posteriorly by two postnasals, ventrally by first supralabial; 9(R, L) rectangular supralabials extending to just beyond upturn of labial margin, tapering abruptly below midpoint of eye; 9(R,L) infralabials tapering in size posteriorly; scales on rostrum and lores weakly raised, larger than granular scales on top of head and occiput, those on posterior portion of canthus rostralis bony frontal ridges bordering orbit confluent with bony, transverse, parietal ridge; dorsal superciliaries elongate, smooth, largest anteriorly; mental triangular, bordered laterally by first infralabials and posteriorly by left and right, rectangular postmentals which contact medially for 70% of their length; single row of slightly enlarged, elongate chinshields extending posteriorly to seventh infralabials; small, granular to flat gular scales grading posteriorly into larger, flat, smooth, imbricate, pectoral and ventral scales.

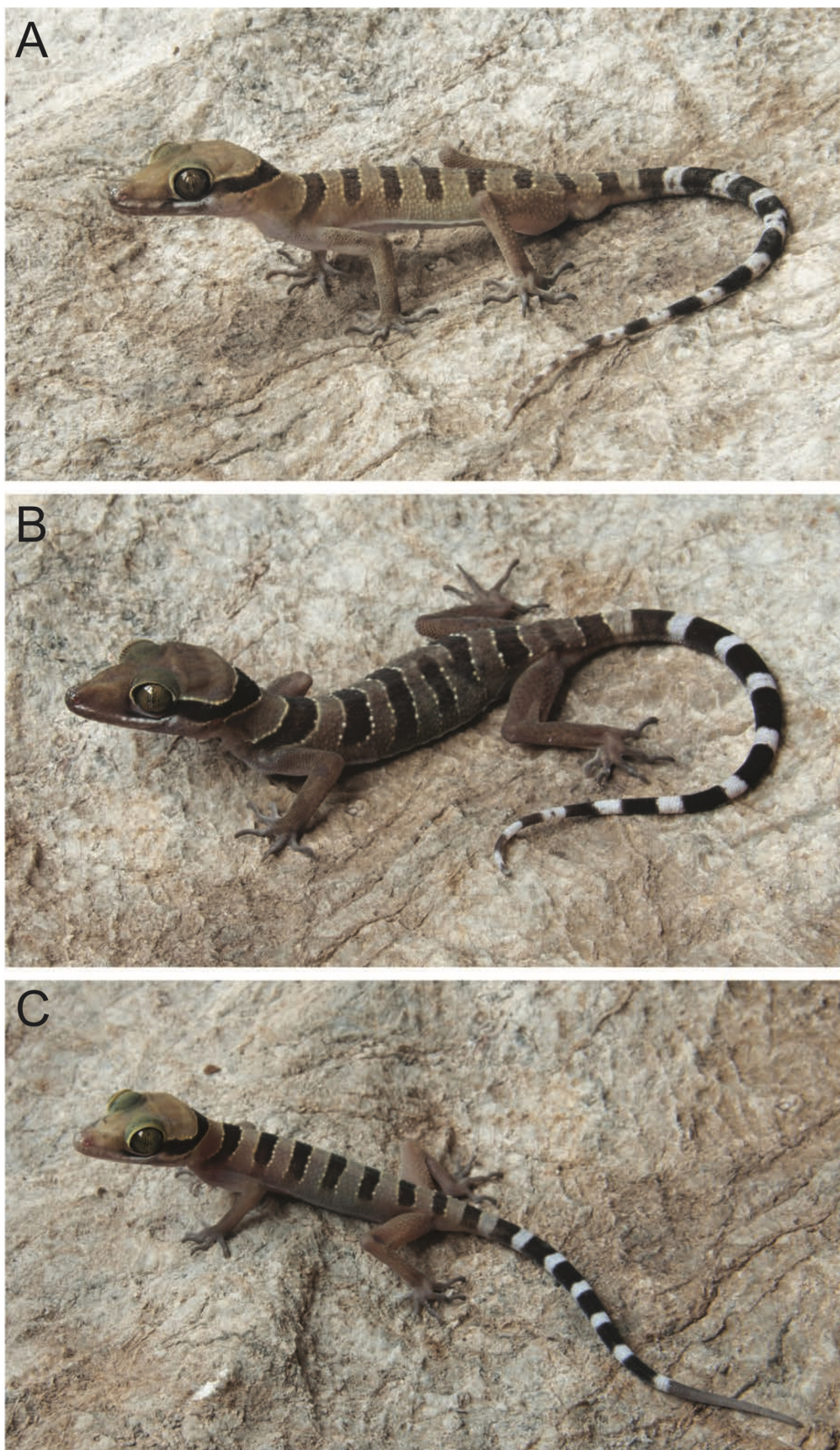


FIGURE 5. Type series of *C. evanquahi* **sp. nov.** in life, from Gunung Baling, Kedah, Malaysia. (A) adult male holotype (BYU 53435); (B), adult female paratype (BYU 53436), and (C) juvenile female paratype (BYU 53437).



FIGURE 6. Type series of *C. evanquahi* **sp. nov.** from Gunung Baling, Kedah, Malaysia. From left to right: adult male holotype (BYU 53435), middle, adult female paratype (BYU 53436), and juvenile female paratype (BYU 53437).

Body relatively short (AG/SVL 0.43) with well-defined, non-tuberculate, ventrolateral folds; dorsal scales small, granular, interspersed with low, regularly arranged, keeled tubercles, smaller intervening tubercles occasionally present; tubercles extend from top of head to caudal constriction and onto anterior one-fifth of tail; tubercles on occiput and nape small, those on body largest; approximately 18 longitudinal rows of tubercles at midbody; 33 paravertebral tubercles; 33 flat imbricate ventral scales between ventrolateral body folds; ventral scales larger than dorsal scales; precloacal scales large, smooth; shallow precloacal groove.

Forelimbs moderate in stature, relatively short (FL/SVL 0.16); scales on dorsal surfaces of forelimbs, small, juxtaposed, intermixed with large tubercles in close contact with one another; scales of ventral surface of forearm flat, subimbricate, tubercles absent; palmar scales weakly rounded; digits well-developed, inflected at basal, interphalangeal joints; subdigital lamellae rectangular proximal to joint inflection, only slightly expanded distal to inflection; digits more narrow distal to joints; claws well-developed, sheathed by a dorsal and ventral scale; hind limbs more robust than forelimbs, moderate in length (TBL/SVL 0.20), larger tubercles on dorsal surface of legs separated by smaller subimbricate scales; ventral scales of thigh flat, smooth, imbricate, larger than dorsal granular scales; ventral, tibial scales flat, smooth, imbricate; single row of greatly enlarged, flat, rectangular, imbricate, femoroprecloacal scales extend nearly from knee to knee through precloacal region where they are continuous with slightly larger; those on the occiput intermixed with small tubercles; posterior interorbital region tuberculate; large, enlarged, pore-bearing precloacal scales; 36 contiguous, pore-bearing precloacal scales forming an inverted T bearing a shallow, precloacal groove in which 11 pore-bearing scales are found (six on left, five on right); postfemoral scales immediately posterior to enlarged scale row small, nearly granular, forming an abrupt union with postfemoral scales on posteroventral margin of thigh; plantar scales low, slightly raised, slightly round; digits well-developed,

inflected at basal, interphalangeal joints; subdigital lamellae proximal to joint inflection rectangular, only slightly expanded distal to inflection; digits more narrow distal to joints; claws well-developed, sheathed by a dorsal and ventral scale; 22(R) 21(L) subdigital lamellae on 4th toe.

Original tail 199 mm in length, 7.2 mm in width at base, tapering to a point; dorsal scales of tail flat, squarish; subcaudal region bearing large median row of transverse scales; shallow caudal furrow; base of the tail bearding hemipenial swellings; three small, postcloacal tubercles on each hemipenial swelling; postcloacal scales smooth, flat, large, imbricate. Coloration in life. Dorsal ground color of head, body, limbs, and base of tail, light brownish grey, immaculate; no V-shaped line on the rostrum; moderate, dark-brown nuchal loop edged anteriorly and posteriorly by thin, whitish cream line bearing tubercles; six dark-brown body bands between nuchal loop and hind limb insertions edged anteriorly and posteriorly by thin whitish cream lines bearing tubercles; body bands slightly thinner than interspaces; no markings on posterior margin of thigh; ventral surface of head, body, and limbs beige, immaculate except for black stipples in each scale; tail bearing eleven dark bands separated by ten, narrower, beige (anteriorly) to white (posteriorly) bands; subcaudal region tan (Figs 5 and 6).

Variation. The paratypes closely resemble the holotype in all aspects of color and pattern except that the female paratype (BYU 53436) has a darker dorsal ground color, two incomplete dark dorsal bands, and nearly immaculate white bands on the tail (Figs 5 and 6). Additional color pattern and morphological differences are listed in Table 5.

Distribution. *Cyrtodactylus evanquahi* **sp. nov.** is known only from Gunung Baling, Kedah, Peninsular Malaysia (Fig. 1). It is expected to be found at other limestone forested areas near the Gunung Baling karst formation.

Etymology. The specific epithet honors Dr. Evan S. H. Quah, who suggested the urgency to document the herpetofaunal diversity of Gunung Baling, Kedah, which is under constant threat from two cement companies that are actively mining the limestone. He also participated in the only herpetological survey of the area. Dr. Quah is an extremely productive contributor to the study of herpetology in Malaysia and is a champion for conservation of the region.



FIGURE 7. Limestone forest microhabitat at the type locality of *C. evanquahi* **sp. nov.**, Gunung Baling, Kedah.

Natural History. All specimens were collected at night between 2000–2400 hrs at the type locality in primary limestone forest habitat (Fig. 7). The adult male (BYU 53435) was found on a root at the base of the karst formation. The adult female (BYU 53436) was found on a thin sapling approximately 1.5 m off the ground. The juvenile female (BYU 53437) was found on a sapling close to the karst. None of the specimens were found directly on the karst and all were found on vegetation, so we hypothesize that these are a limestone forest dwelling species and facultative karst-dwellers. The only adult female collected was not gravid so there are no data on the reproductive biology of this species.

TABLE 6. Characters and measurements of the type series of *Cyrtodactylus evanquahi* **sp. nov.** from Gunung Baling, Kedah Peninsular Malaysia. M=male, F=female, J=juvenile, /=data unavailable, R=regenerated, B=broken. W=weak, P=prominent. Other abbreviations are listed in the Materials and Methods.

	BYU	BYU	BYU
	53435	53436	53437
	holotype	paratype	paratype
Sex	M	F	J
Supralabials	9	9	10
Infralabials	9	10	9
Tuberculation weak, moderate, strong	P	P	P
Tubercles on ventral surface of forelimbs	No	No	No
Tubercles in gular region	No	No	No
Ventrolateral fold tuberculate	No	No	No
No. of paravertebral tubercles	33	31	34
No. longitudinal rows of tubercles	18	23	19
Tubercles on at least anterior 1/3 of tail	No	No	No
No. of ventral scales	33	32	29
No. of subdigital lamellae on 4th toe	22	22	23
No. of femero-precloacal pores	36	32	32
Deep precloacal groove in males	Shallow	/	/
Body bands	7	6	7
Body band/interspace ratio	0.82	0.99	1.1
Scattered white dorsal tubercles	No	No	No
No. bands on original tail	11	11	9
Posterior portion of tail white in adults	Yes	Yes	NA
Immaculate white caudal bands in adults	No	No	No
SVL	85	96	60
TL	119	122	68
TW	7.2	6.64	4.3
FL	13.7	13.9	9.7
TBL	16.4	16.85	11.29
AG	36.8	40.1	26.1
HL	24.7	25	17.79
HW	16.3	16.2	11.38
HD	9.8	10.0	7.1
ED	5.2	6.35	4.89
EE	7.3	6.9	4.34
ES	10.7	11.1	6.6
EN	8.3	8.8	6.1
IO	5.9	5.8	4.94
EL	0.8	1.4	0.86
IN	3.2	3.1	2.35

Comparisons. *Cyrtodactylus evanquahi* **sp. nov.** differs from all other species in the *C. pulchellus* complex by having prominent tuberculation, more dark body bands, and a smaller maximum SVL (Table 5). It is further differentiated from all other species by having a combination of prominent tuberculation on the body; no tubercles on the ventral surface of the forelimbs, gular region, or in the ventrolateral folds; 31–34 paravertebral dorsal tubercles; 18–23 longitudinal rows of tubercles; 29–33 ventral scales; 22–23 subdigital lamellae on the fourth toe; 32–36 fem-

oroprecloacal pores; a shallow precloacal groove in males; body bands and nuchal loop edged with a thin white line bearing tubercles; no scattered white spots on the dorsum; six or seven dark body bands thinner than interspaces; 9–11 dark caudal bands on original tail; bands on the original tail separated by not imperfect white caudal bands (Table 4). Additional comparisons between *C. evanquahi* **sp. nov.** and other members of the *C. pulchellus* complex can be found in Table 4.

Within the *C. pulchellus* complex, *C. evanquahi* **sp. nov.** is the sister species to *C. pulchellus* and can be further differentiated from it by having prominent tuberculation as opposed to moderate–moderate+; shallow precloacal groove in males opposed to a deep groove; having more dark dorsal body bands (six or seven vs. four); having thinner dark body bands; hatchlings and juveniles with white tail tips as opposed to no white tail tips; white caudal bands in adults not immaculate; adults having a posterior caudal region white (Table 5).

Conservation and Threats. Based on the what we know about the limited distribution of this species and the fact that the type locality has cement quarries on either side of it (Figs. 8–9), it is likely that the continued mining of limestone will result in the extinction of this species if this species does not occur in other localities. Gunung Baling is also a popular hiking destination and the increased traffic of tourists also pose a threat to habitat. For example, there have been multiple human induced fires that inflicted considerable damage to the area. We suggest that this species be listed as “Vulnerable” in accordance with the formulaic conservation status assessment criterion of the International Union for Conservation of Nature (IUCN 2019), based on its small population size and the threat of nearby habitat destruction from mining and quarrying.

Discussion

The molecular analyses demonstrate with strong support that *C. evanquahi* **sp. nov.** is deeply nested within the *C. pulchellus* complex (Fig. 2). *Cyrtodactylus evanquahi* **sp. nov.** is geographically separated from its insular endemic sister species *C. pulchellus* by a straight-line distance of ~76 km to the southwest. We hypothesize that there is sufficient evidence of reproductive isolation and that absence of gene flow between these two isolated populations, along with the molecular and the morphological data to consider that *C. evanquahi* **sp. nov.** is a distinct species on its own evolutionary trajectory. The recovery of *C. evanquahi* **sp. nov.** (limestone forest-dweller) as sister to *C. pulchellus* (granite-dweller) from Pulau Pinang provides another instance of convergent adaptation to karst habitat in the *C. pulchellus* complex (Grismer *et al.* 2016d). Based on current distributions and presumably limited dispersal capabilities, one might expect that *C. evanquahi* **sp. nov.** would be more closely related to the almost syntopic species *C. bintangrendah* or *C. macrotuberculatus*, and not an insular endemic ~76 km to the east (Fig. 1).

The phylogenetic analyses recovered *C. bintangrendah* from Belukur, Semang, Perak as the sister species to a population of *C. bintangrendah* from Bukit Palong, Kedah, which is ~10 km to the southeast. Previously, Grismer *et al.* (2012) listed a population of *C. bintangrendah* from the Lenggong Valley, Perak, which is on the east side of the Bintang range, but later described that population as *C. lenggongensis* Grismer, Wood, Anuar, Grismer, Quah, Murdoch, Muin, Davis, Auilar, Klabacka, Cobos, Aowphol & Sites (Grismer *et al.* 2014b, 2016b). Our results add a new population of *C. bintangrendah* back to the eastern side of the Bintang range and further support the hypothesis that these lowland forest dwelling species have a much larger distribution than previously thought (Grismer *et al.* 2012, 2014b, 2016b).

The discovery of yet another new species of karst-associated species of *Cyrtodactylus* adds to the growing body of literature of limestone endemics being discovered on the Thai-Malaya Peninsula and its off shore islands (e.g. Grismer *et al.* 2014a,b,c, 2016a,b,c; Wood *et al.* 2017, and references therein). The distribution of the *C. pulchellus* complex ranges as far north as the Isthmus of Kra in Thailand and encompasses many unexplored karst areas. There are eleven species of the *C. pulchellus* complex endemic to Malaysia and four endemics to Thailand and two species that occur in both Malaysia and Thailand (*C. astrum* Grismer, Wood, Quah, Anuar, Muin, Sumontha, Ahmad, Bauer, Wangkulangkul, Grismer & Pauwels and *C. macrotuberculatus*). It is well documented that there has been considerably more herpetological surveys in Malaysia and we hypothesize that additional field exploration on the Thai portion of the Malay Peninsula and its offshore islands will result in the discovery of new populations and species in the *C. pulchellus* complex, as well as other species.



FIGURE 8. (A) Image of the limestone mining quarry on the North side of the type locality (Cement quarry 1 in Figure 7). (B) Image of the type locality, Gunung Baling, Kedah. (C) Image of the limestone mining quarry on the south side of the type locality (Cement quarry 2 in Figure 7).

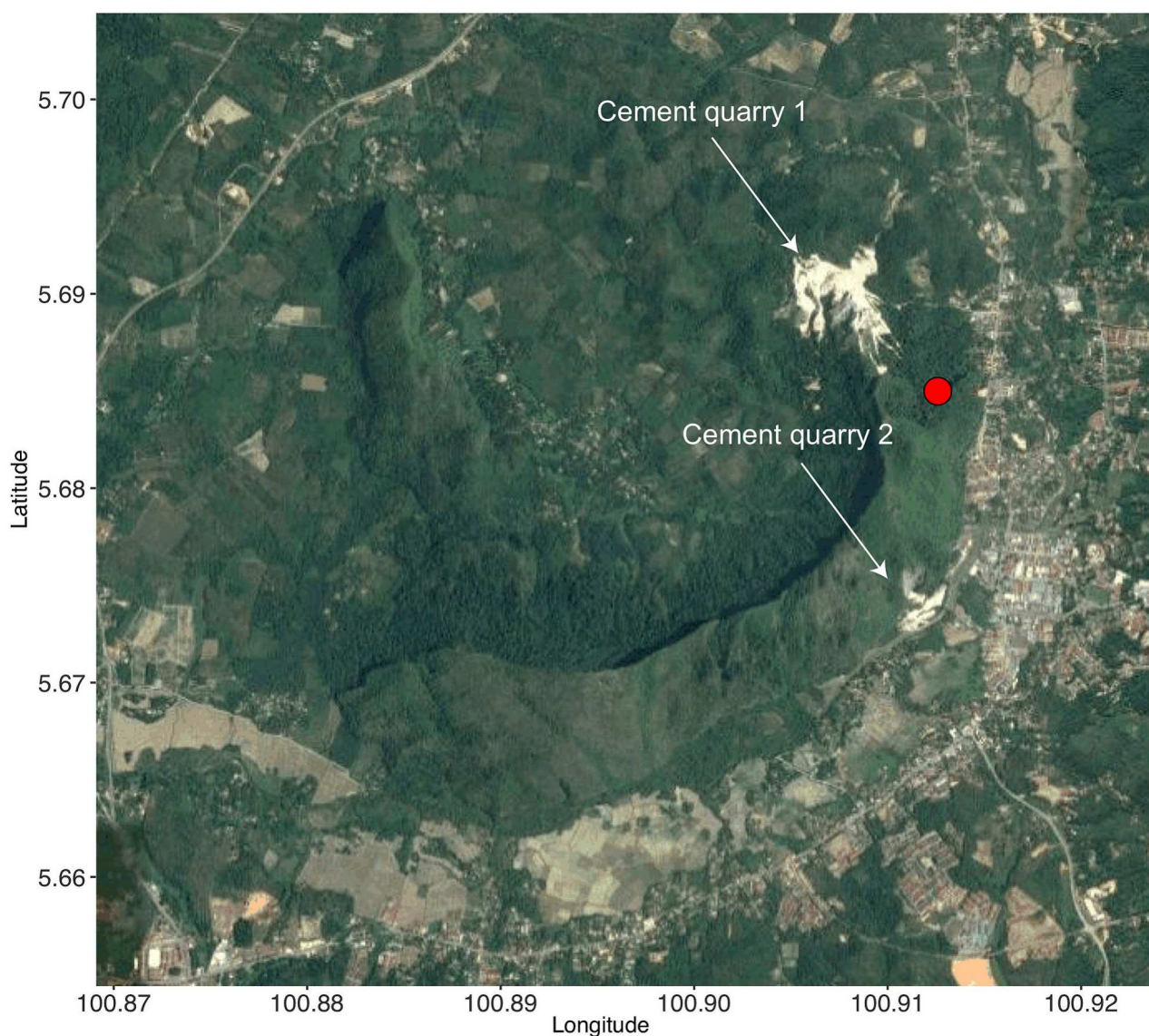


FIGURE 9. Type locality of *C. evanquahi* **sp. nov.** (the red circle) showing the extent of the limestone mining on both sides of the type locality. Landsat/Copernicus image was constructed using Imagery ©2018 CNES/ Airbus, DigitalGlobe, (Google), in the R package *ggmap* (Kahle & Wickham 2013).

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Appendix. Comparative material examined.

Cyrtodactylus australotitiwangsaensis Grismer, Wood, Quah, Anuar, Muin, Sumontha, Ahmad, Bauer, Wangkulangkul, Grismer & Pauwels: BYU 51804–51805, Jeriau Road, Fraser’s Hill, Pahang, Malaysia.

Cyrtodactylus evanquahi sp. nov. BYU 53435–37, Gunung Baling, Kedah, Malaysia.
Cyrtodactylus lenggongensis BYU 51802–51803, Lenggong, Perak, Malaysia.
Cyrtodactylus macrotuberculatus BYU 51869–51870, Kuala Nerang, Kedah, Malaysia.

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