A new insular species of the *Cyrtodactylus pulchellus* group (Reptilia, Gekkonidae) from Tarutao Island, southern Thailand revealed by morphological and genetic evidence

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Academic editor: Thomas Ziegler | Received 29 August 2021 | Accepted 4 October 2021 | Published 12 November 2021

http://zoobank.org/FDBBD099-29F0-4521-9B18-AF841BC88F41

Citation: Termprayoon K, Rujirawan A, Ampai N, Wood Jr PL, Aowphol A (2021) A new insular species of the *Cyrtodactylus pulchellus* group (Reptilia, Gekkonidae) from Tarutao Island, southern Thailand revealed by morphological and genetic evidence. ZooKeys 1070: 101–134. https://doi.org/10.3897/zookeys.1070.73659

Abstract

The bent-toed geckos of the *Cyrtodactylus pulchellus* group are widely distributed along the Thai-Malay Peninsula. Although taxonomic and phylogenetic studies of this species group have been continuously conducted, only some populations from Thailand have been included, resulting in hidden diversity within this group. In this study, we used morphological and molecular data to clarify the taxonomic status and describe a new population from Tarutao Island, Satun Province, southern Thailand. *Cyrtodactylus stellatus sp. nov.* can be distinguished from its congeners by the combination of the following morphological characters: body size; tuberculation; number of dark body bands, ventral scales, and femoroprecloacal pores in males; presence of precloacal pores in females; and scattered pattern on dorsum. Phylogenetic analyses of the mitochondrial ND2 gene recovered the new species as the sister species to *C. astrum*, with an uncorrected pairwise divergence of 9.78–12.37%. *Cyrtodactylus stellatus sp. nov.* is currently only known from Tarutao Island, Thailand. The discovery of this species suggests that the diversity within the *C. pulchellus* group remains underestimated and future exploration of unsurveyed areas are needed to further the understanding of this group and its geographic range.
Keywords
Cyrtodactylus astrum, Cyrtodactylus stellatus sp. nov., karst, morphology, phylogeny, taxonomy

Introduction

Bent-toed geckos in the genus Cyrtodactylus Gray, 1827 are geographically widespread and inhabit lowland (e.g., peat swamps, karst formations, and limestone forests) to mountainous regions (> 1,500 m a.s.l) of South Asia to Melanesia, ranging from India, Myanmar, Thailand, Vietnam, Cambodia, Malaysia, Java, Papua New Guinea to northern Australia (Wood et al. 2012; Nielsen and Oliver 2017; Pauwels et al. 2018; Purkayastha et al. 2020; Riyanto et al. 2020; Grismer et al. 2020a, 2021a, 2021b). This genus is the most diverse group of gekkotans, comprising 314 nominal species (Uetz et al. 2021). During the last two decades, the number of new species described in this genus has significantly increased with the exploration of unsurveyed karst formations (Luu et al. 2016; Nazarov et al. 2018; Davis et al. 2019; Grismer et al. 2018, 2020b). Moreover, genetic data has become a useful tool for taxonomic studies, revealing hidden diversity within the genus (Murdoch et al. 2019; Chomdej et al. 2020; Neang et al. 2020; Riyanto et al. 2020; Kamei and Mahony 2021; Liu and Rao 2021). Recent molecular studies have further supported the monophyly of this genus based on the most complete phylogenetic analysis to date, and have recognized 31 species groups (Grismer et al. 2021b).

One clade of particular interest is the Cyrtodactylus pulchellus group. This relatively diverse group is distributed along the Thai-Malay Peninsula and has high morphological and molecular variation. Cyrtodactylus pulchellus Gray, 1827 was thought to be a single wide-ranging species across their distributional range, but following an integrative approach many new species have been described (e.g., C. bintangrendah Grismer et al., 2012, C. langkawiensis Grismer et al., 2012, and C. sharkari Grismer et al., 2014). This species group has been recovered as monophyletic and currently contains 16 recognized species, based on multiple phylogenetic studies (Grismer et al. 2012, 2014, 2016; Quah et al. 2019; Wood et al. 2020; Termprayoon et al. 2021). This group is distributed from the south of the Isthmus of Kra, southern Thailand to southern Peninsular Malaysia and some of its offshore islands (Grismer and Ahmad 2008; Sumontha et al. 2012; Grismer et al. 2012, 2014, 2016; Quah et al. 2019; Wood et al. 2020; Termprayoon et al. 2021). During field surveys, specimens of the C. pulchellus group were collected from Tarutao Island, Satun Province, southern Thailand. Initially, these specimens were recognized as an insular population of C. astrum Grismer et al., 2012 due to their superficial resemblance in coloration pattern and dorsal tuberculation. A re-examination of these specimens showed morphological differences from its other congeners and mitochondrial DNA sequence data revealed corroborative evidence that the new population of Cyrtodactylus from Tarutao Island represents a distinct monophyletic lineage and is the sister species to C. astrum from the adjacent mainland. Based on integrative analyses, we considered this new Cyrtodactylus population from Tarutao Island as distinct and described it as a new species below.
Materials and methods

Sampling

Field surveys were conducted on Tarutao Island, Mueang Satun District, Satun Province, southern Thailand from November 2017 to November 2019 (Fig. 1). Specimens of the *C. pulchellus* group were collected from karst forest at night (1900–2200 h). Ecological data (air temperature and relative humidity) were recorded using a Kestrel 4000 Weather Meter, and habitat use of each specimen was noted. Geographical coordinates and elevation were recorded using a Garmin GPSMAP 64s. For molecular studies, liver tissue was taken from each euthanized specimen, individually preserved in 95% ethyl alcohol, and stored at -20 °C. Specimens were initially fixed in 10% formalin and later transferred into 70% ethyl alcohol for permanent storage. Voucher specimens were deposited in the herpetological collections of the Zoological Museum, Kasetsart University, Thailand (ZMKU). Additional preserved specimens were examined in the holdings of the Thailand Natural History Museum (THNHM), Thailand, and the La Sierra University Herpetological Collection (LSUHC), La Sierra University, Riverside, California, USA.

DNA extraction and PCR amplification

Total genomic DNA was extracted from ethanol-preserved liver tissue of five *Cyrtodactylus* specimens from Tarutao Island (Table 1) using a NucleoSpin Tissue Kit (Macherey-Nagel GmbH & Co. KG, Germany). A fragment of mitochondrial NADH dehydrogenase subunit 2 (ND2) gene and its flanking tRNAs was amplified using a double-stand Polymerase Chain Reaction (PCR) under the following conditions: initial denaturation at 94 °C for 4 min, followed by 35 cycles of denaturation at 94 °C for 30 sec, annealing at 48–52 °C for 30 sec, extension at 72 °C for 1 min 30 sec, and final extension at 72 °C for 7 min using the primers Metf6 (5' AAGCTTTCGGGCCATTACC 3'; Macey et al. 1997), and COIH (5' AGRGTGCCAATGTCTTTGTGRTT 3'; Macey et al. 1997). PCR products were purified using NucleoSpin Gel and PCR Clean-Up kit (Macherey-Nagel GmbH & Co. KG, Germany). Purified products were sequenced for both strands using the same amplifying primers on an ABI 3730XL DNA Sequencer (Applied Biosystems, CA, USA). Sequences were visually checked and aligned in Geneious R11 (Biomatters, Ltd, Auckland, New Zealand). The protein-coding region of ND2 was translated to amino acids and checked to confirm the lack of premature stop codons. All sequences were deposited in GenBank under the accession numbers OK094494–OK094503 (Table 1).

Phylogenetic analyses

Phylogenetic trees were reconstructed using two different methods, Maximum Likelihood (ML) and Bayesian Inference (BI). The best substitution model for each partition was determined using the Bayesian Information Criterion (BIC) under the
Figure 1. Map showing the type locality of *Cyrtodactylus stellatus* sp. nov. from Tarutao Island, Mueang Satun District, Satun Province, Thailand and the type localities of closely related species, *C. astrum*, *C. dayangbuntingensis*, *C. langkawiensis*, and *C. lekaguli*.

greedy search algorithm as implemented in PartitionFinder2 on XSEDE (Lanfear et al. 2016). The selected models for ML and BI were TIM+G for 1st and 2nd codon positions of ND2, TVM+I+G for 3rd codon position of ND2 and TRN+I+G for tRNAs. The ML analysis was performed in IQ-TREE web server v1.6.12 (Trifinopoulos et al. 2016) with 1,000 bootstrap replicates using ultrafast bootstrap approximation (Minh et al. 2013). The BI analysis was performed in MrBayes 3.2.6 on XSEDE (Ronquist et al. 2012) using the CIPRES Science Gateway v3.3 (Miller et al. 2010). Two simultaneous runs were performed with four chains per run, three hot and one cold under the default settings. The analysis was run for 10,000,000 generations and sampled every 1,000 generations from the Markov chain Monte Carlo (MCMC), with the first 25% of each run discarded as burn-in. Stationarity and the effective sample sizes (ESS) for all parameters were assessed in Tracer v1.7.1. (Rambaut et al. 2018). Nodes with ultrafast bootstrap support (UFB) of ≥ 95 and Bayesian posterior probabilities (BPP) of ≥ 0.95 were considered to be strongly supported (Huelsenbeck and Ronquist 2001; Wilcox et al. 2002; Minh et al. 2013). Intraspecific and interspecific uncorrected pairwise genetic divergences (*p*-distance) were calculated in MEGA X 10.0.5 using the pairwise deletion option for the treatment of gaps and missing data in the dataset (Kumar et al. 2018).
Table 1. Samples used in the molecular analyses, including their GenBank accession number (ND2), voucher number and locality. WM = West Malaysia; TH = Thailand.

| Species                  | Locality                                                                 | Museum No.     | GenBank Accession No. | Reference               |
|--------------------------|---------------------------------------------------------------------------|----------------|-----------------------|-------------------------|
| **Outgroup**             |                                                                           |                |                       |                         |
| Agamura persica          | Pakistan, Baluchistan Province, Makran District, Gwadar division          | FMNH 247474    | JX440515              | Wood et al. (2012)      |
| Hemidactylus frenatus    | Unknow                                                                   | NC 00155       | JX519468              | Grismer et al. (2012)   |
| Tropiocolotes steudneri  | captive                                                                   | JB 28          | JX440520              | Wood et al. (2012)      |
| C. elok                  | WM, Pahang, Fraser’s Hill, The Gap                                       | LSUHC 6471     | JQ889180              | Wood et al. (2012)      |
| C. hontreensis           | Vietnam, Kien Giang Province, Kien Hai District, Hon Tic Island          | LSUHC 8583     | JX440539              | Wood et al. (2012)      |
| C. intermedius           | TH, Chantaburi Province, Khao Khitchakut District                        | LSUHC 9513     | JX519469              | Grismer et al. (2012)   |
| C. interdigitalis        | Lao, Khammouan Province, Nakai District                                  | FMNH 255454    | JQ889181              | Wood et al. (2012)      |
| Cyrtodactylus sp.        | TH, Loei, Phu Rua                                                        | FMNH 265806    | JX519471              | Grismer et al. (2012)   |
| **Ingroup**              |                                                                           |                |                       |                         |
| C. astrum                | WM, Perlis, Guad Kelam                                                   | LSUHC 8068     | JX519481              | Grismer et al. (2012)   |
|                          | WM, Perlis, Guad Kelam                                                   | LSUHC 8067     | JX519478              | Grismer et al. (2012)   |
|                          | WM, Perlis, Guad Kelam                                                   | LSUHC 8068     | JX519479              | Grismer et al. (2012)   |
|                          | WM, Perlis, Guad Kelam                                                   | LSUHC 8069     | JX519480              | Grismer et al. (2012)   |
|                          | WM, Perlis, Kuala Perlis                                                 | LSUHC 8815     | JX519482              | Grismer et al. (2012)   |
|                          | WM, Perlis, Kuala Perlis                                                 | LSUHC 8816     | JX519483              | Grismer et al. (2012)   |
|                          | WM, Perlis, Kuala Perlis                                                 | LSUHC 8817     | JX519473              | Grismer et al. (2012)   |
|                          | WM, Perlis, State Park                                                   | LSUHC 9026     | JX519475              | Grismer et al. (2012)   |
|                          | WM, Perlis, State Park                                                   | LSUHC 9025     | JX519476              | Grismer et al. (2012)   |
| C. australotitiwangaensis| WM, Pahang, Fraser’s Hill                                                | LSUHC 8086     | JX519486              | Grismer et al. (2012)   |
|                          | WM, Pahang, Fraser’s Hill                                                | LSUHC 8087     | JX519485              | Grismer et al. (2012)   |
|                          | WM, Pahang, Genting Highlands                                            | LSUHC 6637     | JX519484              | Grismer et al. (2012)   |
| C. bintangrendah         | WM, Kedah, Bukit Mertajam                                                | LSUHC 10351    | MN125076              | Quah et al. (2019)      |
|                          | WM, Kedah, Bukit Mertajam                                                | LSUHC 10519    | MN125077              | Quah et al. (2019)      |
|                          | WM, Kedah, Bukit Mertajam                                                | LSUHC 10520    | MN125078              | Quah et al. (2019)      |
| C. bintangtinggi         | WM, Perak, Bukit Larat                                                   | LSUHC 8862     | JX519493              | Grismer et al. (2012)   |
|                          | WM, Perak, Bukit Larat                                                   | LSUHC 9006     | JX519494              | Grismer et al. (2012)   |
| C. dayangbuntingensis    | WM, Kedah, Dayang Bunting Island                                          | LSUHC 14355    | MN125090              | Quah et al. (2019)      |
|                          | WM, Kedah, Dayang Bunting Island                                          | LSUHC 14354    | MN125091              | Quah et al. (2019)      |
|                          | WM, Kedah, Dayang Bunting Island                                          | LSUHC 14355    | MN125092              | Quah et al. (2019)      |
| C. evanquahi             | WM, Kedah, Gunung Baling                                                  | BYU 53435      | MN586889              | Wood et al. (2020)      |
|                          | WM, Kedah, Gunung Baling                                                  | BYU 53436      | MN586890              | Wood et al. (2020)      |
|                          | WM, Kedah, Gunung Baling                                                  | BYU 53437      | MN586891              | Wood et al. (2020)      |
| C. bidupelamamya         | WM, Kelantan, Felda Chiku 7                                              | LSUHC 12161    | KX011415              | Grismer et al. (2016)   |
|                          | WM, Kelantan, Felda Chiku 7                                              | LSUHC 12162    | KX011416              | Grismer et al. (2016)   |
|                          | WM, Kelantan, Felda Chiku 7                                              | LSUHC 12163    | KX011417              | Grismer et al. (2016)   |
|                          | WM, Kelantan, Felda Chiku 7                                              | LSUHC 12173    | KX011420              | Grismer et al. (2016)   |
| Species          | Locality                                      | Museum No.          | GenBank Accession No. | Reference                  |
|------------------|-----------------------------------------------|---------------------|-----------------------|----------------------------|
| *C. jelawangensis* | WM, Gunung Stong, Kelantan                   | LSUHC 11060         | KJ659850              | Grismer et al. (2014)      |
|                  | WM, Gunung Stong, Kelantan                   | LSUHC 11062 (holotype) | KJ659852              | Grismer et al. (2014)      |
|                  | WM, Kelantan, Gunung Stong                   | LSUHC 11061 (paratype) | KJ659851              | Grismer et al. (2014)      |
| *C. langkawiensis* | WM, Kedah, Pulau Langkawi, Wat Wanaram       | LSUHC 9120          | JX519502              | Grismer et al. (2012)      |
|                  | WM, Kedah, Pulau Langkawi, Wat Wanaram       | LSUHC 9122          | JX519501              | Grismer et al. (2012)      |
|                  | WM, Kedah, Pulau Langkawi, Wat Wanaram       | LSUHC 9123          | JX519500              | Grismer et al. (2012)      |
|                  | WM, Kedah, Pulau Langkawi, Wat Wanaram       | LSUHC 9124 (paratype) | JX519499              | Grismer et al. (2012)      |
|                  | WM, Kedah, Pulau Langkawi, Wat Wanaram       | LSUHC 9125          | JX519496              | Grismer et al. (2012)      |
|                  | WM, Kedah, Pulau Langkawi, Wat Wanaram       | LSUHC 9434          | JX519498              | Grismer et al. (2012)      |
|                  | WM, Kedah, Pulau Langkawi, Wat Wanaram       | LSUHC 9435          | JX519495              | Grismer et al. (2012)      |
|                  | WM, Kedah, Pulau Langkawi, Wat Wanaram       | LSUHC 9437          | JX519497              | Grismer et al. (2012)      |
|                  | WM, Kedah, Pulau Langkawi, Wat Wanaram       | LSUHC 14347         | MN125093              | Quah et al. (2019)         |
|                  | WM, Kedah, Pulau Langkawi, Wat Wanaram       | LSUHC 14348         | MN125094              | Quah et al. (2019)         |
| *C. lekaguli*    | TH, Phang-nga Province, Mueang Phang-nga District | ZMKUR 00720         | KX011425              | Grismer et al. (2016)      |
|                  | TH, Phang-nga Province, Mueang Phang-nga District | ZMKUR 00721         | KX011426              | Grismer et al. (2016)      |
|                  | TH, Phang-nga Province, Mueang Phang-nga District | ZMKUR 00722         | KX011427              | Grismer et al. (2016)      |
|                  | TH, Phang-nga Province, Mueang Phang-nga District | ZMKUR 00723         | KX011428              | Grismer et al. (2016)      |
|                  | TH, Trang Province, Na Yong District          | ZMKUR R 00918       | OK094494              | This study                 |
|                  | TH, Trang Province, Na Yong District          | ZMKUR R 00919       | OK094495              | This study                 |
|                  | TH, Trang Province, Na Yong District          | ZMKUR R 00920       | OK094496              | This study                 |
|                  | TH, Trang Province, Na Yong District          | ZMKUR R 00921       | OK094497              | This study                 |
|                  | TH, Trang Province, Na Yong District          | ZMKUR R 00922       | OK094498              | This study                 |
| *C. lenggongensis* | WM, Perak, Lenggong Valley                   | LSUHC 9974 (holotype) | JX519490              | Grismer et al. (2012)      |
|                  | WM, Perak, Lenggong Valley                   | LSUHC 9975 (paratype) | JX519488              | Grismer et al. (2012)      |
|                  | WM, Perak, Lenggong Valley                   | LSUHC 9976 (paratype) | JX519489              | Grismer et al. (2012)      |
|                  | WM, Perak, Lenggong Valley                   | LSUHC 9977 (paratype) | JX519491              | Grismer et al. (2012)      |
| *C. macrotuberculatus* | TH, Phuket Province, Kathu District, Kathu Waterfall | ZMKUR R 00890       | MW809301              | Termprayoon et al. (2021)  |
|                  | TH, Phuket Province, Kathu District, Kathu Waterfall | ZMKUR R 00891       | MW809302              | Termprayoon et al. (2021)  |
|                  | TH, Phuket Province, Thalang District, Thep Krasatti | ZMKUR R 00894       | MW809305              | Termprayoon et al. (2021)  |
|                  | TH, Phuket Province, Thalang District, Thep Krasatti | ZMKUR R 00895       | MW809306              | Termprayoon et al. (2021)  |
|                  | TH, Phuket Province, Thalang District, Thep Krasatti | ZMKUR R 00896       | MW809307              | Termprayoon et al. (2021)  |
|                  | TH, Satun Province, Mueang Satun District, Adang Island | ZMKUR R 00875       | MW809295              | Termprayoon et al. (2021)  |
|                  | TH, Satun Province, Mueang Satun District, Rawi Island | ZMKUR R 00883       | MW809299              | Termprayoon et al. (2021)  |
|                  | TH, Satun Province, Mueang Satun District, Rawi Island | ZMKUR R 00887       | MW809300              | Termprayoon et al. (2021)  |
|                  | TH, Songkhla Province, Hat Yai District, Thung Tam Sao | ZMKUR R 00876       | MW809296              | Termprayoon et al. (2021)  |
|                  | TH, Songkhla Province, Hat Yai District, Thung Tam Sao | ZMKUR R 00887       | MW809277              | Termprayoon et al. (2021)  |
|                  | TH, Songkhla Province, Hat Yai District, Thung Tam Sao | ZMKUR R 00878       | MW809298              | Termprayoon et al. (2021)  |
|                  | WM, Kedah, Hutan Lipur Sungai Tupah           | LSUHC 9671          | JX519510              | Grismer et al. (2012)      |
|                  | WM, Kedah, Hutan Lipur Sungai Tupah           | LSUHC 9672          | JX519511              | Grismer et al. (2012)      |
|                  | WM, Kedah, Hutan Lipur Sungai Tupah           | LSUHC 9693          | JX519517              | Grismer et al. (2012)      |
|                  | WM, Kedah, Pulau Langkawi, Gunung Machinschang | LSUHC 9448          | JX519507              | Grismer et al. (2012)      |
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| Species          | Locality                                      | Museum No.  | GenBank Accession No. | Reference      |
|------------------|-----------------------------------------------|-------------|-----------------------|---------------|
| C. macrotuberculatus | WM, Kedah, Pulau Langkawi, Gunung Raya     | LSUHC 9428  | JX519506              | Grismer et al. (2012) |
|                  | WM, Kedah, Pulau Langkawi, Lubuk Sembilang | LSUHC 6829  | JX519505              | Grismer et al. (2012) |
|                  | WM, Perlis, Bukit Cita, Langkawi             | LSUHC 10037 | JX519519              | Grismer et al. (2012) |
|                  | WM, Perlis, Bukit Cita, Langkawi             | LSUHC 10038 | JX519518              | Grismer et al. (2012) |
| C. pulchellus    | WM, Penang, Pulau Pinang, Empangan Air Itam | LSUHC 6668  | JX519523              | Grismer et al. (2012) |
|                  | WM, Penang, Pulau Pinang, Mon gate Trail     | LSUHC 6727  | JX519526              | Grismer et al. (2012) |
|                  | WM, Penang, Pulau Pinang, Mon gate Trail     | LSUHC 6728  | JX519525              | Grismer et al. (2012) |
|                  | WM, Penang, Pulau Pinang, Mon gate Trail     | LSUHC 6729  | JX519528              | Grismer et al. (2012) |
| C. sbarkari      | WM, Pahang, Metapoh, Gua Gunting             | LSUHC 11022 | KJ659853              | Grismer et al. (2014) |
| Cyrtodactylus stellatus sp. nov. | TH, Satun Province, Muang Satun District, Tarutao Island | ZMKU R 00903 (holotype) | OK094499 | This study |
|                  | TH, Satun Province, Muang Satun District, Tarutao Island | ZMKU R 00905 (paratype) | OK094500 | This study |
|                  | TH, Satun Province, Muang Satun District, Tarutao Island | ZMKU R 00906 (paratype) | OK094501 | This study |
|                  | TH, Satun Province, Muang Satun District, Tarutao Island | ZMKU R 00907 (paratype) | OK094502 | This study |
|                  | TH, Satun Province, Muang Satun District, Tarutao Island | ZMKU R 00908 (paratype) | OK094503 | This study |
| C. timur        | WM, Gunung Tebu, Terengganu                  | LSUHC 10886 | KJ639834              | Grismer et al. (2014) |
|                  | WM, Gunung Tebu, Terengganu                  | LSUHC 11183 | KJ639835              | Grismer et al. (2014) |
|                  | WM, Gunung Tebu, Terengganu                  | LSUHC 11184 | KJ639856              | Grismer et al. (2014) |
|                  | WM, Gunung Tebu, Terengganu                  | LSUHC 11185 | KJ639857              | Grismer et al. (2014) |
| C. trilatofasciatus | WM, Pahang, Cameron Highlands               | LSUHC 10064 | JX519529              | Grismer et al. (2012) |
|                  | WM, Pahang, Cameron Highlands               | LSUHC 10065 | JX519530              | Grismer et al. (2012) |
|                  | WM, Pahang, Cameron Highlands               | LSUHC 10066 | JX519531              | Grismer et al. (2012) |

Morphology

The morphological characters and their definition used in this study were modified from previous studies of the C. pulchellus group (Grismer and Ahmad 2008; Grismer et al. 2012, 2014, 2016; Quah et al. 2019; Wood et al. 2020), and abbreviations are derived from Grismer et al. (2018, 2020c). All mensural characters were taken with digital calipers to the nearest 0.01 mm on the left side, while scale counts were made on both sides when possible. Scalation and external morphology were evaluated under a Nikon SMZ745 dissecting microscope. Measurement and meristic characters are shown in Table 2, and external morphological characters evaluated are described below.

External morphological characters examined in the C. pulchellus group were the degree of body tuberculation, weak tuberculation referring to dorsal body tubercles that are low and rounded whereas prominent tuberculation refer to tubercles that are raise and keeled; the presence or absence of tubercles on the dorsal and ventral surface of the forearms; the presence or absence of tubercles in the gular region, throat, and ventrolateral body folds; the width of the dark body bands relative to the width of the interspace between the bands; the presence or absence of dark pigmentation infused in the white caudal bands of adults; the presence or absence of a precloacal depression or groove; the presence or absence of scattered white/yellow tubercles on the dorsum; and
the presence or absence of white tail tip on the posterior portion of the original tail in hatchlings and juveniles. Color pattern characteristics were taken from digital images of live specimens in both sexes and of all possible age classes prior to preservation.

**Statistical analyses**

All analyses were performed using the base statistical software in R v3.6.1 (R Core Team 2019). To eliminate bias of sexual dimorphism, adult males and females were analyzed separately. Morphological analyses were run on 15 mensural characters. Tail length (TL) was not included due to their different condition (e.g., original, regenerated, and broken). All measurements of each species were size-adjusted in order to remove potential effects of allometry using the following allometric equation: $X_{\text{adj}} = \log[X ± \beta(SVL ± SVL_{\text{mean}})]$, where $X_{\text{adj}}$ = adjusted value; $X$ = measured value; $\beta$ = unstandardized regression coefficient for each OTU; SVL = measured snout–vent length; SVL_{\text{mean}}
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Morphological measurements of *C. astrum*, *C. dayangbuntingensis* Quah et al., 2019, *C. langkawiensis* and *C. lekaguli* Grismer et al., 2012 were obtained from their original descriptions (Grismer et al. 2012; Quah et al. 2019). Additional preserved specimens of *C. astrum* (from Malaysia) and *C. lekaguli* (topotypes) were examined and included in the analyses (Appendix I). Morphometric adjustments were conducted separately on each species and then concatenated into a single data frame to ensure there was no interspecific conflation of variation (Reist 1985; McCoy et al. 2006). Specimens were assigned into five groups (= species) based on phylogenetic analyses which are *Cyrtodactylus* Tarutao Island samples (*N* = 5 males, 5 females), *C. astrum* (*N* = 5 males, 3 females), *C. dayangbuntingensis* (*N* = 2 males), *C. langkawiensis* (*N* = 2 males, 4 females), and *C. lekaguli* (*N* = 7 males, 9 females).

Principal components analysis (PCA) was performed on size-adjusted data for each sex using FactoMineR package (Lê et al. 2008) and were visualized with the R package ggplot2 (Wickham 2016). For univariate analysis, Shapiro-Wilk test was used to evaluate data to meet normality assumptions (*p* ≥ 0.05) and Levene’s test for testing for equality of variance (*p* ≥ 0.05). Morphological differences were compared using Analysis of variance (ANOVA) or Kruskal-Wallis test. ANOVA was conducted on normally distributed data with homogeneous variances and were subjected to Tukey HSD post hoc tests (Tukey’s test) to determine which characters had statistically different mean values for which pairs of species if ANOVA had a *p*-value of less than 0.05. Kruskal-Wallis test was performed on non-normally distributed data and followed by a post hoc Dunn’s multiple comparison (Dunn’s test). Due to limited sample sizes, *C. dayangbuntingensis* (*N* = 2 males) and males of *C. langkawiensis* (*N* = 2 males) were excluded from the univariate analysis.

**Results**

**Phylogenetic relationships**

The aligned matrix contained 1,429 mtDNA characters from 93 individuals of the *C. pulchellus* group and nine individuals of outgroup species (Table 1). The standard deviation of split frequencies among the two simultaneous BI runs was 0.002676, and the ESS values of all parameters were greater than or equal to 2,494.4. The maximum likelihood value of the best ML tree was lnL = -15,115.412.

The topologies of ML and BI analyses were largely concordant. The ML and BI analyses recovered the *C. pulchellus* group as monophyletic with strong support (≥ 95 UFB, ≥ 0.95 BPP) which is comprised of two major clades referred to as Clades A and B (Figs 2, 3). The *Cyrtodactylus* specimens from Tarutao Island represented a strongly supported monophyletic group (≥ 95 UFB, ≥ 0.95 BPP) within Clade A containing
Figure 2. The Maximum Likelihood tree of the *Cyrtodactylus pulchellus* group based on 1,429 bp of the ND2 gene and flanking tRNAs. Support values on branches are ultrafast bootstrap (UFB). Black circles represent nodes strongly supported (UFB ≥ 95).
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**Figure 3.** The Bayesian consensus tree of the *Cyrtodactylus pulchellus* group based on 1,429 bp of the ND2 gene and flanking tRNAs. Support values on branches are Bayesian posterior probabilities (BPP). Black circles represent nodes strongly supported (BPP ≥ 0.95).
C. astrum, C. dayangbuntingensis, C. langkawiensis, and C. lekaguli. The Tarutao Island samples were weakly recovered as a sister species to C. astrum from the adjacent Peninsular Malaysian mainland (64 UFB, 0.82 BPP). Clade B is composed of all other species including C. australotitiwangsaensis Grismer et al., 2012, C. bintangrendah, C. bintangtinggi Grismer et al., 2012, C. evanquahi Wood et al., 2020, C. hidupselamanya Grismer et al., 2016, C. jelawangensis Grismer et al., 2014, C. lenggongensis Grismer et al., 2016, C. macrotuberculatus Grismer and Ahmad, 2008, C. pulchellus, C. sharkari, C. timur Grismer et al., 2014 and C. trilatofasciatus Grismer et al., 2012. Uncorrected pairwise genetic divergences (p-distance) range from 0.00–1.17% within the Tarutao Island specimens and 8.46–12.37% between the Tarutao Island specimens and other species in Clade A (Table 3).

Morphology

The PCA was conducted on members from Clade A. The plots on the first two PC axes showed that the Tarutao Island specimens are clustered separately from other species in both sexes (Fig. 4). In male, the first two principal components explained 66.95% of the morphological variation (Table 4). The first principal component (PC1) accounted for 45.88% of the variation and was heavily loaded on FL adj, TBL adj, HW adj, HD adj, EE adj, ES adj, and EN adj; and the PC2 accounted for 21.07% of the variation and was heavily loaded on TW adj, AG adj, IO adj, and EL adj. PC analysis of females accounted for 56.74% of the variation in first two components. The PC1 accounted for 34.81% of the variation and was heavily loaded on TBL adj, HW adj, EE adj, ES adj, and EN adj; and the PC2 accounted for 21.93% of the variation and was heavily loaded on TW adj, IO adj and IN adj.

The univariate analyses (ANOVA or Kruskal-Wallis test) were significantly different (p < 0.05) in most morphological characters among the members of Clade A (except C. dayangbuntingensis). In the comparison of adult males, the Tarutao Island population was significantly different from C. astrum and C. lekaguli in twelve morphological characters (ANOVA or Kruskal-Wallis test, p < 0.001–0.006) except AG adj, ED adj, and IN adj (ANOVA or Kruskal-Wallis test, p = 0.051–0.122). Subsequent Tukey’s test or Dunn’s test demonstrated that Tarutao Island population was significantly different from C. astrum in SVL adj, FL adj, TBL adj, HL adj, HW adj, HD adj, EE adj, ES adj, and EN adj; and C. lekaguli in SVL adj, TW adj, FL adj, HL adj, HW adj, HD adj, EE adj, ES adj, IO adj, and EL adj. In adult females, the Tarutao Island population was significantly different

| Table 3. Percentage uncorrected pairwise genetic divergence (p-distances) of Cyrtodactylus stellatus sp. nov. and closely related species (Clade A) calculated from 1,429 base pairs of mitochondrial ND2 gene and flanking tRNAs. |
|---|---|---|---|---|---|---|
| Species | N | 1 | 2 | 3 | 4 | 5 |
| --- | --- | --- | --- | --- | --- | --- |
| 1. Cyrtodactylus stellatus sp. nov. | 5 | 0.48 (0.00–1.17) | | | | |
| 2. C. astrum | 12 | 10.50 (9.78–12.37) | 1.37 (0.00–2.97) | | | |
| 3. C. dayangbuntingensis | 3 | 9.90 (9.56–10.88) | 9.86 (9.51–11.21) | | 0.14 (0.07–0.22) | |
| 4. C. langkawiensis | 10 | 10.49 (9.86–11.69) | 10.19 (9.71–11.59) | 7.62 (7.39–7.83) | 0.42 (0.00–0.69) | |
| 5. C. lekaguli | 9 | 9.33 (8.46–10.80) | 9.94 (8.98–11.77) | 8.58 (8.00–9.59) | 9.39 (8.42–10.54) | 2.30 (0.00–4.27) |
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**Figure 4.** Plots of the first two principal components of *Cyrtodactylus stellatus* sp. nov. and the closely related species in Clade A based on adjusted mensural characters of A males and B females. The letters in the scatter plots refer to holotype (= H), paratype (= P), and topotype (= T).
from *C. astrum*, *C. langkawiensis* and *C. lekaguli* in nine characters (ANOVA, \( p < 0.001–0.007 \)) except SVL_{adj}, TW_{adj}, AG_{adj}, HL_{adj}, ED_{adj} and EL_{adj} (ANOVA or Kruskal-Wallis test, \( p = 0.052–0.631 \)). Subsequent Tukey’s test revealed that the Tarutao Island population was significantly different from *C. astrum* in FL_{adj}, TBL_{adj}, HW_{adj}, HD_{adj}, EE_{adj}, ES_{adj} and EN_{adj}; *C. langkawiensis* in HW_{adj}, ES_{adj}, EN_{adj} and IN_{adj}; and *C. lekaguli* in HD_{adj}, IO_{adj} and IN_{adj}.

Summary pairwise results (Tukey’s test or Dunn’s test) of significant differences in morphological characters for adult males and females of Clade A are shown in Table 5. Additional differences in meristic characters and coloration are discussed in the comparison sections.

Table 4. Summary statistics and factor loadings of the first three principal components (PC) of 15 mensural characters for males and females of *Cyrtodactylus stellatus* sp. nov. and its closely related species including *C. astrum*, *C. dayangbuntingensis*, *C. langkawiensis*, and *C. lekaguli*. Bold texts indicate high loadings.

| Characters | Males | | | Females | | |
|---|---|---|---|---|---|---|
| | PC1 | PC2 | PC3 | PC1 | PC2 | PC3 |
| SVL_{adj} | 0.660 | -0.284 | 0.293 | 0.374 | -0.097 | -0.127 |
| TW_{adj} | 0.436 | 0.795 | -0.073 | 0.380 | 0.845 | 0.194 |
| FL_{adj} | 0.855 | -0.228 | -0.051 | 0.693 | 0.111 | 0.003 |
| TBL_{adj} | 0.951 | 0.098 | -0.032 | 0.881 | 0.181 | 0.102 |
| AG_{adj} | -0.261 | -0.728 | 0.364 | -0.030 | 0.157 | 0.824 |
| HL_{adj} | 0.459 | -0.508 | -0.560 | 0.532 | -0.194 | 0.537 |
| HW_{adj} | 0.943 | -0.168 | 0.177 | 0.785 | -0.350 | -0.197 |
| HD_{adj} | 0.838 | -0.325 | 0.188 | 0.526 | -0.647 | 0.170 |
| ED_{adj} | 0.552 | -0.195 | -0.491 | 0.137 | -0.086 | 0.612 |
| EE_{adj} | 0.829 | -0.171 | 0.194 | 0.755 | -0.410 | 0.266 |
| ES_{adj} | 0.932 | 0.113 | 0.054 | 0.900 | -0.078 | -0.271 |
| EN_{adj} | 0.875 | 0.246 | 0.142 | 0.922 | 0.122 | -0.263 |
| IO_{adj} | 0.143 | 0.850 | 0.435 | 0.361 | 0.854 | 0.033 |
| EL_{adj} | 0.303 | 0.770 | -0.417 | 0.343 | 0.690 | -0.298 |
| IN_{adj} | -0.105 | 0.093 | 0.560 | -0.089 | 0.719 | 0.238 |
| Eigenvalue | 6.882 | 3.161 | 1.587 | 5.222 | 3.289 | 1.835 |
| Percentage of variance | 45.879 | 21.073 | 10.583 | 34.813 | 21.928 | 12.235 |
| Cumulative proportion | 45.879 | 66.952 | 77.533 | 34.813 | 56.741 | 68.976 |

Table 5. Summary pairwise results of statistically significant characters (Tukey’s test; \( p < 0.05 \)) from 15 mensural characters for males and females of *Cyrtodactylus stellatus* sp. nov. and closely related species (Clade A). Abbreviations are listed in Table 2. Key: * tested by Dunn’s test; M = male; F = female.

| Characters | Males | | | Females | | |
|---|---|---|---|---|---|---|
| | Cyrtodactylus stellatus sp. nov. | | | *C. astrum* | | |
| | M | F | M | F | M | F |
| Cyrtodactylus stellatus sp. nov. | M | – | – | – | – | – |
| | F | – | – | – | – | – |
| *C. astrum* | M | SVL, FL, TBL, HL, HW, HD, EE, ES*, EN | – | – | – | – |
| | F | FL, TBL, HW, HD, EE, ES, EN | – | – | – | – |
| *C. langkawiensis* | M | – | – | – | – | – |
| | F | HW, ES, EN, IN | – | HW, IN | – | – |
| *C. lekaguli* | M | SVL, TW, FL, HL, HW, HD, EE, ES*, IO, EL | – | TW, FL, TBL, HW, EN, IO, EL | – | – |
| | F | HD, IO, IN | – | FL, TBL, HW, ES, EN, IO, EL | – | ES |
Taxonomic hypotheses

_Cyrtodactylus_ samples from Tarutao Island, Mueang Satun District, Satun Province differed from its congeners in mtDNA, morphometrics and morphological comparisons. These corroborated lines of evidence provide sufficient support to warrant them specific species status and is described as new below.

Taxonomy

_Cyrtodactylus stellatus_ sp. nov.
http://zoobank.org/F2AF3CB9-F0FE-4749-9785-F57C7CAC021C
Figures 5–11
Stellar Bent-toed Gecko

Holotype. Adult male (ZMKU R 00905, Figs 5–7) collected from Thailand, Satun Province, Mueang Satun District, Tarutao National Park, Tarutao Island, Pha (= cliff) Toe Boo (6°42.185’N; 99°38.895’E; 2 m a.s.l.), on 11 March 2019 by Korkhwan Termprayoon, Anchalee Aowphol, Attapol Rujirawan, Natee Ampai and Siriporn Yodthong.

Paratypes (Figs 8–9). Two adult males (ZMKU R 00906–00907) and two adult females (ZMKU R 00908–00909), same data as holotype. One adult female (ZMKU R 00913) same data as holotype except collected on 12 May 2019. One adult male (ZMKU R 00903) and two adult females (ZMKU R 00899–00900), same data as holotype, except collected on 5 November 2017 by Korkhwan Termprayoon, Attapol Rujirawan, Natee Ampai, and Siriporn Yodthong. One adult male (ZMKU R 00915) collected from Thailand, Satun Province, Mueang Satun District, Tarutao National Park, Tarutao Island, Tarutao Outcrop (6°41.617’N; 99°38.796’E; 3 m a.s.l.) on 12 March 2019 by Korkhwan Termprayoon, Anchalee Aowphol, Attapol Rujirawan, Natee Ampai and Siriporn Yodthong.

Referred specimens. ZMKU R 00901 (immature male) and ZMKU R 00902 (immature female) same data as holotype except collected on 5 November 2017 by Korkhwan Termprayoon, Attapol Rujirawan, Natee Ampai, and Siriporn Yodthong. ZMKU R 00904 (immature male) same data as holotype, except collected on 5 April 2018. ZMKU R 00910–00911 (two immature males) and ZMKU R 00912 (immature female) same data as holotype. ZMKU R 00914 (immature female) same data as holotype except collected on 12 May 2019. ZMKU R 00916 (immature male) and ZMKU R 00917 (juvenile) collected from Thailand, Satun Province, Mueang Satun District, Tarutao National Park, Tarutao Island, Tarutao Outcrop (6°41.617’N; 99°38.796’E; 3 m a.s.l.) on 12 March 2019 by Korkhwan Termprayoon, Anchalee Aowphol, Attapol Rujirawan, Natee Ampai and Siriporn Yodthong.

Diagnosis. _Cyrtodactylus stellatus_ sp. nov. can be distinguished from all other species of the _C. pulchellus_ group by the combination of the following characters: (1) SVL 86.3–95.9 mm in adult males, 86.6–96.1 mm in adult females; (2) 12–15 supralabial and 10–13 infralabial scales; (3) weak tuberculation on body; (4) no tubercles on ven-
tral surfaces of forelimbs, gular region, or in ventrolateral body folds; (5) 32–47 para-vertebral tubercles; (6) 19–23 longitudinal rows of dorsal tubercles; (7) 32–40 rows of ventral scales; (8) 20–23 subdigital lamellae on the dorsal tubercles; (9) 24–29 femoropre-cloacal pores in adult males; (10) precloacal pores present in adult females; (11) deep precloacal groove in males; (12) dorsum bearing a scattered pattern of white tubercles; (13) four dark dorsal body bands; (14) 10–12 dark caudal bands on original tail; (15) white caudal bands in adults heavily infused with dark pigmentation; and (16) posterior portion of tail in hatchlings and juveniles white.

**Description of holotype.** Adult male SVL 94.2 mm; head large, moderate in length (HL/SVL 0.29) and wide (HW/HL 0.61), somewhat flattened (HD/HL 0.38), distinct from neck, and triangular in dorsal profile; lores concave anteriorly, inflated posteriorly; frontal and prefrontal regions deeply concave; canthus rostralis rounded anteriorly; snout elongate (ES/HL 0.39), rounded in dorsal profile, laterally constricted; eye large (ED/HL 0.25); ear opening elliptical, moderate in size (EL/HL 0.09), obliquely oriented; eye to ear distance slightly greater than diameter of eye; rostral rectangular, divided dorsally by an inverted Y-shaped furrow, bordered posteriorly by left and right supranasals and internasal, bordered laterally by first supralabials; external nares bordered anteriorly by rostral, dorsally by a large anterior supranasal, posteriorly by two postnasals, ventrally by first supralabial; 13/14 (left/right) rectangular supralabials extending to just beyond upturn of labial margin, tapering abruptly below midpoint of eye; second supralabial slightly larger than first; 11/11 infralabials tapering in size posteriorly; scales of rostrum and lores slightly raised, larger than granular scales on top of head and occiput, those on posterior portion of canthus rostralis slightly larger; scales on occiput intermixed with small tubercles; large, boney frontal ridges bordering orbit confluent with bone, V-shaped, transverse, parietal ridge; dorsal superciliaries elongate, smooth, largest anteriorly; mental triangular, bordered laterally by first infralabials and posteriorly by left and right, trapezoidal postmentals which contact medially for 50% of their length; one row of slightly enlarged, elongate sublabials extending posteriorly to the seventh (left) and fifth (right) infralabials; small, granular, gular scales grading posteriorly into larger, flat, smooth, imbricate, pectoral and ventral scales.

Body relatively short (AG/SVL 0.46) with well-defined, non-tuberculate, ventrolateral folds; dorsal scales small, granular, interspersed with low, regularly arranged, weakly keeled tubercles, smaller intervening tubercles occasionally present; tubercles extend from occiput to caudal constriction, absent from regenerated portion of tail; tubercles on occiput and nape relatively small, those on body largest; approximately 21 longitudinal rows of tubercles at midbody; 36 paravertebral tubercles; 33 flat imbricate ventral scales between ventrolateral body folds; ventral scales larger than dorsal scales; precloacal scales large, smooth; deep precloacal groove.

Forelimbs moderate in stature, relatively short (FL/SVL 0.16); scales on dorsal surfaces of forelimbs granular intermixed with larger tubercles; scales of ventral surface of forearm flat, subimbricate, tubercles absent; palmar scales small, weakly rounded; digits well-developed, inflected at basal, interphalangeal joints; subdigital lamellae rec-
A new insular species of the *Cyrtodactylus pulchellus* group

Figure 5. Adult male holotype of *Cyrtodactylus stellatus* sp. nov. (ZMKU R 00905) from Tarutao Island, Satun Province. A specimen in life and immediately before preservative; B dorsal and C ventral views.
tangular proximal to joint inflection, only slightly expanded distal to inflection; digits narrower distal to joints; claws well-developed, sheathed by a dorsal and ventral scale; the fifth digit broken on left forearm; hind limbs more robust than forelimbs, moderate in length (TBL/SVL 0.19), larger tubercles on dorsal surface of legs separated by smaller juxtaposed scales; ventral scales of thigh flat, smooth, imbricate, larger than dorsal granular scales; ventral, tibial scales flat, smooth, imbricate; a single row of 34 enlarged femoroprecloacal scales extend nearly from knee to knee through precloacal region where they are continuous with enlarged, pore-bearing precloacal scales; 27 separated pore-bearing femoroprecloacal scales (Fig. 10A), forming an inverted T bearing a deep, precloacal groove; six pore-bearing scales bordering groove (three on each side
A new insular species of the *Cyrtodactylus pulchellus* group

**Figure 7.** Male holotype of *Cyrtodactylus stellatus* sp. nov. (ZMKU R 00905) in preservation. **A** dorsal and **B** ventral views **C** tuberculation on dorsum, and **D** ventral view of left foot.
of groove); 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 weakly rounded to flat; digits well developed, inflected at basal, interphalangeal joints; subdigital lamellae proximal to joint inflection rectangular, only slightly expanded distal to inflection; digits narrower distal to joints; claws well-developed, sheathed by a dorsal and ventral scale; 21/22 subdigital lamellae on the 4th toe.

Tail 94.8 mm in length, completely regenerated, 9.2 mm in width at base, tapering to a point; regenerated tail covered with small, smooth, rectangular scales dorsally; base of tail bearing hemipenial swellings; one row of 4/4 medium-sized postcloacal tubercles on each hemipenial swelling; postcloacaal scales smooth, flat, large, imbricate.

**Coloration in life (Fig. 5).** Dorsal ground color of head, body, and limbs light-brownish grey; a wide, dark-brown nuchal band bordered anteriorly and posteriorly by thin, creamy-white lines bearing tubercles that extend from the posterior margin of one eye to the posterior margin of other eye; the color of nuchal band and creamy-white lines is faded above left ear opening; four dark-brown body bands between nuchal loop and hind limb insertions that are also bordered anteriorly and posteriorly by thin, creamy-white lines bearing tubercles, first band terminates at shoulders, second and third bands terminate just dorsal of ventrolateral folds, the fourth band terminates at

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**Figure 8.** Male paratypes of *Cyrtodactylus stellatus* sp. nov. in preservation. **A** dorsal and **B** ventral views; from left to right: ZMKU R 00903, ZMKU R 00906, ZMKU R 00907, and ZMKU R 00915.
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**Figure 9.** Female paratypes of *Cyrtodactylus stellatus* sp. nov. in preservation. A dorsal and B ventral views; from left to right: ZMKU R 00899, ZMKU R 00900, ZMKU R 00908, ZMKU R 00909, and ZMKU R 00913.

femurs; dark body bands slightly larger than light-colored interspaces; creamy-white to light-yellow tubercles scattered on dorsal surfaces of nape, body, and limbs; one additional dark-brown band posterior to hind limbs; light-brown regenerated tail, bearing yellowish pigment on some scales; ventral surfaces of head smudged with brown; abdomen and limbs beige, with slightly darker, lateral regions.

**Coloration in preservative (Figs 6, 7).** The overall color pattern of head, body, limbs, and tail similar to that in life with some fading. Ground color of head, body, limbs, and dorsum light-brown; dark body bands lighter than in life. Colored tuberculation on dorsum fade to off-white. Tan colored on the ventral surface.

**Variation.** *Cyrtodactylus stellatus* sp. nov. usually varies in coloration and banding pattern (Figs 8–11; Tables 6, 7). All specimens possess a clear dark-brown nuchal band which is less clearly defined in ZMKU R 00903 and the holotype. In adult females, precloacal pores are present but they lack the precloacal groove (Fig. 10B). Four specimens (ZMKU R 00903, ZMKU R 00907, ZMKU R 00911, and ZMKU R 00913) have prominent light-yellow tubercles scattered on the dorsum and limbs. Male paratype (ZMKU R 00907) has continuous pore-bearing femoroprecloacal scales. Original
tails (ZMKU R 00899, ZMKU R 00901–00902, ZMKU R 00910, ZMKU R 00912, and ZMKU R 00916) have 10–12 dark caudal bands (Fig. 11A, B), light bands diffused with dark pigment in adults (immaculate in immature and juvenile), subcaudal scales transversely enlarged and shallow caudal furrows. Male paratypes have a single row of 3–4L/2–4R postcloacal tubercles on each hemipenial swelling except ZMKU R 00907 which has two rows of 4/5 on each side. This character in female paratypes is very small, and a single row of 2–4L/2–4R on each side at the base of tail.

In life, the juvenile (ZMKU R 00917; SVL 43.1 mm) had a body pattern similar to the adults but with less prominent tuberculation, brownish yellow ground color of body, dark body bands are bordered by yellow lines, some bearing tubercles, the original tail has approximately 10 dark caudal bands, the posterior portion of tail is white, and light caudal bands are immaculate (Fig. 11C).
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Figure 11. Variation of Cyrtodactylus stellatus sp. nov. A adult female ZMKU R 00899 having 11 dark caudal bands on the original tail and white caudal bands infused with dark pigmentation B immature female ZMKU R 00902 (field number AA 05272) having 12 dark caudal bands on the original tail with immaculate white caudal bands, and C juvenile ZMKU R 00917 having light-yellow color on the body and bearing white tail tip.
Distribution. *Cyrtodactylus stellatus* sp. nov. is currently known only from Tarutao Island, Satun Province, Thailand (Figs 1, 12A).

Natural history. All specimens of *C. stellatus* sp. nov. were collected from a karst forest at night (1950–2100 h) with temperatures between 27.1–32.2 °C and relative humidity between 71.4–93.0%. The specimens were found on karst walls, within karst crevices and on nearby karst boulders. Some specimens occurred on tree trunks or

Table 6. Descriptive measurement (millimeters), meristic (left/right) and color pattern characters of the type series of *Cyrtodactylus stellatus* sp. nov. Key: H = holotype; P = paratype; M = male; F = female; / = data unavailable or unapplicable; b = broken; r = regenerated. Morphological abbreviations are defined in Table 2.

| Specimen | ZMUKR 00905 | ZMUKR 00903 | ZMUKR 00906 | ZMUKR 00907 | ZMUKR 00913 | ZMUKR 00915 | ZMUKR 00909 | ZMUKR 00908 |
|----------|--------------|--------------|--------------|--------------|--------------|--------------|--------------|--------------|
| Sex | M | M | M | M | F | F | F | F |
| SVL | 94.2 | 95.9 | 94.6 | 87.9 | 86.3 | 96.1 | 93.6 | 94.8 | 90.4 | 86.6 |
| TL | 94.8 | 96.8 | 92.3 | 69.0 | 69.6 | 124.4 | 70.5 | 107.5 | 81.7 | 102.3 |
| TW | 9.2 | 9.7 | 9.2 | 8.4 | 7.6 | 9.1 | 9.1 | 10.3 | 7.1 | 10.3 |
| FL | 15.4 | 15.3 | 15.1 | 14.4 | 14.1 | 14.9 | 14.5 | 15.9 | 15.6 | 14.8 |
| TBL | 18.1 | 18.3 | 17.8 | 17.4 | 17.6 | 17.7 | 17.3 | 18.1 | 17.8 | 16.5 |
| AG | 43.3 | 43.7 | 43.9 | 44.4 | 39.6 | 46.0 | 44.5 | 44.5 | 45.4 | 39.9 |
| HL | 27.6 | 26.3 | 27.0 | 25.2 | 24.8 | 26.5 | 26.9 | 27.3 | 26.4 | 25.7 |
| HW | 16.7 | 16.3 | 17.3 | 15.4 | 14.7 | 16.4 | 16.8 | 17.2 | 15.7 | 15.2 |
| HD | 10.4 | 9.6 | 10.8 | 9.2 | 8.7 | 10.4 | 10.2 | 10.1 | 9.4 | 9.2 |
| ED | 6.8 | 6.7 | 6.7 | 5.9 | 5.8 | 6.4 | 6.8 | 6.6 | 6.6 | 5.6 |
| EE | 7.1 | 7.6 | 7.2 | 6.5 | 6.2 | 6.9 | 7.0 | 7.0 | 6.7 | 6.8 |
| ES | 10.8 | 10.7 | 10.9 | 9.8 | 9.8 | 10.9 | 10.8 | 10.7 | 10.4 | 10.1 |
| EN | 8.5 | 8.3 | 8.3 | 7.8 | 7.5 | 8.2 | 8.3 | 8.5 | 8.1 | 7.9 |
| TO | 5.9 | 6.2 | 6.6 | 5.8 | 5.5 | 6.0 | 6.4 | 6.1 | 5.7 | 6.2 |
| EL | 2.4 | 2.5 | 2.2 | 2.0 | 2.0 | 2.0 | 2.8 | 2.7 | 2.1 | 2.3 |
| TN | 2.9 | 3.2 | 3.5 | 3.1 | 3.0 | 3.8 | 3.3 | 3.2 | 3.2 | 2.6 |
| SL | 13/14 | 14/13 | 15/12 | 13/14 | 13/12 | 13/13 | 13/13 | 13/12 | 12/12 | 13/13 |
| TL | 11/11 | 10/10 | 11/12 | 12/12 | 11/11 | 11/11 | 12/11 | 12/12 | 10/11 | 11/11 |
| PVT | 36 | 35 | 41 | 38 | 43 | 38 | 40 | 40 | 40 | 47 |
| LRT | 21 | 20 | 21 | 19 | 22 | 20 | 21 | 19 | 22 | 22 |
| VS | 33 | 37 | 36 | 35 | 36 | 37 | 39 | 37 | 37 | 36 |
| 4TL | 21/22 | 21/21 | 21/21 | 21/20 | 23/22 | 22/22 | 21/21 | 22/23 | 22/20 | 20/20 |
| FPP in adult males | 27 | 25 | 24 | 29 | 27 | / | / | / | / | / |
| PP in adult females | / | / | / | / | / | 15 | 12 | 14 | 11 | 11 |
| BB | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 |
| DCB | / | / | / | / | / | 11 | / | / | / | / |
| Body band/ interspace ratio | 1.12 | 1.20 | 1.04 | 1.10 | 1.68 | 1.07 | 1.03 | 1.23 | 1.06 | 0.92 |
| Precloacal groove | Deep | Deep | Deep | Deep | Deep | Absent | Absent | Absent | Absent | Absent |
| Femoroprecoacal pores continuous | No | No | No | Yes | No | / | / | / | / | / |
| Tuberculation | Weak | Weak | Weak | Weak | Weak | Weak | Weak | Weak | Weak | Weak |
| Tubercles on ventral surface of forelimb | No | No | No | No | No | No | No | No | No | No |
| Tubercles in gular region | No | No | No | No | No | No | No | No | No | No |
| Ventrolateral fold tuberculate | No | No | No | No | No | No | No | No | No | No |
| Dorsum bearing scattered pattern of white tubercles | Yes | Yes | Yes | Yes | Yes | Yes | Yes | Yes | Yes | Yes |
| Hatching/juveniles with white tail tip | / | / | / | / | / | / | / | / | / | / |
| Adult posterior caudal region white | / | No | / | / | / | No | / | No | / | / |
| White caudal bands in adults immaculate | / | No | / | / | / | No | / | No | / | No |
A new insular species of the Cyrtodactylus pulchellus group

Table 7. Descriptive meristic (left/right) and color pattern characters of the referred specimens of Cyrtodactylus stellatus sp. nov. Key: RF = referred specimen; IM-M = immature male; IM-F = immature female; J = juvenile; / = data unavailable or unapplicable. Morphological abbreviations are defined in Table 2.

| ZMKU R 00901 | ZMKU R 00902 | ZMKU R 00904 | ZMKU R 00905 | ZMKU R 00910 | ZMKU R 00911 | ZMKU R 00912 | ZMKU R 00914 | ZMKU R 00916 | ZMKU R 00917 |
|--------------|--------------|--------------|--------------|--------------|--------------|--------------|--------------|--------------|--------------|
| RF | RF | RF | RF | RF | RF | RF | RF | RF | RF |
| Age | IM-M | IM-F | IM-M | IM-M | IM-F | IM-F | IM-M | J |
| SVL | 77.4 | 68.4 | 72.5 | 82.5 | 81.8 | 73.8 | 81.9 | 79.9 | 43.1 |
| SL | 12/12 | 13/13 | 12/12 | 12/13 | 14/14 | 14/14 | 13/13 | 13/13 | 13/14 |
| IL | 10/11 | 11/12 | 10/11 | 11/11 | 10/12 | 13/11 | 10/11 | 10/11 | / |
| PVT | 38 | 38 | 32 | 41 | 41 | 41 | 42 | 40 | / |
| LRT | 20 | 21 | 19 | 22 | 19 | 19 | 22 | 23 | / |
| VS | 34 | 40 | 34 | 37 | 32 | 37 | 38 | 37 | / |
| 4TL | 22/21 | 22/22 | 21/20 | 21/21 | 20/21 | 23/23 | 22/21 | 21/22 | / |
| FFP in adult males | / | / | / | / | / | / | / | / | / |
| PP in adult females | / | / | / | / | / | / | / | / | / |
| BB | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 |
| DCB | 11 | 12 | / | 11 | / | 10 | / | 11 | / |
| Body band/ interspace ratio | 1.35 | 1.36 | 1.40 | 1.09 | 0.99 | 1.44 | 1.22 | 1.39 | / |
| Prefoal groove | / | / | / | / | / | / | / | / | / |
| Tuberculation | Weak | Weak | Weak | Weak | Weak | Weak | Weak | Weak | / |
| Tubercles on ventral surface of forelimb | No | No | No | No | No | No | No | No | No |
| Tubercles in gular region | No | No | No | No | No | No | No | No | No |
| Ventrolateral fold tuberculate | No | No | No | No | No | No | No | No | No |
| Dorsum bearing scattered pattern of white tubercles | Yes | Yes | Yes | Yes | Yes | Yes | Yes | Yes | No |
| Hatchlings/juveniles with white tail tip | No | No | No | No | No | No | No | No | Yes |
| Adult posterior caudal region white | / | / | / | / | / | / | / | / | / |
| White caudal bands in adults immaculate | / | / | / | / | / | / | / | / | / |

vines near the karst formations (Fig. 12). The holotype was found on a karst wall approximately 1 m above the ground within karst forest. Eight specimens (ZMKU R 00900, ZMKU R 00906, ZMKU R 00908, ZMKU R 00911–00912, ZMKU R 00913, and ZMKU R 00915–00916) were found on karst walls from 0.5–3.0 m above the ground. ZMKU R 00907, ZMKU R 00910, and ZMKU R 00914 were found in karst crevices. Three specimens (ZMKU R 00901, ZMKU R 00903, and ZMKU R 00909) were found on karst boulders. Four specimens (ZMKU R 00899, ZMKU R 00902, ZMKU R 00904, and ZMKU R 00917) were perched on vegetation near karst walls or karst boulders.

Two gravid females (ZMKU R 00899–00900) were collected in November 2017 and contained two eggs (externally visible). The juvenile was found on a vine in May 2019. Cyrtodactylus stellatus sp. nov. appears to be nocturnal and sympatric with two other gekkonids, Gehyra mutilata Wiegmann, 1834 and the diurnal species Cnemaspis tarutaoensis Ampai et al., 2019.

Etymology. The specific epithet stellatus is Latin word, meaning starry or starred, and refers to scattered pattern of light-colored tubercles on dorsum and limbs. The name corresponds with the sister taxon C. astrum that shared similar diagnostic character (scattered light-colored tubercles pattern on dorsum).
Comparison. *Cyrtodactylus stellatus* sp. nov. can be distinguished from other species in the *C. pulchellus* group by having a combination of weak tuberculation on the body; no tubercles on ventral surface of forelimbs, gular region, or in ventrolateral body folds; 19–23 longitudinal tubercle rows; 32–40 ventral scales; 20–23 subdigital lamellae on the fourth toe; 24–29 femorprecloacal pores in males; deep precloacal

Figure 12. Habitat of *Cyrtodactylus stellatus* sp. nov. at the type locality, Tarutao Island, Satun Province, Thailand. **A** Pha Toe Boo karst formation **B** karst microhabitat structure and **C** vegetation (vine) used by a juvenile in karst habitat.
Table 8. Diagnostic characters of *Cyrtodactylus stellatus* sp. nov. and its related species within the *C. pulchellus* group. W = weak; P = prominent; / = data unavailable. Some information was collected from the following literature (Grismer et al. 2012, 2014, 2016; Quah et al. 2019, Wood et al. 2020, and Termprayoon et al. 2021).

| Character                  | Clade A | Clade B |
|----------------------------|---------|---------|
|                            | *stellatus* sp. nov. | *astrum* |
|                            | *dayangbuntingensis* | *australotitiwangsaensis* |
|                            | *langkawiensis* | *bintangrendah* |
|                            | *bintangtinggi* | *evanquahi* |
|                            | *hidupselamanya* | *jelawangensis* |
|                            | *lenggongensis* | *macrotuberculatus* |
|                            | *pulchellus* | *sharkari* |
|                            | *timur* | *trilatofasciatus* |
| Sample size                | 10      | 13      |
| Maximum SVL                | 96.1    | 108.3   |
| SL                         | 12–15   | 10–12   |
| IL                         | 10–13   | 9–12    |
| PVT                        | 32–47   | 40–57   |
| LRT                        | 19–23   | 20–29   |
| VS                         | 32–40   | 31–46   |
| 4TL                        | 20–23   | 20–24   |
| FPP in adult males         | 24–29   | 28–38   |
| PP in adult females         | 11–15   | Absent  |
| No. of body bands          | 4       | 4       |
| Body band/ interspace ratio| 0.92–1.08 | 0.98–2.07 |
| DCB                        | 10–12   | 13 or 14 |
| Precloacal groove in males | Both    | Absent  |
| Femoroprecloacal pores continuous | Deep | Deep |
| Tuberculation              | W       | W       |
| Tubercles on ventral surface of fordist | No | No |
| Tubercles in gular region  | No | No |
| Ventrolateral fold tuberculate | No | No |
| Dorsum bearing scattered pattern of white tubercles | Yes | Yes |
| Hatchlings/juveniles with white tail tip | Yes | Yes |
| Adult posterior caudal region white | No | No |
| White caudal bands in adults immaculate | No | No |

| Diagnostic characters         | Clade A | Clade B |
|-------------------------------|---------|---------|
|                            | *stellatus* sp. nov. | *astrum* |
|                            | *dayangbuntingensis* | *australotitiwangsaensis* |
|                            | *langkawiensis* | *bintangrendah* |
|                            | *bintangtinggi* | *evanquahi* |
|                            | *hidupselamanya* | *jelawangensis* |
|                            | *lenggongensis* | *macrotuberculatus* |
|                            | *pulchellus* | *sharkari* |
|                            | *timur* | *trilatofasciatus* |
| Sample size                | 10      | 13      |
| Maximum SVL                | 96.1    | 108.3   |
| SL                         | 12–15   | 10–12   |
| IL                         | 10–13   | 9–12    |
| PVT                        | 32–47   | 40–57   |
| LRT                        | 19–23   | 20–29   |
| VS                         | 32–40   | 31–46   |
| 4TL                        | 20–23   | 20–24   |
| FPP in adult males         | 24–29   | 28–38   |
| PP in adult females         | 11–15   | Absent  |
| No. of body bands          | 4       | 4       |
| Body band/ interspace ratio| 0.92–1.08 | 0.98–2.07 |
| DCB                        | 10–12   | 13 or 14 |
| Precloacal groove in males | Both    | Absent  |
| Femoroprecloacal pores continuous | Deep | Deep |
| Tuberculation              | W       | W       |
| Tubercles on ventral surface of fordist | No | No |
| Tubercles in gular region  | No | No |
| Ventrolateral fold tuberculate | No | No |
| Dorsum bearing scattered pattern of white tubercles | Yes | Yes |
| Hatchlings/juveniles with white tail tip | Yes | Yes |
| Adult posterior caudal region white | No | No |
| White caudal bands in adults immaculate | No | No |
groove in males; 11–15 precloacal pores in females; scattered pattern of white, cream or light-yellow tubercles on dorsum; 10–12 dark caudal bands on original tail; white caudal bands on original tail infused with dark pigmentation in adults; and juveniles with white tail tip. Additional comparisons between C. stellatus sp. nov. and other species in the C. pulchellus group are in Table 8.

Based on phylogenetic tree, C. stellatus sp. nov. is embedded in Clade A along with C. astrum, C. dayangbuntingensis, C. langkawiensis, and C. lekaguli. It can be distinguished from all four species by having smaller maximum SVL of 96.1 mm (vs. 108.3 mm in C. astrum, 99.0 mm in C. dayangbuntingensis, 99.8 mm in C. langkawiensis, and 108.3 in C. lekaguli); 24–29 femoroprecloacal pores in males (vs. 28–38 in C. astrum, 30 in C. langkawiensis, and 30–40 in C. lekaguli); 11–15 precloacal pores in females (vs. absent in C. astrum, C. dayangbuntingensis, C. langkawiensis, and C. lekaguli); scattered pattern of white, cream or light-yellow tubercles on dorsum (vs. absent in C. langkawien-sis, and C. lekaguli); the ratio of dark body bands to the light color interspaces 0.92–1.68 (vs. 0.75 in C. dayangbuntingensis); 10–12 dark caudal bands (vs. 13 or 14 in C. astrum).

Discussion

The discovery of C. stellatus sp. nov. brings the total number of species in the C. pulchellus group to 17, of which four have been reported from Thailand. This new species is only known from karst habitats on Tarutao Island and seems to have a narrow geographic distribution (endemic to Tarutao Island). Molecular analyses recovered it as the sister taxon to C. astrum and is closely related to C. dayangbuntingensis, C. langkawiensis, and C. lekaguli. Although C. stellatus sp. nov. showed a similar morphological pattern to its sister species, morphological analyses and comparisons of meristic characters revealed that this new species is clearly different from its congeners species of Cyrtodactylus. Among Cyrtodactylus, most useful diagnostic characters are associated with the femoral and precloacal pores (Harvey et al. 2015). These characters are easily detected in males, but those in females are superficial and only found in some species (e.g., C. marmoratus Gray, 1831; C. psarops Harvey et al., 2015; C. sworderi Smith, 1925). We found differences in pore-bearing scales between C. stellatus sp. nov. and other species in the C. pulchellus group, that proved to be useful in distinguishing among species. Members of the C. pulchellus group mostly possess a continuous series of enlarged, pore-bearing femoropreco-local scales in males, but C. stellatus sp. nov. presents a discontinuous row of femoroprecloacal pores except one individual (ZMKU R 00907), which has a continuous series. Moreover, the presence of precloacal pores were found in females of C. stellatus sp. nov., which has not been reported in the other species (Grismer et al. 2012; Quah et al. 2019; Wood et al. 2020, Termprayoon et al. 2021).

In addition, we found that the reported sampling localities of C. lekaguli (ZMKU R 00720–00723) were incorrectly stated as “Thailand, Changwat Province, Takua Pa District, Phangnga” in previous studies (i.e., Grismer et al. 2016; Quah et al. 2019;
Wood et al. 2020, Termprayoon et al. 2021). Therefore, we corrected the sampling localities to “Thailand, Phang-nga Province, Mueang Phang-nga District” (see Table 1).

The discovery of this new species suggests that undiscovered species of the Cyrtodactylus pulchellus group may still occur in southern Thailand where there are still numerous unexplored karst areas. Additional surveys are needed to determine the extent of the geographic range of C. stellatus sp. nov. and the Cyrtodactylus pulchellus group in as a whole in the region.

Acknowledgments

This research was supported by the Center of Excellence on Biodiversity (BDC), Office of Higher Education Commission (BDC-PG4-160022). Research protocol was approved by the Institutional Animal Care and Use Committee of Faculty of Science, Kasetsart University (project number ACKU61-SCI-006). KT was supported by a grant from the Faculty of Science, Kasetsart University (50th Anniversary of Faculty of Science). AR and AA were supported by Kasetsart University Research and Development Institute (KURDI), the Department of Zoology, and International SciKU Branding (ISB), Faculty of Science, Kasetsart University. NA was supported by Sri-nakharinwirot University Research Grant. The Department of National Parks, Wildlife and Plant Conservation, Thailand for providing permission to conduct the research in Tarutao National Park and Khao Banthat Wildlife Sanctuary. Kanchanapan Kamhang (Tarutao National Park) and Bamrungrat Ploydam (Khao Banthat Wildlife Sanctuary) for facilitating the fieldwork. L. Lee Grismer (La Sierra University), Wachara Sangansombat and Sunchai Makchai (Thailand Natural History Museum) made specimens in their care available for study. Siriporn Yodthong assisted with fieldwork. This paper is contribution number 950 of the Auburn University Museum of Natural History. We thank L. Lee Grismer and Evan S.H. Quah for providing their suggestions, which greatly improved the manuscript.

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Appendix I

Specimens examined

_Cyrtodactylus astrum_: **Peninsular Malaysia**, Perlis, Gua Wang Burma: LSUHC 09928 (female) and LSUHC 100075 (male).

_Cyrtodactylus lekaguli_: **Thailand**, Trang Province, Na Yong District: ZMKU R 00918, THNHM 017781, THNHM 017784, THNHM 017787, THNHM 017791 (5 males), and ZMKU R 00919, ZMKU R 00921, THNHM 017694, THNHM 017777, THNHM 017788, THNHM 017790 (6 females).