



A new species of *Cyrtodactylus* (Reptilia: Gekkonidae) from the southern Western Ghats of India

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Abstract

A new species of *Cyrtodactylus* is described from the southern Western Ghats of India. It is distinguished from all species of the *Cyrtodactylus collegalensis* species complex in colour pattern and resembles the Srilankan endemic *C. yakhuna* in overall colouration. Phylogenetic analysis of mitochondrial ND2 DNA sequences indicates that the new species is most closely related to species in the *C. collegalensis* complex and differs from them by an uncorrected pairwise genetic distance of 10.5–12.9%.

Keywords

Colour pattern, *Cyrtodactylus*, phylogeny, Tamil Nadu, Western Ghats

Introduction

The gekkonid genus *Cyrtodactylus* Gray, 1827 is currently the most species-rich group of geckos in the world with about 330 nominal species (Uetz et al. 2022). More than 50% of this diversity was documented in the last two decades, the genus is distributed largely in south and south-east Asia, and in the Western Pacific Islands (Grismer et al. 2021a, b). Many of these species are morphological-

ly cryptic, despite their high dissimilarity in the genetic data. This morphological crypsis and high species diversity adds to the difficulty in formulating appropriate species diagnosis and overburdens with comparing species that are distantly related and geographically unrelated. To resolve this, Grismer et al. (2021a, b) recently built a near-complete comprehensive phylogeny for this genus

and recognized 32 well-supported monophyletic species groups. They also suggested future works focus on comparing the new species with the congeners of the group they fall in and geographically proximate species.

Among these 32 species groups, the *triedrus* group is endemic to peninsular India and Sri Lanka comprising two well-supported clades “*fraenatus* and *triedrus*” with 19 nominal and six undescribed species (Grismer et al. 2021a). The *fraenatus* clade comprises six nominal species that are scansorial and all endemic to Sri Lanka (De Silva and Ukuwela 2020; Grismer et al. 2021a). The *triedrus* clade comprises 13 nominal species distributed in peninsular India and Sri Lanka are terrestrial species which were previously classified in separate genus *Geckoella*, now a subgenus (Agarwal and Karanth 2015; Grismer et al. 2021a; Amarasinghe et al. 2022). Out of these 13 species, *Cyrtodactylus triedrus* (Günther, 1864), *C. vedda* Amarasinghe, Karunarathna, Campbell, Gayan, Ranasinghe, De Silva & Mirza, 2022, *C. punctatus*, *C. yakhuna* (Deraniyagala, 1945) are endemic to Sri Lanka and the remaining nine species, viz., *C. albofasciatus* (Boulenger, 1885), *C. deccanensis* (Günther, 1864), *C. jeyporensis* (Beddome, 1878), *C. nebulosus* (Beddome, 1878), *C. collegalensis* (Beddome, 1870), *C. rishivalleyensis* Agarwal, 2016, *C. speciosus* (Beddome, 1870), *C. srilekhae* Agarwal, 2016, *C. varadgirii* Agarwal, Mirza, Pal, Maddock, Mishra & Bauer, 2016 are endemic to peninsular India and the last five including the Sri Lankan *C. yakhuna* belong to the *collegalensis* species complex (Agarwal et al. 2016).

Although multiple records of species from *collegalensis* complex are known from across southern India, the type localities of the formally described Indian species are restricted to areas above 10° N latitude (Agarwal and Karanth 2015; Agarwal 2016; Agarwal et al. 2016). All other records known from the south are attributed to either *C. collegalensis* or *C. cf. speciosus* based only on photographic records (Srinivasulu et al. 2014; Ganesh and Arumugam 2016; Bhupathy and Sathishkumar 2013; Chaitanya et al. 2018). Members of this complex have highly conserved morphology and the recent descriptions were mainly based on the colour pattern and genetic data (Agarwal 2016; Agarwal et al. 2016). We investigated the southernmost (below 10° N) population of *Cyrtodactylus* from the Western Ghats and describe it as a new species based on morphological and molecular evidence.

Materials and Methods

Molecular analysis

We generated DNA sequences for two specimens viz, ZSI-R 28275 and ZSI-R 28280 (Fig. 1). Specimens were euthanized, fixed in 4% formalin, rinsed with distilled water and transferred to 70% ethanol for preservation. All specimens collected in this study are deposited in the Zoological Survey of India, Kolkata with the following registration numbers ZSI-R 28275–28280.

We extracted genomic DNA from liver tissue or tail tip samples stored in absolute ethanol at -20°C, using the Dneasy (Qiagen™) blood and tissue kit. We amplified the partial sequence (1038 base pairs) of the mitochondrial *ND2* gene using the following primers: MetF1 (Forward) and H5934 (Reverse) (Macey et al. 1997). PCR conditions were as follows: initial denaturation at 95°C for 3 min, followed by 39 cycles of denaturation at 95°C for 35 sec, annealing at 56°C for 40 sec and extension at 72°C for 1 min 30 sec. The final extension was at 72°C for 5 min. PCR amplifications were carried out in an S1000™ Thermal Cycler (Bio-Rad, USA). Amplified PCR products were run on a 2% agarose gel and viewed with an Essential V4 (UVITEC Cambridge, UK) gel documentation system. PCR products were Sanger sequenced in both directions at Barcode Biosciences (Bangalore, India).

Bidirectional sequences were manually checked using the Software CHROMAS v.2.6.6 (<http://technelysium.com.au/wp/chromas>) and aligned using ClustalW (Thompson et al. 1994) with default prior settings implemented in MEGA 7 (Kumar et al. 2016). We checked for unexpected stop codons by translating the sequence to amino acids in MEGA7 (Kumar et al. 2016). The new sequence generated in this study was aligned with data for 39 other *Cyrtodactylus* species downloaded from the Genbank (supplementary Table S1). *Cyrtodactylus fraenatus* and *C. soba* were used as an outgroup following the phylogeny from Grismer et al. (2021) and Amarasinghe et al. (2022).

Maximum Likelihood (ML) analysis was carried out with RAxML GUI version 2.0 (Edler et al. 2021) implementing the GTRGAMMA model of sequence evolution, which is recommended over GTR+G+I because the 25 rate categories account for potentially invariant sites (Stamatakis 2006). A Bayesian Inference (BI) analysis was carried out using the program MrBayes 3.2 (Ronquist et al. 2012), with default prior settings. The dataset was partitioned by codon positions using PartitionFinder v1.1.1 (Lanfear et al. 2012) with default settings to find the best-fit model of sequence evolution. Partition finder suggested three partitions as follows, position1: HKY+G, position2: TrN+G, position3: TIM+I+G. Four separate runs were set up with eight Markov chains each initiated from random trees and allowed to run for 10 million generations, sampling every 100 generations. Analyses were terminated when the standard deviation of split frequencies was less than 0.001, the first 25% of trees were discarded as “burn-in”, and trees were constructed under 50% majority consensus rule. We obtained ESS values using Tracer v 1.6 (Rambaut et al. 2018) and confirmed the convergence for all the priors (ESS>200). Support for the internal branches for the ML and BI was quantified using thorough bootstrap (BS) with 1000 replicates and posterior probabilities (PP), respectively. Bayesian posterior probabilities (BPP) values above 0.95 and BS values above 75 are considered strong support (Huelsenbeck et al. 2001). The resulting tree was edited in Figtree (<http://tree.bio.ed.ac.uk/software/figtree>). Uncorrected pairwise genetic distances were calculated in MEGA 7 using the default setting selecting a pairwise deletion option.

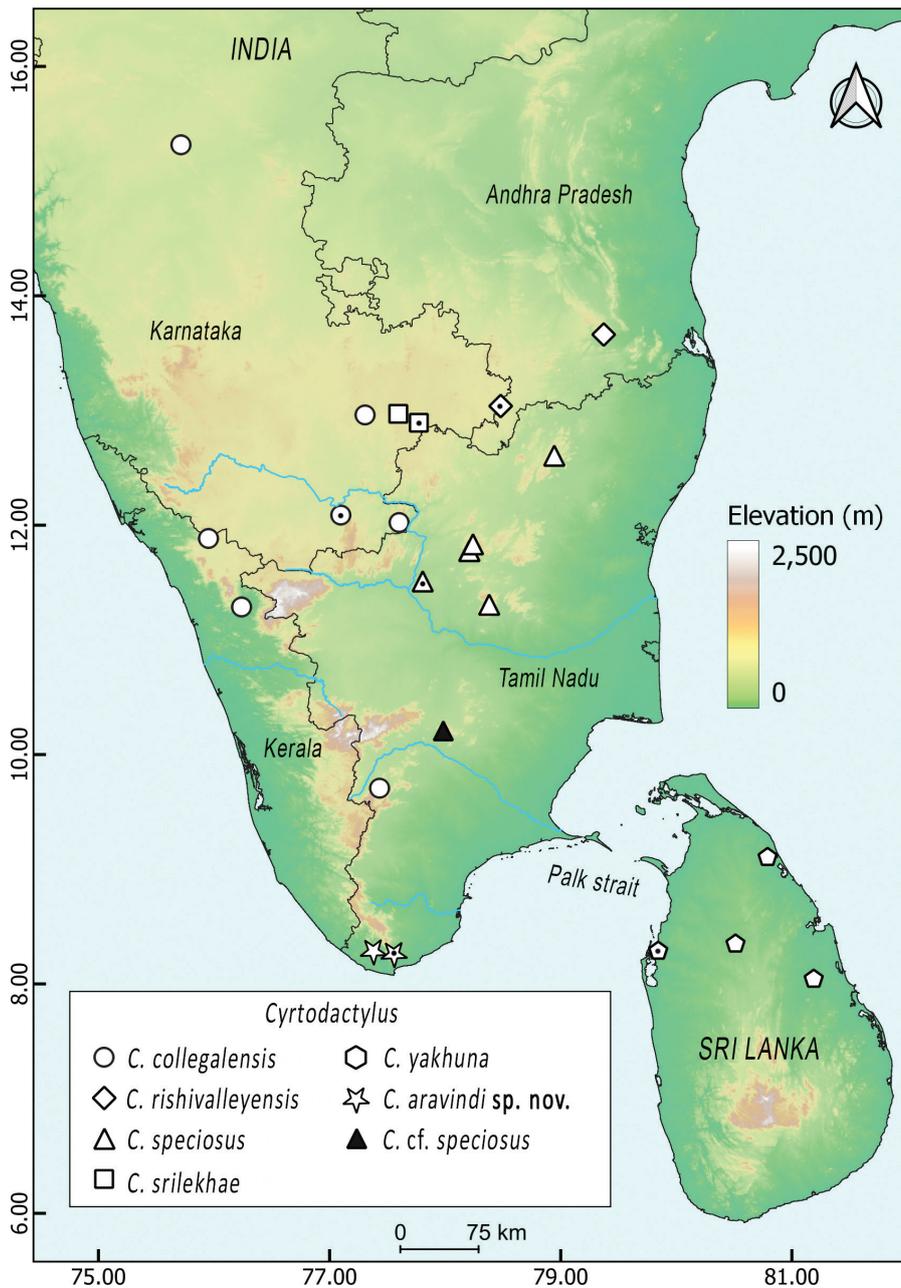


Figure 1. Map showing distribution of species in the *collegalensis* complex from southern peninsular India and Sri Lanka. Type localities are marked with a dot inside the symbols. *Cyrtodactylus varadgirii* which is distributed in Maharashtra, Madhya Pradesh and Gujarat states is not shown on this map.

Morphological analysis

All the morphological characters examined (mensural and meristic) and colour pattern follow (Agarwal et al. 2016 and Agarwal 2016). Measurements and meristic data from the collected specimens for this study were taken under a Nikon microscope and were measured using a Mitutoyo digital vernier caliper to the nearest 0.1 mm. Photographs were taken using Canon EOS 7D mounted with a 100mm macro lens and two external flashes. Measurements and meristic characters include: axilla to groin length (AGL, from posterior margin of forelimb insertion to anterior margin of hindlimb insertion); body width (BW, maximum body width); crus length (CL, from the posterior surface of the knee while flexed 90° to the base of the heel); eye diameter (ED, greatest horizontal diameter of eye); eye to naris distance (EN, distance between anterior margin of eye and posterior edge

of nostril); eye to snout distance (ES, distance between anterior margin of eye and tip of snout); eye to ear distance (EE, distance from anterior edge of ear opening to posterior margin of eye); ear length (EL, maximum horizontal length of ear opening); head length (HL, distance from the posterior margin of the retroarticular process to the tip of the snout); head width (HW, maximum width of head); head depth (HD, maximum head depth at occiput); internarial distance (IN, distance between nares); interorbital distance (IO, shortest distance between left and right supraciliary scale rows); snout vent length (SVL, from tip of snout to vent); tail length (TL, from vent to tip of tail); tail width (TW, measured at widest point of tail). Abbreviations for the meristic characters include SL: number of supralabials; SL(M): supralabial at the position of midorbital; IL: number of infralabials; IL (M): infralabial at the position of midorbital; PCT: Preloacal tubercles; MVSR: the number of ventral scale

rows at mid-body between the lowest rows of dorsal scales.

Comparative data for the members of the *collegalensis* complex were obtained from original descriptions (Beddome 1870; Agarwal 2016; Agarwal et al. 2016). Morphological data and colour patterns for the *Cyrtodactylus yakhuna* and its subspecies *C. yakhuna zonatus* were obtained from Deraniyagala (1945) (*vide* Amarasinghe et al. 2009). Additionally, we also examined some of the type series of *Cyrtodactylus yakhuna* var. *zonatus* (ZSI 20469).

Results

Molecular analysis

Both the ML and BI analyses recovered a similar topology for the *triedrus* group as reported in (Amarasinghe et al. 2022). The monophyly of the *collegalensis* complex is well supported in both analyses and recovered *Cyrtodactylus varadgirii* as sister lineage for the remainder of this clade with strong support in ML (BS 100) and BI (PP 1.0). The new species described here is nested within the clade containing all the members of the *collegalensis* species complex (Fig. 2). The new species is recovered as sister to four Indian species *C. srilekhae*, *C. rishivalleyensis*, *C. speciosus*, *C. collegalensis*, and the Sri Lankan *C. yakhuna* with moderate support in ML (BS 67) and strong support in BI analysis (PP 0.94).

The uncorrected pairwise genetic distance between the new species and other congeners within the *collegalensis* clade range from 10.5% to 12.9% and there is 1.5% intraspecific variation between the two samples of the new species (Table 1). Within the *collegalensis* clade, the lowest and highest pairwise genetic distance between any two species is 8.8–9.1% (*C. srilekhae* & *C. rishivalleyensis*) 13.9–15.5% (*C. speciosus* & *C. varadgirii*), respectively. The new species has a genetic divergence of 10.5% with *C. yakhuna* and a range of 11–12.9% to other species in the clade.

Cyrtodactylus aravindi sp. nov.

<http://zoobank.org/B0A93527-4976-479A-9520-CF-2B76C56103>

Figures 3–6; Tables 1,2

Type locality. Muppandal, Nagercoil, Kanyakumari district, Tamil Nadu, India (8.260862°N, 77.557513°E, 108 m above sea level).

Holotype. ZSI-R 28275, adult male collected from Muppandal, Nagercoil, Kanyakumari district, Tamil Nadu, India (8.260862°N, 77.557513°E, 108 m above sea level) collected by P. Hopeland and Amirtha Balan on 4 April 2022 (Figs 3, 4, 6A).

Paratypes (n=5). ZSI-R 28276 (adult male), ZSI-R 28277 (adult female), ZSI-R 28278 (adult male), ZSI-R 28279 (subadult male) collections details same as the holotype (Figs 5A–D); ZSI-R 28280 (adult female) collected from Thuckalay, Kanyakumari district, Tamil Nadu, India (8.285148°N, 77.379105°E, 371 above sea level) collected by Roshin Tom & Sandeep Das on 7 August 2021 (Figs 5E and 6B).

Etymology. The specific epithet is a patronym honouring Dr N. A. Aravind, Senior Fellow at ATREE, Bengaluru, India for his support towards herpetological research. Aravind is a malacologist who has also contributed to amphibian systematics and his lab support has been instrumental in our research for the past few years. We suggest a common name for the new species as Aravind's ground gecko.

Diagnosis. A small-sized *Cyrtodactylus*, SVL less than 45 mm ($n=6$); body moderately stout, limbs and digits short, slender; dorsal pholidosis on trunk homogeneous with smooth and granular scales; 16–20 dorsal midbody scale rows across trunk contained within one eye diameter; 33–36 ventral scales across belly; preloacal groove, enlarged preloacal and femoral scales, preloacal or femoral pores absent in both the sexes. Tail without a series of enlarged median subcaudal scales. Subdigital scancers smooth, entire (except one or two on some digits divided), unnotched; 5 or 7 basal 7 or 8 distal on digit IV of the manus. Dorsal pattern with a single thick band medially between the fore and hind limb insertions and a single moderately sized spot posterior to the band. Post-occipital collar complete extending from the posterior margin of one orbit to the other, no regular spots on the flanks. Venter tan brown with irregular dark mottling.

Description of Holotype. Morphometric and meristic data are provided in Table 2. Adult male. Specimen in good condition, and a small piece (3mm) of the tail was removed from the posterior end for DNA extraction (Fig. 3). Body relatively slender (BW/AGL 0.42), trunk almost half of SVL (AGL/SVL 0.47) without ventrolateral folds. SVL 40.7 mm, head short (HL/SVL 0.31), wide (HW/HL 0.64), not strongly depressed (HD/HL 0.32), as broad as body (HW/BW ratio 1.01), and distinct from neck. Loreal region slightly inflated, canthus rostralis not prominent. Snout less than half the head length (ES/HL 0.37), slightly longer than eye diameter (ED/ES 0.61); scales on snout, canthus rostralis, and loreal region large, sub-circular, smooth and, weakly conical; much larger than granular scales on the forehead and interorbital region; occipital and temporal region with smaller, smooth granules. Eye small (ED/HL 0.23); pupil vertical with crenate margins; supraciliaries short, larger anteriorly, not elongate; interorbital scale rows across narrowest point of frontal 12 or 13; 33–38 scale rows between left and right supraciliaries at mid-orbit. Ear-opening oval, small (EL/HL 0.09); eye to ear distance similar to eye diameter (EE/ED 1.06). Rostral wider (1.9 mm) than deep (1.1 mm), incompletely divided by weakly developed rostral groove

Table 1. Uncorrected pairwise genetic distances between *Cyrtodactylus aravindi* sp. nov. and other species in *collegalensis* complex.

S. no	Species	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
1	<i>Cyrtodactylus aravindi</i> sp. nov.	-																		
2	<i>Cyrtodactylus aravindi</i> sp. nov.	1.5																		
3	<i>Cyrtodactylus yakkhuna</i>	10.5	10.1																	
4	<i>Cyrtodactylus varadgiri</i>	12.3	10.8	11.8																
5	<i>Cyrtodactylus varadgiri</i>	11.0	10.8	11.2	1.1															
6	<i>Cyrtodactylus varadgiri</i>	12.4	11.7	11.9	1.1	1.6														
7	<i>Cyrtodactylus varadgiri</i>	10.9	10.7	10.9	0.8	0.6	1.4													
8	<i>Cyrtodactylus varadgiri</i>	11.6	11.0	11.1	0.1	1.3	0.7	1.0												
9	<i>Cyrtodactylus collegalensis</i>	12.8	12.6	10.9	13.0	12.4	13.9	12.0	12.9											
10	<i>Cyrtodactylus collegalensis</i>	12.5	11.6	11.2	12.8	12.2	13.3	11.8	12.3	3.7										
11	<i>Cyrtodactylus collegalensis</i>	12.6	11.6	11.2	12.8	12.2	13.3	11.8	12.3	3.7	0.0									
12	<i>Cyrtodactylus collegalensis</i>	12.0	11.6	11.3	12.1	11.6	12.8	11.3	11.9	3.9	1.3	1.3								
13	<i>Cyrtodactylus collegalensis</i>	12.9	12.5	11.0	11.8	10.7	12.7	10.2	11.5	4.7	3.1	3.1	3.1							
14	<i>Cyrtodactylus speciosus</i>	12.6	13.8	13.1	14.3	14.4	15.5	13.9	15.2	12.6	11.8	11.9	11.8	11.9						
15	<i>Cyrtodactylus speciosus</i>	12.8	12.7	12.5	12.4	12.9	13.8	12.5	12.6	13.1	11.8	11.8	12.0	11.9	6.4					
16	<i>Cyrtodactylus srilekhae</i>	12.0	11.9	11.9	13.3	12.2	13.6	11.8	12.6	12.2	11.6	11.6	11.4	10.8	12.3	11.4				
17	<i>Cyrtodactylus srilekhae</i>	11.8	12.1	11.8	12.8	11.6	13.1	11.3	12.2	11.6	12.0	12.1	11.8	11.6	11.1	10.4	0.8			
18	<i>Cyrtodactylus srilekhae</i>	12.1	11.8	11.8	13.0	11.6	13.1	11.3	12.0	12.0	11.3	11.3	11.1	10.8	11.9	10.8	0.9	1.0		
19	<i>Cyrtodactylus rishivalleyensis</i>	11.6	12.9	11.7	10.7	10.5	10.9	10.2	11.1	10.6	10.6	10.6	10.4	10.0	12.3	11.7	8.4	8.5	8.5	
20	<i>Cyrtodactylus rishivalleyensis</i>	12.2	12.8	12.1	11.6	11.0	11.4	10.7	11.6	11.6	11.7	11.7	11.4	11.1	12.2	11.8	8.8	9.1	8.8	0.6

dorsally covering more than half of its height; a single enlarged supranasal on each side, more than twice the size than postnasals, separated from each other by a single enlarged internasals on the snout; two subequal postnasals, much smaller than supranasals; rostral in contact with nostril, supralabial 1, supranasals, internasals, and postnasals on either side; nostrils rounded, directed outwards, covering most of the nasal scale; four or five rows of smaller scales separate the orbit from the supralabials. Mental enlarged, triangular, wider (2.6 mm) than long (1.9 mm); one pair of postmentals, slightly longer (1.3 mm) than mental, in strong contact with each other below mental; sublabials half the size of postmentals; chin shields bordering postmentals and infralabials flat, smooth, smaller than outermost postmentals, rest flattened, small, smooth; two or three rows of enlarged elongated scales separating gular scales from infralabials. Nine supralabials up to angle of jaw and seven at midorbital position on each side; eight infralabials up to angle of jaw and seven infralabials at midorbital position on both sides.

Dorsal pholidosis on trunk homogeneous; granular scales smooth to feebly keeled. Granular scales on occiput and nape slightly smaller than those on body dorsum; granular scales on flank slightly larger than those on dorsum. Ventral scales larger than granular scales on dorsum, smooth, subimbricate, subequal from chest to vent; 33 ventral scales across belly between lowest rows of granular scales on flank. Scales on throat slightly smaller than those on belly; gular region with much smaller. No enlarged precloacal or femoral scales, no precloacal or femoral pores; no precloacal groove. Scales on palm and soles granular, smooth, rounded; scales on dorsal aspects of limbs heterogeneous in shape and size; mixture of small, granules similar to dorsum and many smooth flattened and imbricate scales which are much larger than granules on the body dorsum.

Forelimbs and hindlimbs slightly long, slender (LAL/SVL 0.14; CL/SVL 0.15); digits short, slender, with a strong, recurved claw, moderately inflected, distal portions laterally compressed. Series of unpaired lamellae on basal portion of digits except one or two which on some digits which are paired, separated from narrower distal lamellae by a single large lamella at the inflection; basal lamellae series: 3-6-6-6-5 right manus, 3-6-7-9-6 right pes, 3-6-5-6-3 left manus; 3-6-7-9-6 left pes; distal lamellae series: 8-7-9-8-7 right manus, 9-9-10-9-10 right pes, 7-7-9-8-7 left manus; 9-8-10-9-10 left pes. Relative length of digits (measurements in mm in parentheses): IV

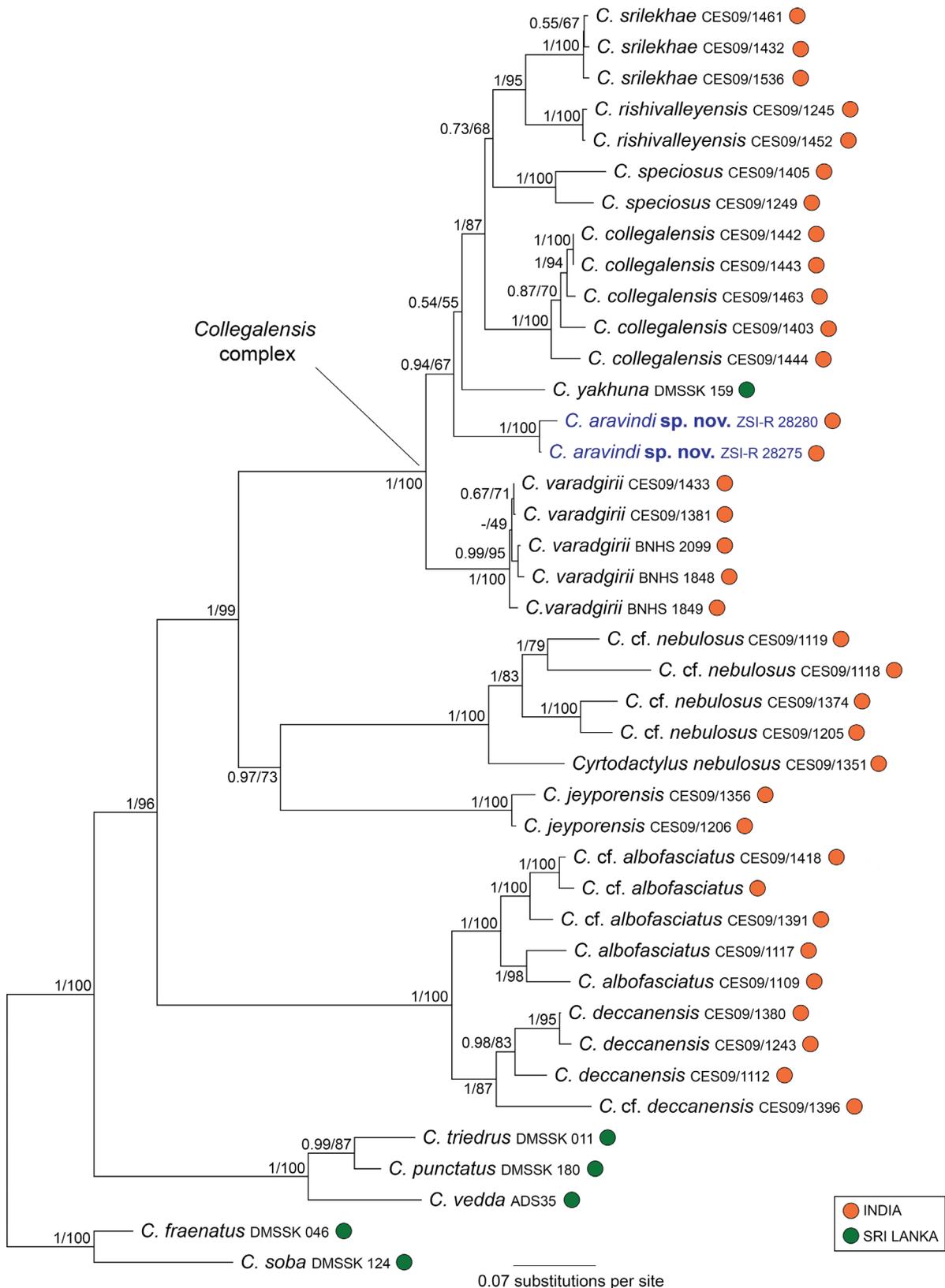


Figure 2. Maximum Likelihood tree showing the relationship of *Cyrtodactylus aravindi* sp. nov. with other congeners of the *triedrus* group. Numbers at internal branches are posterior probability and ML bootstrap support values, respectively.

(3.0) > III (2.7) > II (2.6) > V (2.3) > I (1.7) (right manus);
IV (3.9) > III (3.6) > V (3.5) > II (3.1) > I (1.9) (right pes).

Original tail circular in cross-section, relatively thick, tapering gradually to tip, unsegmented, slightly shorter than snout-vent length (TL/SVL ratio 0.81). Scales on

dorsal aspect of tail base similar to body dorsum; scales on dorsal aspect of tail large flat, slightly elongated, smooth, and imbricate, becoming larger towards the lateral aspect, largest on ventral side, but not forming median row of transversely enlarged subcaudal scales. Three and

Table 2. Morphometric and meristic data for the type series of *Cyrtodactylus aravindi* sp. nov. * denote incomplete tail, numbers in brackets are the length of the tail tip collected for DNA. Bilateral scale counts separated by a comma are given in left, right order.

Specimen number	ZSI-R 28275	ZSI-R 28276	ZSI-R 28277	ZSI-R 28278	ZSI-R 28279	ZSI-R 28280
Type status	Holotype	Paratype	Paratype	Paratype	Paratype	Paratype
Sex	Male	Male	Female	Male	Male	Female
SVL	40.7	39.5	33.7	38.6	28.7	44.7
TL	29.8 (+3)*	26.6	19.5(+4)*	18.5	14.8(+6)*	24.8
TW	3.9	3.9	2.5	3.3	2.8	3.1
AGL	19.2	15.9	16	17	13.3	16.1
BH	5.3	5.7	4.3	5.6	4.6	4.9
BW	8	7.9	6.8	6.5	5.3	9.5
CL	6.3	4.7	5.6	6.1	5.6	7
ED	2.9	2.9	2.6	2.8	2	3.4
EE	3.1	3.1	3.2	3.4	2.4	3.9
EL	1.2	1	1	1.1	0.8	1.2
EN	4.1	2.9	2.5	3	2.2	3.4
ES	4.7	4.5	3.7	4.4	3.2	5
HD	4.1	4.3	3.6	3.9	2.9	4.2
HL	12.7	12.4	11.2	11.5	9.4	14.9
HW	8.1	7.9	6.7	8	5.8	8.5
IN	0.9	1.1	1.3	1.6	0.9	1.3
IO	3.1	2.9	3	3.4	2.7	3.7
LAL	5.7	3	5.2	5.7	4.1	6.6
SL (L&R)	9,9	9,10	9,9	8,8	9,9	10,10
IL (L&R)	8,8	7,7	8,8	7,7	8,8	9,9
SL M (L&R)	7,7	8,9	7,7	6,6	7,7	8,8
IL M (L&R)	6,6	6,6	6,6	5,5	6,6	7,7
MVSR	33	36	33	33	35	35
DLam1F (L&R)	5,6	6,7	5,6	6,6	5,6	5,6
BLam1F (L&R)	3,3	2,3	3,3	3,3	3,3	3,3
DLam4F (L&R)	7,7	7,7	7,7	8,8	7,7	7,7
BLam4F (L&R)	6,6	5,5	6,6	6,6	6,6	6,6
DLam1T (L&R)	5,5	6,6	6,6	7,7	7,7	8,8
BLam1T (L&R)	3,3	3,3	2,2	3,3	2,2	2,2
DLam4T (L&R)	9,9	9,9	8,8	8,8	8,8	8,8
BLam4T (L&R)	6,6	6,6	7,6	6,6	7,6	6,6
PCT (L&R)	3,2	2,1	2,2	2,2	2,2	2,2
PCT (L&R)	3,2	2,1	2,2	2,2	2,2	2,2

two small, smooth, subequal, conical postcloacal spurs on the right and left side of the tail base, respectively; prominent hemipenial swelling, flap of skin covering cloacal aperture

Colouration. Dorsal head pattern has six distinct dark spots; one spot in the frontal region that is slightly narrow; two dark elongated spots between the occiputs just parallel to the supraciliaries and three dark spots in the parietal region, the one in the middle much longer than the other two. All the markings on the head are distinctly separated from each other. Laterally a dark streak through the eye and continues as dark postocular stripes that connect to form the collar band. Labials are mostly whitish with some dark markings on the first four labials and the area below the eye. Ventral aspect of the body pale with irregular black mottling mostly towards the flank and with dark spots in the trunk region. Ventral aspect of the head has numerous thick streaks on infralabials grading

into a thin dark network in the gular region; ventral aspect of tail is dark with some scattered light scales. Dorsal colour heterogeneous, creamish white to brown, one thick dark-brown band on the mid-body extending into the lateral sides where it becomes broader, covering the region between the fore and hind limb insertions; and one dark brownish prominent spot behind the band mid dorsally (between the band and sacral region). Tail dorsum is darker with irregular black mottling and one dark spot (roughly bell-shaped) at the tail base. The area between the collar band and the band is much lighter than the area between the band and tail base. Limbs are brownish with irregular black mottling and the thigh has a few small scattered dark streaks. Collar is dark brown and roughly inverted bell-shaped. In preservative, the creamish colour turned slightly paler.

Variations among the paratypes. Mensural and meristic data for the type series are given in Table. 2. Paratypes

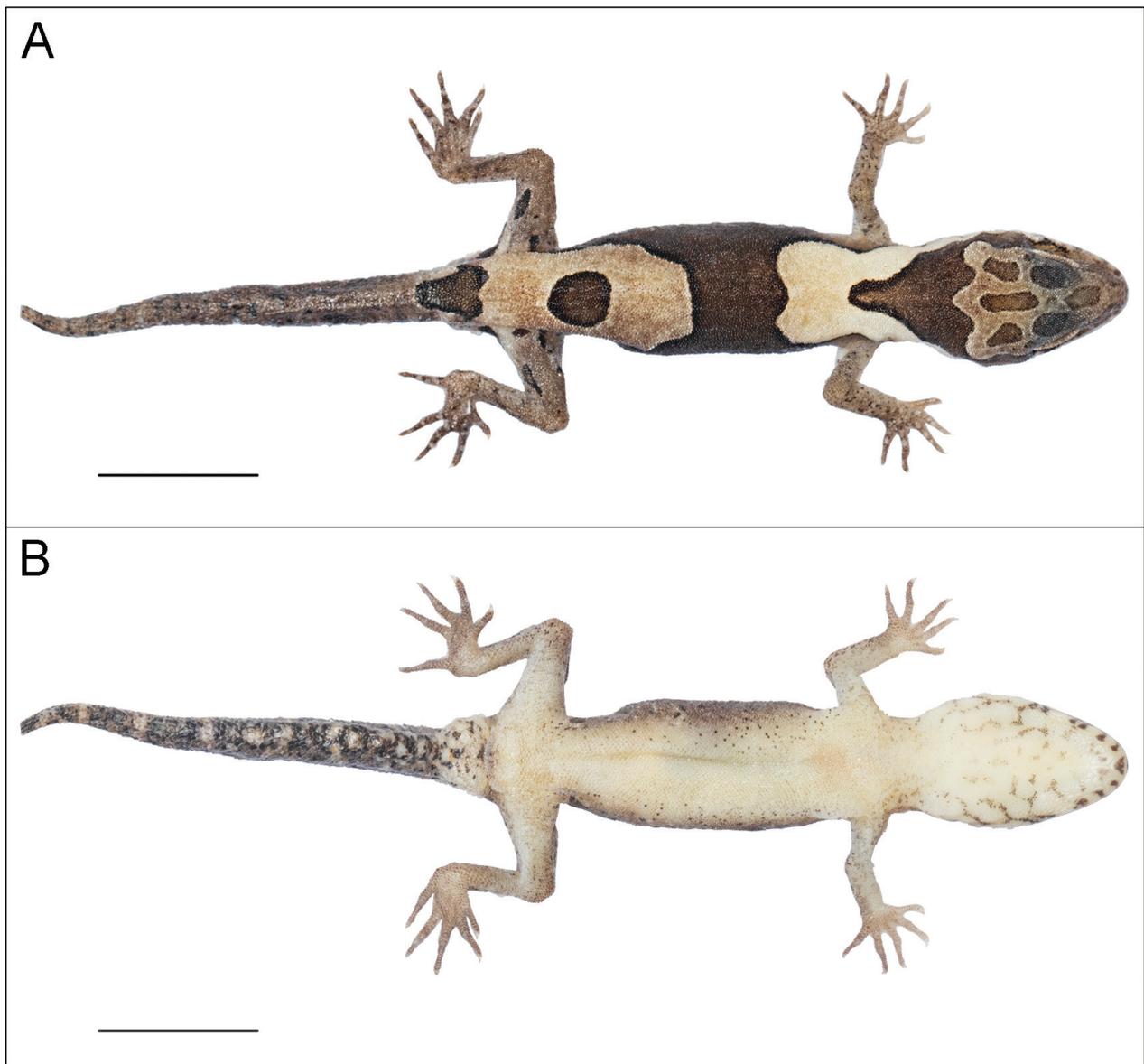


Figure 3. **A** Dorsal (upper) and **B** ventral (lower) aspects of the holotype (ZSI-R 28275) of *Cyrtodactylus aravindi* **sp. nov.** Scale bar = 10mm.

of both male and female specimens range in SVL from 28.7–44.7 mm. All paratypes resemble the holotype in overall morphology except as follows: Two internasals in ZSI-R 28280. The scales between outer postmentals are five (three large and two small) in ZSI-R 28279, two in ZSI-R 28276, four in ZSI-R 28278 and two in ZSI-R 28280. The position on the outer postmentals is slightly lower in ZSI-R 28276, ZSI-R 28277 and ZSI-R 28279. The outermost postmental on the left side is covered by four scales. Tail incomplete in ZSI-R 28277 and ZSI-R 28279 (less than 10mm was cut for the DNA extraction). Tails of all the paratypes original except in ZSI-R 28278 that has regenerated from the base of the tail but complete. In colouration, the frontal spot and parietal spot (middle one) are much narrower in ZSI-R 28276 and the parietal spot (middle one) narrower in ZSI-R 28276, ZSI-R 28277 and ZSI-R 28280. Head markings are feeble or inconspicuous in ZSI-R 28278 and ZSI-R 28279. The dorsal band does not extend into the flank covering the whole area

between fore and hindlimb insertion in ZSI-R 28277, ZSI-R 28279 and ZSI-R 28280. The collar band in all the paratypes differ from that of the holotype posteriorly; in ZSI-R 28278 and ZSI-R 28279 it is somewhat a straight line, slightly notched inwards in ZSI-R 28276 and ZSI-R 28280 and roughly V-shaped in ZSI-R 28277. Paratype ZSI-R 28280 has one small dark spot between the collar band and middorsal band and the dark spot in the tail base is medially divided in ZSI-R 28278 and ZSI-R 28280.

Comparison with the members of the collegalensis complex. *Cyrtodactylus aravindi* **sp. nov.** can be differentiated from all the members of the *collegalensis* complex by the presence of a single band on the dorsum (Vs. three pairs of dark spots that may be fused forming horizontal 8 shaped markings in *C. collegalensis* two broad dark bands on dorsum in *C. rishivalleyensis*, three rows of irregular blotches in *C. srilekhae*), two broad dark bands on dorsum in *C. speciosus*, 4–6 pairs of spots on

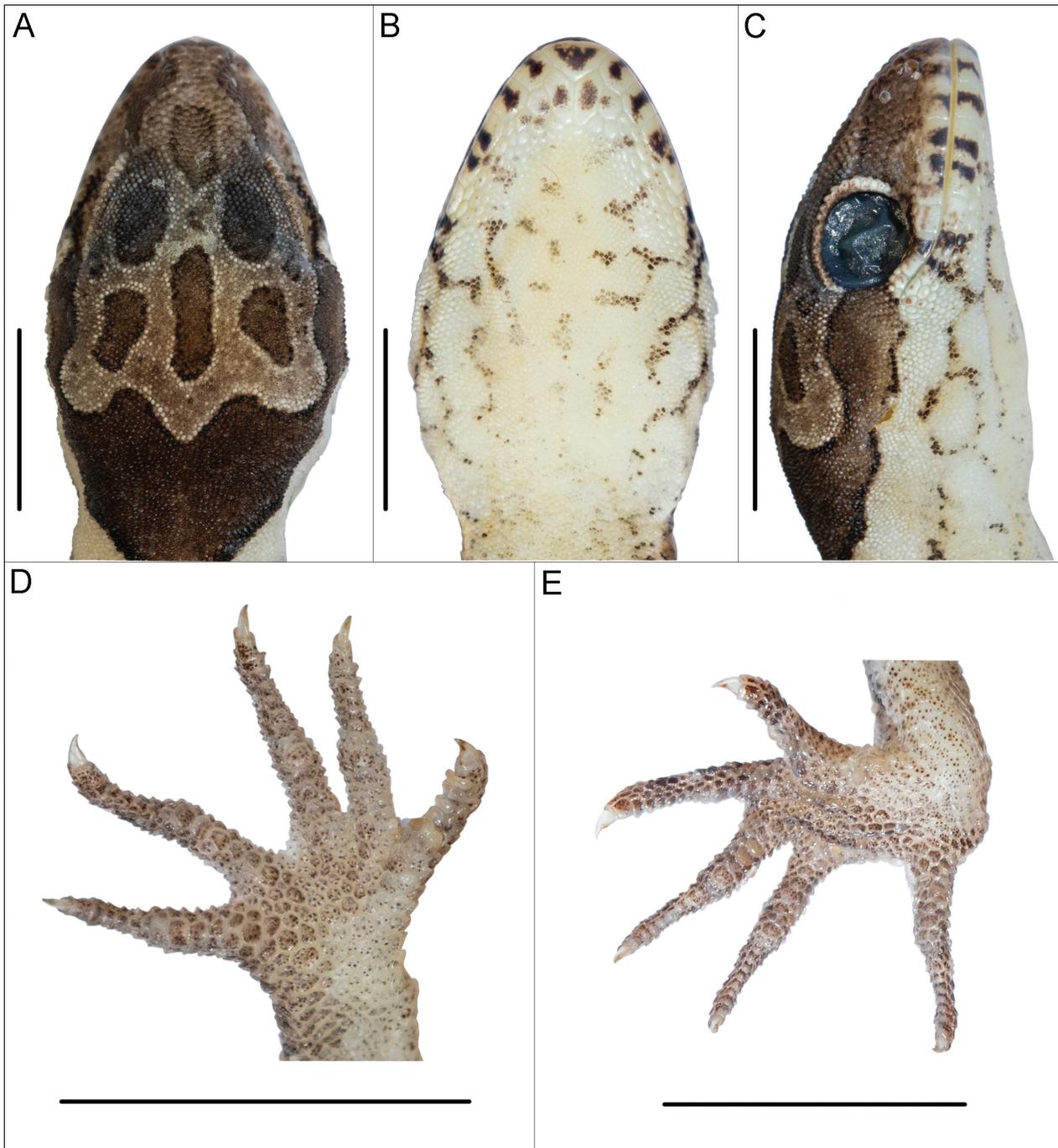


Figure 4. *Cyrtodactylus aravindi* sp. nov. (holotype, ZSI-R 28275). **A** head in dorsal view, **B** ventral view, **C** lateral view, **D** ventral view of right manus, and **E** right pes. Scale bar = 5mm.

dorsum in *C. varadgirii*). From the closely related Sri Lankan species *C. yakhuna* including its variety “*zonatus*” the new species can be differentiated by a combination of characteristics, presence of a single dark band and a single dark spot anterior to the hindlimb insertions on the dorsum (Vs. one or two dark bands on the dorsum (the posterior mark is much larger making it look like a band than a spot)); the dorsal band is always in mid-dorsum *i.e.* its edges on both ends are equally spaced between the fore and hindlimb insertions (Vs. the band is always on the anterior of the body, more closely to the forelimb insertion). Additionally, *Cyrtodactylus aravindi* sp. nov. has higher number of ventral scales across belly (MVSR)

33–36 compared to *C. collegalensis* (27–29) and *C. speciosus* (29–34).

Distribution and Natural History. *Cyrtodactylus aravindi* sp. nov. is currently known from the two locations 20 kilometres from each other in straight-line distance in the Agasthaymalai hill range in the southern Western Ghats of India. The type locality is in the rain shadow region with very high winds on the eastern slopes of the Western Ghats close to the Aralvaimozhi pass (Fig. 7A) and Thuckalay is situated more towards the western slopes at the southernmost end of the Western Ghats (Fig. 7B) receiving an annual rainfall of about 600–900

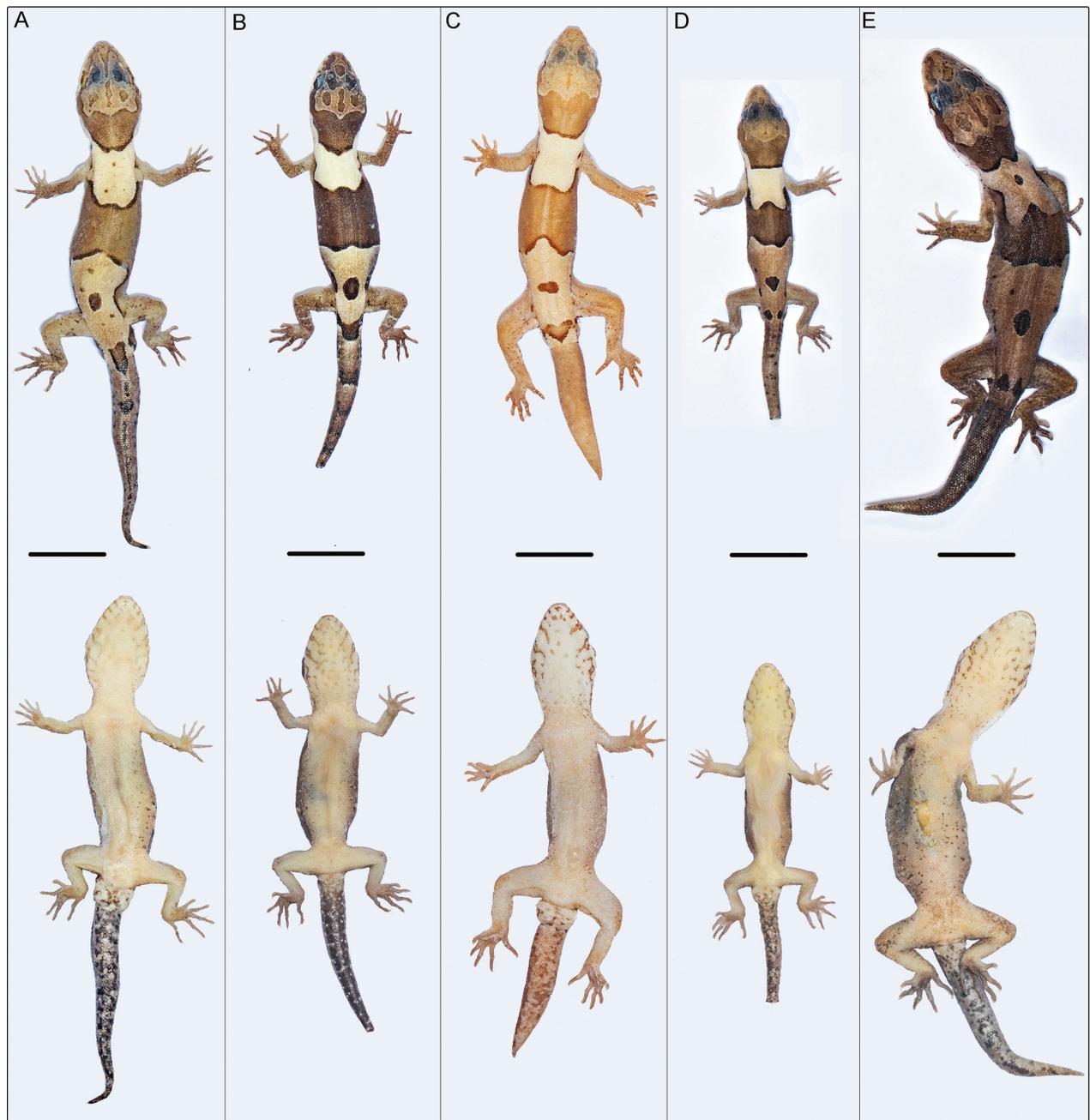


Figure 5. Dorsal (top) and ventral (bottom) aspects of the paratypes of *Cyrtodactylus aravindi* **sp. nov.** A ZSI-R 28276, B ZSI-R 28277, C ZSI-R 28278, D ZSI-R 28279 and E ZSI-R 28280. Scale bar = 10mm.

mm and 900–1200 mm, respectively (Pascal et al. 2004). *Cyrtodactylus aravindi* **sp. nov.** is a nocturnal species and the type series was collected from the ground at night between 19:30–22.00 hrs. The holotype and the four paratypes (ZSI-R 28276–ZSI-R 28279) were all collected from a small area (ca. 60 acres) in the type locality, an isolated southern tropical dry evergreen scrub forest patch, the woody trees *Tamarindus indicus*, *Ficus religiosa* and other shrubs with some history of agriculture about two decades ago. At both sites, *Cyrtodactylus aravindi* **sp. nov.** appears to be a rather uncommon species. The holotype (ZSI-R 28275) was collected from the bottom of a shrub, ZSI-R 28277 was collected from leaf litter covered by a Banyan tree, paratypes ZSI-R 28276, ZSI-R 28278 and ZSI-R 28279 were found in

the mud path covered by vegetation consisting of bushes and grasses. Paratype ZSI-R 28280 was collected from hilly terrain mainly composed of rubber plantations intermixed with coffee and coconut plantations. In both locations the new species is found in sympatry with a few geckonids namely: *Hemidactylus acanthophilis* Mirza & Sanap, 2014, *H. leushnualiti* Duméril & Bibron, 1836, *H. parvimaculatus* Deraniyagala, 1953 and *H. triedrus* (Daudin, 1802).

At the type locality, individuals were seen in the months of October (2021) and April (2022). They were not recorded in the months of November–December (2021) and May (2022) when field effort was made at Muppandal as a part of the ecological study commissioned by the landholder Dohnavur Fellowship. This spe-



Figure 6. Live images of *Cyrtodactylus aravindi* sp. nov. **A** Holotype (ZSI-R 28275), **B** Paratype (ZSI-R 28280), **C** uncollected juvenile female from the type locality.



Figure 7. General habitat of *C. aravindi* sp. nov. **A** Muppandal (type locality) and **B** Thuckalay (paratype locality), Kanyakumari district, Tamil Nadu, India.

cies seems to occur in lower density in open scrub habitat but prefers areas with high grass, shrub and tree cover with open edges.

At the type locality, agriculture was practised in the past but with the absence of intervention in over two decades, ecological succession has occurred. But when agriculture was paused, wind farms had been set up and run for over two decades since. Currently, both the known locations of *C. aravindi* sp. nov. do not fall under any

protected area network. However, the type locality Muppandal is set at less than one kilometre from the border of Kanyakumari Wildlife Sanctuary but is isolated by the linear infrastructure of highways in the East, West and North among other landuse. It also demonstrates the role private properties like Dohnavur Fellowship can play in conservation of lesser-known or lesser charismatic species outside the protected area networks in southern Tamil Nadu state.

Discussion

Description of yet another species of *Cyrtodactylus* from the Agasthyamalai landscape makes it the fourth *Cyrtodactylus* for Tamil Nadu state. The southern tip of the Western Ghats (Agasthyamalai) is known for its endemic reptilian fauna and multiple new species were described recently, both in the mountains (Krishnan 2008; Mallik et al. 2019; Mallik et al. 2021) as well as in the lowlands (Harikrishnan et al. 2012; Srikanthan et al. 2018; Narayanan et al. 2021; Pal et al. 2021; Khandekar et al. 2022). This highlights the hidden species diversity in this landscape and shows the poor exploration of these well-known hill ranges. As mentioned above, this is the first species of *Cyrtodactylus* formally described from below 10° N latitudes in peninsular India. It is surprising that despite the vastly similar drier habitat along the eastern slopes of the Western Ghats there are distinct undescribed species. Identifying species with highly conserved morphology from previously unreported locations, especially “*Geckoella*” where the colour pattern is critical, should be treated with caution, preferably supported by molecular data to avoid underestimation of species diversity. This further warrants investigation of the other populations below 10° latitudes that are previously reported as *C. collegalensis* and *C. cf. speciosus* (Ganesh and Arumugam 2016; Bhupathy and Sathishkumar 2013; Chaitanya et al. 2018).

South Asian geckonids in general are described based on the number of femoral pores, precloacal pores, poreless scales between or the combination of these. However, the absence of these scales/pores makes it very difficult to morphologically diagnose the species in the *collegalensis* complex. Morphological crypsis is previously highlighted among the members of the *collegalensis* complex (Agarwal 2016; Agarwal et al. 2016) and most of the species in this clade are diagnosed based on the colour pattern including the recently described *C. srilekhae* and *C. rishvalleyensis* (Agarwal 2016). This is also the case with *C. aravindi* **sp. nov.** as our description is largely based on the colour pattern and supported by the deep genetic divergence between its congeners in the ND2 mitochondrial gene. Within the type series, there are some variations in the colour pattern on the head and body (Figs 4 and 5). The most distinct among the six specimens is the paratype (ZSI-R 28280) with a relatively short band closer to the anterior of the body than the midbody. However, we only found minor genetic difference in the sequence of this individual compared to the holotype.

A recent phylogeny encompassing all available *Cyrtodactylus* species also recovered *C. yakhuna* as a species nested within the *C. collegalensis* complex with moderate support (Grismer et al. 2021b). If *C. yakhuna* is indeed nested within the *C. collegalensis* complex, this indicates multiple dispersals from Sri Lanka to India or a back dispersal of a single lineage back to Sri Lanka. Similar dispersal scenarios between peninsular India and Sri Lanka have been hypothesized for some freshwater fishes, frogs, geckos and freshwater crabs (Bossuyt et al. 2004;

Lajmi et al. 2018; Meegaskumbura et al. 2019). The main difference in *Cyrtodactylus* is that the sister lineages for *triderus* group are all from Southeast Asia and the older lineages within *triderus* group are endemic to Sri Lanka (Grismer et al. 2021b) and hence the initial dispersals were presumably from Sri Lanka to peninsular India and not vice versa.

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Supplementary material 1

Table S1

Authors: Narayanan S, Das S, Balan A, Tom R, Divakar N, Rajkumar KP, Hopeland P, Deepak V (2022)

Data type: .xlsx

Explanation note: Sequences generated and other GenBank sequences used to build phylogenies.

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