

A new species of swamp-dwelling skink (*Tytthoscincus*) from Singapore and Peninsular Malaysia

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Abstract. *Tytthoscincus temasekensis* is a new species of swamp-dwelling skink from Singapore and the vicinity of Tanjung Malim, Perak, Peninsular Malaysia and the third species in the swamp clade of *Tytthoscincus*. It is distinguished from all other species of *Tytthoscincus* by the combination of having two loreals; two postsupralabials; 10–12 superciliaries; four supraoculars; interparietal contacting the 2nd–4th supraoculars; a shallow, pigmented tympanum; slightly enlarged, isolated, pectoral scales; 27–29 midbody scale rows; 55–65 paravertebral scales; 54–63 ventral scales; 9–11 subdigital lamellae on the fourth toe; keeled, subdigital lamellae; and a dorsal pattern of light-coloured stripes and/or linearly arranged spots. The growing diversity of the swamp clade in Singapore and Peninsular Malaysia begins to underscore the underappreciated contribution of swamplands to herpetological endemism and diversity as well as the need for its conservation.

Key words. Scincidae, *Tytthoscincus*, Singapore, Malaysia, swamp forests, new species

INTRODUCTION

In a recent phylogenetic analysis of the scincid genus *Tytthoscincus*, Grismer et al. (2016a) demonstrated that there are two distantly related, ecologically distinct lineages on the Thai-Malay Peninsula they referred to as the montane and swamp clades. Grismer et al. (2017) noted that the lowland swamp clade contained at least two species from three widely allopatric populations: *T. sibuensis* Grismer, 2006 from Pulau Sibul, Johor; *T. panchoensis* Grismer, Muin, Wood, Shahrul & Linkem, 2016a from Bukit Pancho, Penang; and a population referred to as *T. cf. sibuensis* from Singapore. In the absence of molecular data, the *conferre* designation of the latter was based on its generally striped colour pattern and its geographic proximity to *T. sibuensis*. With the acquisition of a tissue sample of *T. cf. sibuensis* from a specimen collected at Pasir Laba, Singapore (ZRC 2.6490), a phylogenetic analysis based on the mitochondrial gene ND2, indicated that the Singapore population is neither *T. sibuensis* or *T. panchoensis* but basal to them (Grismer et al., 2017). Morphological analyses support the molecular phylogenetic analyses and also demonstrate that there is an

additional population of this new species from the peat swamp forests near Tanjung Malim, Perak, Peninsular Malaysia, approximately 380 km to the north (Fig. 1). These data and the description of this new species are presented below.

MATERIAL AND METHODS

Phylogenetic analysis. A dataset composed of 1,026 bp of the mitochondrial gene NADH dehydrogenase subunit 2 (ND2) was constructed from three individuals of the swamp clade of *Tytthoscincus* that comprised the ingroup plus 48 individuals from 17 other species of *Tytthoscincus* that, along with one specimen of *Larutia seribuensis* Grismer, Leong, Yaakob, 2003 composed the outgroups based on Grismer et al. (2017; Table 1). Total genomic DNA was isolated from liver or skeletal muscle from specimens stored in 95% ethanol using the Qiagen DNeasyTM tissue kit (Valencia, CA, USA). The ND2 gene was amplified using a double-stranded Polymerase Chain Reaction (PCR) under the following conditions: 1.0 µl genomic DNA (~10–33 µg), 1.0 µl (10 µM) light strand primer (5'-AAGCAGTTGGGCCCATACC-3': Macey et al., 1997), 1.0 µl (10 µM) heavy strand primer (5'-AACCAAACCCAACTACGAAAAAT-3': Macey et al., 1997), 1.0 µl dinucleotide pairs (1.5 µM), 2.0 µl 5× buffer (1.5 µM), 1.0 µl MgCl 10× buffer (1.5 µM), 0.18 µl Taq polymerase (5u/µl), and 7.5 µl H₂O. PCR reactions were run on an Eppendorf Mastercycler gradient thermocycler under the following conditions: initial denaturation at 95°C for 2 min, followed by a second denaturation at 95°C for 35 s, annealing at 52°C for 35 s, followed by a cycle extension at 72°C for 35 s, for 33 cycles. All PCR products were visualised on a 1% agarose gel electrophoresis. Successfully amplified PCR products were vacuum purified using MANU 30 PCR Millipore plates and purified products were resuspended in sterile molecular grade water. Purified PCR products were

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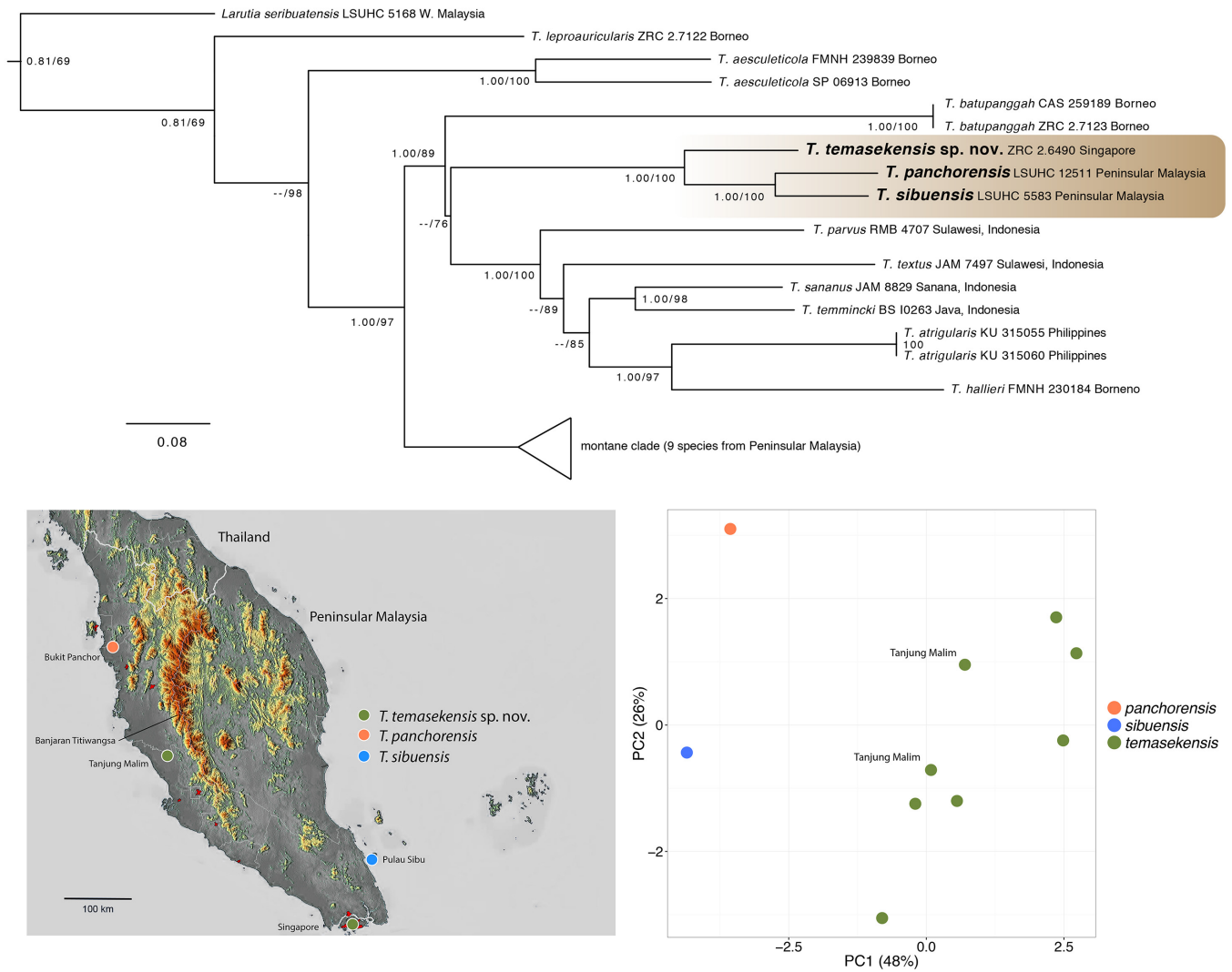


Fig. 1. Upper: Maximum Likelihood phylogram depicting the relationships of species within the swamp clade of *Tythoscincus* (brown highlight) and their relationship to other *Tythoscincus* lineages. Bayesian posterior probabilities and ultrafast bootstrap values, respectively, are listed at the nodes. Lower left: Distribution map of the species of the swamp clade of *Tythoscincus*. Lower right: Principal Component Analysis of the species of the swamp clade of *Tythoscincus*.

Table 1. GenBank accession numbers for ND2 sequences and catalogue numbers of the voucher specimens used in this study.

Species	Voucher	Locality	GenBank No.
<i>Larutia seribuatensis</i>	LSUHC 5168	West Malaysia, Johor, Pulau Tuali	HQ906968
<i>Tythoscincus aesculeticolus</i>	FMNH 239839	East Malaysia, Sabah Sipitang District	JF498209
<i>T. aesculeticolus</i>	SP 06913	East Malaysia, Sabah Sipitang District	JF498208
<i>T. atrigularis</i>	KU 315055	Philippines, Zamboanga City “Province” Pasaonca Natural Park	JF497971
<i>T. atrigularis</i>	KU 315060	Philippines, Zamboanga City “Province” Pasaonca Natural Park	JF497972
<i>T. batupanggih</i>	CAS 259189	East Malaysia, Sarawak, Gunung Penrissen	KU587723
<i>T. batupanggih</i>	ZRC 2.7123	East Malaysia, Sarawak, Gunung Penrissen	KU587725
<i>T. hallieri</i>	FMNH 230184	East Malaysia, Sabah Lahad Datu District	JF497973
<i>T. leproauricularis</i>	LSUHC 7860	East Malaysia, Sarawak, Gunung Penrissen	KU587724
<i>T. parvus</i>	RMB 4707	Indonesia, Sulawesi	JF498213
<i>T. sananus</i>	JAM 8829	Indonesia, Sanana Island	KY989394
<i>T. temmincki</i>	BS 10263	Indonesia, Java	KY989396
<i>T. textus</i>	JAM 7497	Indonesia, Sulawesi	KY989397
Swamp clade			
<i>T. panchorensis</i> (holotype)	LSUHC 4801	West Malaysia, Penang, Bukit Panchor State Park	KU872741
<i>T. sibuensis</i>	LSUHC 5583	West Malaysia, Johor, Pulau Sibiu	KU872743
<i>T. temasekensis</i> sp. nov.	JAM 7233	Pasir Laba Road, Singapore	KY9893945

Species	Voucher	Locality	GenBank No.
Upland clade			
<i>T. bukitensis</i>	LSUHC 12750	West Malaysia, Pahang, Genting Highlands, Awana Rd.	KY989398
<i>T. bukitensis</i>	LSUHC 12237	West Malaysia, Pahang, Genting Highlands, Awana Rd.	KY989399
<i>T. bukitensis</i> (holotype)	ZRC 2.6245	West Malaysia, Pahang, Fraser's Hill, Bishops's Trail	KY989400
<i>T. bukitensis</i>	LSUHC 12686	West Malaysia, Pahang, Fraser's Hill, Jeriau	KY989401
<i>T. bukitensis</i>	LSUHC 12687	West Malaysia, Pahang, Fraser's Hill, Jeriau	KY989402
<i>T. bukitensis</i>	LSUHC 12226	West Malaysia, Pahang, Fraser's Hill, Jeriau	KY989403
<i>T. bukitensis</i>	LSUHC 11771	West Malaysia, Pahang, Fraser's Hill, Telecom Loop	KY989404
<i>T. butleri</i>	LSUHC 9206	West Malaysia, Perak, Bukit Larut	KU872732
<i>T. butleri</i>	LSUHC 12429	West Malaysia, Perak, Bukit Larut	KY989406
<i>T. butleri</i>	LSUHC 12432	West Malaysia, Perak, Bukit Larut	KY989406
<i>T. butleri</i>	LSUHC 12433	West Malaysia, Perak, Bukit Larut	KY989407
<i>T. butleri</i>	LSUHC 9204	West Malaysia, Perak, Bukit Larut	KU872731
<i>T. butleri</i>	LSUHC 12516	West Malaysia, Penang, Penang Island, Penang Hill	KY989408
<i>T. butleri</i>	LSUHC 12071	West Malaysia, Penang, Penang Island, Penang Hill	KU872733
<i>T. butleri</i>	LSUHC 11275	West Malaysia, Penang, Penang Island, Penang Hill	KY989410
<i>T. butleri</i>	LSUHC 11552	West Malaysia, Kedah, Pulau Langkawi, Gunung Raya	KU872737
<i>T. butleri</i>	LSUHC 6790	West Malaysia, Kedah, Pulau Langkawi, Gunung Raya	KU872736
<i>T. butleri</i>	LSUHC 11784	West Malaysia, Kedah, Pulau Langkawi, Gunung Raya	KY989411
<i>T. butleri</i>	LSUHC 11785	West Malaysia, Kedah, Pulau Langkawi, Gunung Raya	KU872738
<i>T. butleri</i>	LSUHC 11786	West Malaysia, Kedah, Pulau Langkawi, Gunung Raya	KU872739
<i>T. butleri</i>	LSUHC 9206	West Malaysia, Kedah, Pulau Langkawi, Gunung Raya	KU972732
<i>T. ishaki</i>	LSUHC 5165	West Malaysia, Pahang, Pulau Tioman, Gunung Kajang	KY989413
<i>T. ishaki</i>	LSUHC 6150	West Malaysia, Pahang, Pulau Tioman, Gunung Kajang	KU872735
<i>T. ishaki</i>	LSUHC 6151	West Malaysia, Pahang, Pulau Tioman, Gunung Kajang	KY989414
<i>T. jaripendek</i> (holotype)	LSUHC 11681	West Malaysia, Pahang, Cameron Highlands, Robinson Falls	KU872745
<i>T. jaripendek</i>	LSUHC 11679	West Malaysia, Pahang, Cameron Highlands, Robinson Falls	KU872746
<i>T. jaripendek</i>	LSUHC 11680	West Malaysia, Pahang, Cameron Highlands, Robinson Falls	KU872747
<i>T. jaripendek</i>	LSUHC 11987	West Malaysia, Pahang, Cameron Highlands, Robinson Falls	KU872748
<i>T. kakikecil</i>	LSUHC 11769	West Malaysia, Pahang, Fraser's Hill, Richmond Rd.	KY989415
<i>T. kakikecil</i>	LSUHC 11770	West Malaysia, Pahang, Fraser's Hill, Richmond Rd.	KY989416
<i>T. kakikecil</i>	LSUHC 11772	West Malaysia, Pahang, Fraser's Hill, Telecom Loop	KY989417
<i>T. kakikecil</i>	LSUHC 12754	West Malaysia, Pahang, Genting Highlands, Ulu Kali	KY989418
<i>T. martae</i>	LSUHC 12688	West Malaysia, Pahang, Fraser's Hill, Hindu Temple	KY989419
<i>T. martae</i>	ZRC 3.6246	West Malaysia, Pahang, Fraser's Hill, Bishop's Trail	KY989420
<i>T. martae</i>	LSUHC 12749	West Malaysia, Pahang, Genting Highlands, Awana Rd.	KY989421
<i>T. martae</i>	LSUHC 12518	West Malaysia, Pahang, Genting Highlands, Awana Rd.	KY989422
<i>T. martae</i>	LSUHC 12751	West Malaysia, Pahang, Genting Highlands, Awana Rd.	KY989423
<i>T. martae</i>	LSUHC 12571	West Malaysia, Pahang, Genting Highlands, Awana Rd.	KY989424
<i>T. perhentianensis</i> (holotype)	LSUHC 9206	West Malaysia, Terengganu, Pulau Perhentian Besar	KU872742
<i>T. temengorensis</i>	LSUHC 9206	West Malaysia, Perak, Temengor Forest Reserve	KU872744
<i>Tytthoscincus</i> sp. nov.	LSUHC 12515	West Malaysia, Terengganu, Tembak Reservoir	MG182075

sequenced using the ABI Big-Dye Terminator v3.1 Cycle Sequencing Kit in an ABI GeneAmp PCR 9700 thermal cycler. Cycle sequencing reactions were purified with Sephadex G-50 Fine (GE Healthcare) and sequenced on an ABI 3730xl DNA Analyser at the BYU DNA Sequencing Center. All sequences were edited in Geneious v6.1.8 (Drummond et al., 2011) and aligned by eye. Mesquite v3.0.2 (Maddison & Maddison, 2015) was used to check for premature stop codons and to ensure the correct amino acid read frame. Uncorrected pairwise sequence divergences were calculated in MEGA7.0 (Kumar et al., 2016).

The phylogenetic analysis applied two model-based methods, Maximum Likelihood (ML) and Bayesian Inference (BI).

The Bayesian Information Criterion (BIC) as implemented in IQ-TREE (Nguyen et al., 2015) calculated TVM+I+G4, HKY+G4, and TPM3+G4 to be the best-fit models of evolution for the first, second, and third codon positions, respectively. Maximum Likelihood analyses using IQ-TREE employed 1,000 bootstrap pseudoreplicates via the ultrafast bootstrap approximation algorithm. A codon-partitioned Bayesian analysis was carried out in MrBayes v3.2.6 (Huelsenbeck & Ronquist, 2001; Ronquist & Huelsenbeck, 2003) on CIPRES (Cyberinfrastructure for Phylogenetic Research; Miller et al., 2010) using default priors. Models of evolution used were approximated from those calculated for the ML analysis and employed GTR+I+ Γ for the first and third codon positions and HKY+ Γ for the second codon

Table 2. Summary statistics and loadings of the Principal Component Analysis from species from the swamp clade of *Tyrrhoscinus*.

	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10
Standard Deviation	2.41065	1.75744	1.15041	0.89153	0.64558	0.49185	0.44804	0.28415	0.20435	0.00000
Proportion of Variance	0.48427	0.25738	0.11029	0.06624	0.03473	0.02016	0.01673	0.00673	0.00348	0.00000
Cumulative Proportion	0.48427	0.74165	0.85194	0.91817	0.95290	0.97306	0.98979	0.99652	1.00000	1.00000
Eigenvalue	5.81122	3.08858	1.32344	0.79482	0.41677	0.24192	0.20074	0.08074	0.04176	0.00000
Snout-forelimb Length/SVL	-0.39699	-0.12068	-0.02600	-0.02609	0.26062	-0.10718	0.15791	-0.14150	-0.01959	0.15044
Axilla-groin Length/SVL	-0.17850	0.35243	0.27639	-0.62900	0.03099	0.10500	-0.04000	-0.12840	0.51188	-0.01454
Head Length/SVL	-0.38953	-0.03951	0.10805	0.16113	0.01414	-0.53792	0.17606	0.09065	-0.09533	0.36457
Head Width/SVL	-0.33663	-0.12526	0.37190	0.30087	0.16820	-0.00616	-0.19690	-0.44071	0.25620	0.04035
Supralabials	0.30636	0.24713	0.28410	-0.32474	-0.17508	-0.44943	-0.19342	-0.11446	-0.34974	0.34636
Infralabials	0.31746	0.15645	0.37534	0.30525	-0.12420	-0.32949	0.45966	-0.12981	0.20675	-0.45671
Postsupralabials	-0.21533	0.35282	-0.45394	-0.01355	-0.25305	-0.11903	0.43586	0.14564	0.27888	0.14488
Loreals	0.35883	-0.22741	-0.03815	0.24002	-0.19523	-0.05315	-0.23717	0.12132	0.60431	0.48504
Midbody Scale Rows	-0.03228	0.44791	0.41369	0.29258	0.27053	0.31786	0.02858	0.55031	-0.07231	0.21752
Paravertebral Scale Rows	0.04283	0.50631	-0.20227	0.33250	-0.15569	0.26059	-0.06301	-0.58058	-0.15652	0.21867
Ventral Scales	0.25123	0.25441	-0.35379	0.04088	0.74062	-0.34963	-0.18839	-0.03316	0.15080	-0.09373
4th Toe Subdigital Lamellae	0.33126	-0.24604	0.08134	-0.18148	0.32932	0.26338	0.60704	-0.23270	-0.04859	0.39229

position. Two simultaneous runs were performed with four chains per run (three hot and one cold) using default priors. The simulation ran for four million generations, was sampled every 4,000 generations with the Markov Chain Monte Carlo (MCMC), and halted after the average standard deviation split frequency was below 0.01. The first 25% of the trees were discarded as burnin using the sumt function. Convergence of all parameters and stationarity distributions were verified and checked in Tracer v1.6 (Rambaut et al., 2014). Nodes having ultrafast ML bootstrap values of 95 and above and BI posterior probabilities of 0.95 and above were considered well-supported (Huelsenbeck et al., 2001; Nguyen et al., 2015; Wilcox et al., 2002).

Morphological analysis. All measurements were made with Mitutoyo digital calipers to the nearest 0.1 mm by LLG. Scale counts were made on the right side of the body when possible with a Nikon SMZ 1500 dissecting microscope. Scale terminology was adapted from Grismer et al. (2009a, b) and Lim (1998). Measurements and scale counts used were snout-vent length (SVL) measured from the tip of the rostral scale to the vent; snout-forelimb insertion (SFL) measured from the anterior margin of the forelimb at its insertion point on the body to the tip of the rostral scale; axilla-groin length (AXG) measured from the anterior margin of the hind limb at its insertion point of the body to the posterior margin of the forelimb measured at its insertion point on the body with the upper limb sections held at right angles to the body; head length (HL) measured from the anterior margin of the ear opening to the tip of the rostral scale; and head width (HW) measured across the widest part of the head posterior to the eyes.

Scale counts taken were midbody scale rows counted as the number of longitudinal scale rows encircling the body at a point midway between the limb insertions; paravertebral scale rows counted as the number of scales in a line from the parietal scales to a point on the dorsum opposite the vent; and ventral scale rows counted as a row of scales between the postmental and the edge of the cloacal plate. Other standard counts include superciliaries (given as two numbers, the first accounting for the anterior smaller scales followed by a second number accounting for the much larger, posteriorly projecting scales preceded by the notation of a ' [e.g., 8'1]), supraoculars, loreals, supralabials, postsupralabials, infralabials, and fourth toe subdigital lamellae. Additional characters examined were the degree of contact between the parietals and supraoculars, enlargement of posterior superciliary scales, degree of contact between the prefrontal scales, presence or absence of enlarged preloacal and pectoral scales, texture of subdigital lamellae, and the degree of development of the tympanum. Colour pattern characters examined were the degree of dark, dorsolateral striping and overall ground colour.

An analysis of variance (ANOVA) was performed to ascertain if statistically significant mean differences ($p < 0.05$) existed among the populations for the scale counts. Statistically different ANOVAs ($p < 0.05$) were subjected to a TukeyHSD test to ascertain which population pairs

Table 3. Percent uncorrected pair-wise sequence divergence for species of *Tytthoscincus* swamp clade.

	<i>temasekensis</i>	<i>panchorensis</i>	<i>sibuensis</i>
<i>temasekensis</i>	**	**	**
<i>panchorensis</i>	0.150	**	**
<i>sibuensis</i>	0.145	0.113	**

differed significantly. A Principal Component Analysis (PCA) as implemented by the `prcomp` command in R v 3.2.1 (R Core Team, 2015), was employed to find the overall best low-dimensional representation of the significant morphological variation in the data and to ascertain if such differences could form the basis of statistically detectable group structure. Characters used in the PCA are listed in Table 2. Ratiometric data (SFL/SVL, AXG/SVL, HL/SVL, HW/SVL, and HDL/SVL) were used only from adults (SVL \geq 30 mm or determined by the possession of eggs or by dissection) to minimise the allometric effects of body size. All PCA characters were log-transformed prior to analysis and then scaled to one standard deviation of their means in order to normalise distributions to ensure characters with very large and very low values did not over-leverage the results due to intervariable nonlinearity.

RESULTS

The ML and the BI analyses produced trees with the same topologies and the ML topology is presented here with BI and ML bootstrap values, respectively placed at the nodes (Fig. 1). The molecular analyses are consistent with those of Grismer et al. (2016a, 2017) indicating that the swamp clade of *Tytthoscincus* is nested within a larger clade of Indonesian, Philippine, and Bornean species and composed of three very distinctive species with uncorrected pairwise sequence divergences ranging 11.3–15.0% among them (Table 3). The analyses demonstrate that the *T. cf. sibuensis* (= *T. temasekensis* [see below]) is not conspecific with *T. sibuensis* but sister to the *T. sibuensis* and *T. panchorensis* lineage and warrants separate species recognition. To consider *T. cf. sibuensis* conspecific with *T. sibuensis* would render the latter paraphyletic.

The morphological analyses support the molecular analyses in confirming the specific identity of *T. cf. sibuensis*. In the PCA analysis (Fig. 1), principal components 1 (PC1) and 2 (PC2) account for 74% of the total variation and PC3 accounts for an additional 11% (Table 2). Ordination of PC1 and PC2 demonstrates that *T. cf. sibuensis* clusters separately from *T. sibuensis* and *T. panchorensis* along PC1, which accounts for 48% of the total variation and loads most heavily for snout-forelimb length/SVL, head length/SVL (which are no doubt correlated), and loreals (Table 2). *Tytthoscincus cf. sibuensis* is also completely separated from *T. panchorensis* along PC2, which loads most heavily for paravertebral scales. The PCA also demonstrates that the specimens from Tanjung Malim cluster with other *T. cf. sibuensis* along both PC1 and PC2 (Fig. 1). *Tytthoscincus cf. sibuensis* specimens and the Tanjung Malim populations show no discrete or statistically

significant differences between them in scales counts, scale morphology, or colour pattern (Tables 4, 5) and are thus considered here to be conspecific. Collectively, however, they differ discretely from *T. sibuensis* in having two versus one loreal and 54–63 versus 52 ventrals (Tables 4, 5). However, with a sample size of one for *T. sibuensis*, these may not turn out to be discrete differences and they are not statistically significantly different. *Tytthoscincus cf. sibuensis* and the Tanjung Malim population differ collectively from *T. panchorensis* in having two versus three postsupralabials, four versus five supraoculars, two versus one loreal, 55–65 versus 68 paravertebral scale rows, and 9–11 versus eight subdigital fourth toe lamellae (Tables 4, 5). The means values of the latter (10.0 versus 8.0, respectively) are the only values that statistically significantly different ($p < 0.05$).

TAXONOMY

The molecular and morphological data indicate thus far that the *Tytthoscincus* populations from Singapore and Tanjung Malim are conspecific and well-differentiated from *T. sibuensis* and *T. panchorensis*. They are therefore described below as:

***Tytthoscincus temasekensis*, new species**
Singapore swamp skink
(Fig. 2)

Tytthoscincus cf. sibuensis — Grismer et al., 2017: in press.

Holotype. ZRC 2.6490 (adult female) collected from Pasir Laba Road, Singapore (N 01°19.526', E 103°40.212'; 24 m elevation) by B. Y. H. Lee on 21 June 2014.

Paratypes. ZRC 2.2557 (juvenile) collected from the Nee Soon Swamp, Singapore (approximately N 01°24.051', E 103°48.537'; 20 m elevation) by K. P. K. Lim on 28 December 1989. ZRC 2.667 (adult male) collected from the Nee Soon Swamp, Singapore (approximately N 01°24.051', E 103°48.537'; 20 m elevation) by K. Young and P. K. L. Ng on 30 April 1990. ZRC 2.3959 (adult male) at Lorong Banir off Upper Thomson Road, Singapore (approximately N 01°23.427', E 103°50.220'; 9 m elevation) by K. P. K. Lim on 24 May 1994. ZRC 2.7111 (juvenile) collected at Upper Seletar Reservoir Park, Singapore (approximately N 01°22.376', E 103°48.434'; 37 m elevation) by N. Baker on 12 September 2015.

Non-types. *Tytthoscincus temasekensis*. ZRC 2.3277 (juvenile) from North Selangor Peat Swamp kilometer marker 34 on road to Tanjung Malim, Selangor, Peninsular

Table 4. Meristic data for the types series of *Tythosincus temasekensis* sp. nov., *T. sibuensis*, and *T. panchorensis*. Tg. = [Tanjung], Bk. = [Bukit], and P. = [Pulau]. Tail tips of ZRC 2.7111 and 2.6490 were removed for DNA analysis. ca = approximately. Diagnostic characters are in bold.

	<i>temasekensis</i>					<i>panchorensis</i>			<i>sibuensis</i>	
	ZRC	ZRC	ZRC	ZRC	ZRC	ZRC	ZRC	ZRC	LSUHC	ZRC
Supralabials	7	6	6	7	6	6	7	7	6	6
Infralabials	7	7	5	7	5	6	7	7	5	5
Postsupralabials	2	2	2	2	2	2	2	2	3	2
Supraoculars	4	4	4	4	4	4	4	4	5	4
Interparietal contacting supraoculars	2,3,4	2,3,4	2,3,4	2,3,4	2,3,4	2,3,4	2,3,4	2,3,4	3,4,5	2,3,4
Superciliaries	9.1	9.1	9.1	10.2	9.1	9.1	9.1	9.1	8.1	10.2
Prefrontals in contact	yes	point	no	no	no	point	no	no	no	no
Loreals	2	2	2	2	2	2	2	2	1	1
Tympanum recessed	yes	yes	yes	yes	yes	yes	yes	yes	yes	yes
Midbody scale rows	29	29	27	29	28	28	28	29	29	29
Paravertebral scale rows	63	61	55	65	61	62	61	62	68	58
Ventral scale rows	54	56	55	63	57	54	57	58	57	52
Enlarged pectoral scales	yes	yes	yes	yes	yes	yes	yes	yes	no	no
4th toe lamellae	9	10	10	10	10	10	11	11	8	9
Adpressed limbs	contact	contact	contact	contact	contact	contact	contact	contact	separate	separate
Color pattern with white lineate markings	yes	yes	yes	yes	yes	yes	yes	yes	no	yes
SVL	28.8	22.5	23.0	34.9	34.9	24.7	36.3	35.4	35.5	17.7
SFL	9.5	8.1	8.7	11.5	12.1	9.0	12.0	11.3	13.8	7.4
AXG	15.5	11.0	11.8	18.4	17.5	12.5	19.0	19.8	20.4	10.2
HL	5.1	4.2	4.3	5.8	6.0	4.5	6.1	5.7	7.2	3.8
HW	3.6	3.1	3.1	4.1	4.3	3.4	4.1	3.9	4.5	3
TL	31.8	22.4	ca 23.7	ca 40.8	46.6	32.5	46.1	44.1	30	16.5

Table 5. Summary statistics for species in the swamp clade of *Tytthoscincus*.

	<i>temasekensis</i> new species	<i>sibuensis</i>	<i>panchorensis</i>
Supralabials	6 or 7	6	6
Mean	6.5	6.0	6.0
SD	±0.53	/	/
Postsupralabials	2	2	3
Mean	2.0	2.0	2.0
SD	/	/	/
Infralabials	5–7	5	5
Mean	6.4	5.0	5.0
SD	±0.92	/	/
Supraoculars	4	4	5
Mean	4.0	4.0	5.0
SD	/	/	/
Loreals	2	1	1
Mean	2.0	1.0	1.0
SD	/	/	/
Midbody scales	27–29	29	29
Mean	28.4	29.0	29.0
SD	±0.74	/	/
Paravertebral scales	55–65	58	68
Mean	61.3	58.0	68.0
SD	±2.92	/	/
Ventral scales	54–63	52	57
Mean	56.8	52.0	57.0
SD	±2.92	/	/
4th toe lamellae	9–11	9–11	8
Mean	10.1	10.0	8.0
SD	±0.64	/	/
n	8	1	1

Malaysia (approximately N 03°42.383', E 101°09.115'; 20 m elevation) collected by NUS 1991–92 Zoology Honours Class on 17 June 1991. ZRC 2.3377 (juvenile) from North Selangor Peat Swamp kilometer marker 47 at Sungai Besar Road on road to Tanjung Malim, Selangor, Peninsular Malaysia (approximately N 03°41.472', E 101°14.062'; 15 m elevation) collected by D. S. L. Chung in April 1993. ZRC 2.7152 from the Nee Soon swamp-forest, Singapore collected by H. H. Tan and others on 23 October 1999.

Diagnosis. *Tytthoscincus temasekensis* sp. nov. can be differentiated from all other species of *Tytthoscincus* in Peninsular Malaysia by having the combination of two loreals, two postsupralabials, 9¹ or 10² superciliaries, four supraoculars; interparietal contacting 2nd–4th supraoculars, a shallow, pigmented tympanum, slightly enlarged pectoral scales, 27–29 midbody scale rows, 55–65 paravertebral scales, 54–63 ventral scales, 9–11 subdigital lamellae on the fourth toe, keeled, subdigital lamellae, and a dorsal pattern of light-coloured stripes and/or linearly arranged spots. All characters are scored across all other *Tytthoscincus* and species of *Sphenomorphus* suspected of being *Tytthoscincus* in Grismer et al. (2016a: 237) and Karin et al. (2016: 416).

Description of holotype. Adult female, SVL 34.9 mm; tail length 40.8 mm, 2 mm of tip removed; axilla-groin length 18.4 mm; head length 5.8 mm; head width 4.1 mm; snout to anterior margin of foreleg 11.5 mm; rostral wider than long, in broad contact with frontonasal; frontonasal wider than long; prefrontals large, contacting on midline; frontal elongate, diamond-shaped, in contact with first two supraoculars; four supraoculars; interparietal in contact posterior to frontal, contacting second, third, and fourth, supraoculars anterolaterally and parietals and interparietal posteriorly; frontoparietals non-overlapping; interparietal diamond-shaped, large, slightly projecting posteriorly, eyespot in posterior projection; parietals large, in medial contact posterior to interparietal, contacting fourth supraocular anteriorly; enlarged nuchal scales absent; nasals small, widely separated, trapezoidal, contacting rostral anteriorly, frontonasal dorsally, first loreal posteriorly, first supralabial ventrally; nostril in center of nasal; supranasals absent; two loreals taller than wide, posterior loreal largest; upper and lower preocular present; 10 superciliaries, posterior two superciliaries elongate and projecting dorsomedially; seven supralabials, third, fourth, and fifth below eye; two postsupralabials; two primary temporals; two pretemporals;



Fig. 2. *Tythoscincus temasekensis* sp. nov. Upper: adult holotype (ZRC 2.6490) from Pasir Laba Road, Singapore. Middle: juvenile paratype (ZRC 2.7111) from Upper Seletar Reservoir Park, Singapore (Photograph by Nick Baker). Lower: uncataloged specimen from 3 km south of the Nee Soon Swamp, Singapore (Photograph by Noel Thomas).

two secondary temporals, uppermost not contacting parietals; lower eyelid transparent, scaly, no enlarged central window; mental twice as wide as long; single, large postmental, contacting first infralabials on each side; two enlarged pairs of chinshields posterior to postmental, anterior pair contacting medially, posterior pair separated posteriorly by a single scale; chinshields contacting infralabials; seven infralabials; external ear opening 0.8 mm wide, approximately one-half diameter of eyeball, subcircular, lacking anterior lobules; and tympanum shallow, pigmented.

Body scales smooth, cycloid, imbricate; ventral scales slightly larger than dorsal scales; some pectoral scales slightly enlarged; 29 longitudinal scale rows around midbody; 65 paravertebral scale rows; 63 ventral scale rows; slightly enlarged precloacal scales, inner precloacals overlap outer precloacals; and tail slightly compressed laterally.

Limbs well-developed, short, contacting but not overlapping when adpressed; scales of dorsal surface slightly larger than those of ventral surface; palmar and plantar scales slightly raised; and digits short, scales of dorsal surface of fourth toe in multiple rows, subdigital keeled, 10 on fourth toe; and rank of toe length I, II, IV, III, V.

Colouration in alcohol (Fig. 2). Overall dorsal ground colour of head, body, limbs, and tail dark-brown; head speckled with light-coloured markings; labials distinctly



Fig. 3. Microhabitat of *Tythoscincus temasekensis* sp. nov. in the Nee Soon Swamp, Singapore.

barred; labials bearing a central light-coloured spot; anterior of flanks and venter to posterior margin of jaws dull-orange; light-coloured, lineate, paravertebral markings extending from postorbital region to groin becoming more of a series of spots closer to the groin and bordered below anteriorly by a thick, dark-coloured stripe; mid-dorsal region bearing a lineate series of light-coloured, paravertebral spots extending from occiput to anterior portion of tail; dorsal surface of limbs and tail speckled; ventral surfaces beige; and plantar and palmar regions dark.

Variation (Fig. 2). Paratypes closely approach the holotype in all aspects of colouration except for the dorsal pattern of ZRC 2.2557 is generally more spotted than lineate. The dorsal patterns of ZRC 2.2667 and 2.3959 are very faded but the same general lineate characteristics are still visible. Colour photos of living ZRC 2.2711 show its dorsal pattern to be much less bold than that of the holotype and nearly unicolour. Both ZRC 2.3277 and 2.3377 from the vicinity of Tanjung Malim bear the same lineate dorsal characteristics of the Singapore specimens. Meristic variation is presented in Table 4.

Distribution. *Tythoscincus temasekensis*, new species, is known from lowland areas in Singapore and near Tanjung Malim, Perak, Peninsular Malaysia (Fig. 1).

Natural history. *Tythoscincus temasekensis* has been found in lowland dipterocarp forests but is far more common along stream banks in peat and freshwater swamp forests up to

DISCUSSION

at least 37 m in elevation (Lim, 1998; Serin, 2015; Fig. 3). Specimens near Tanjung Malim were inadvertently collected while hand-netting for fishes in small streams which may indicate semi-aquatic proclivities as noted by Baker (2013) who states “An example of about 5 cm was seen among forest leaf litter at the edge of a shallow stream. It swam in a sinuous motion across the stream, coming to rest on the opposite side partly submerged, with only the front part of its head including the eyes and nostrils emerged.” ZRC 2.7111 was collected while crossing a paved road running through lowland forest. A juvenile (ZRC 2.6859) was taken from the gut of an *Aheatulla mycterizans* found dead on Old Upper Thomson Road.

Etymology. The specific epithet *temasekensis* is derived from the word Temasek meaning ‘Sea Town’ in Old Javanese and represents the earliest recorded name of a settlement in Singapore. The suffix *-ensis* is Latin meaning ‘of or from a place.’ The specific epithet is in reference to the type locality being on the island of Singapore. The suggested common name is the Singapore swamp skink.

Comparisons. *Tytthoscincus temasekensis*, new species, can be differentiated from all other species of the *Tytthoscincus* of the montane clade by having stripes or longitudinally arranged spots. *Tytthoscincus temasekensis* sp. nov. can be differentiated from all other species of the *Tytthoscincus* of the swamp clade by having two versus one loreal scale, slightly enlarged pectoral scales versus no enlarged pectoral scales, and adpressed limbs making contact versus being separated. *Tytthoscincus temasekensis* sp. nov. can be further differentiated from *T. panchoensis* by the interparietal contacting the 2nd–4th supraoculars versus the 3rd–5th supraoculars and having four versus five supraoculars (these two characters are linked); having 55–65 versus 68 paravertebral scales rows, having 9–11 versus eight subdigital lamellae on the 4th toe; and having white lineate markings in its dorsal pattern (Tables 4, 5). *Tytthoscincus temasekensis* sp. nov. is further differentiated from *T. sibuensis* by having 54–63 versus 52 ventral scale rows.

Remarks. Because the morphology and colour pattern of the Tanjung Malim specimens from Peninsular Malaysia (ZRC 2.3277, 2.3377) are completely subsumed within the variation of those from specimens of the Singapore population, we elect to consider them conspecific given there is no intrinsic evidence to suggest otherwise. However, we do not include the Tanjung Malim specimens as part of the type series. Cryptic within the genus *Tytthoscincus*, has been well-documented and can potentially create taxonomic problems when new species are described in the absence of molecular data (Grismer et al., 2017). If molecular evidence eventually indicates that the Tanjung Malim population is not conspecific with the Singapore population, the type series of *T. temasekensis* sp. nov. will remain intact. This was not the case with the type series of *T. bukitenis* (Grismer, 2007a) that was eventually shown to be composed of two unrelated species (Grismer et al., 2017).

The distribution pattern of the three species in the swamp clade of *Tytthoscincus* from four widely separated populations indicates that this group occupies lowland swampy areas ranging around the southern end and up both sides of the Banjaran [=mountain range] Titiwangsa of Peninsular Malaysia (Fig. 1). This distribution pattern is not unique and is seen in other species of Malaysian amphibians and reptiles, most notably the peat swamp toad *Ingerophrynus kumquat* Das & Lim, 2001 (Sukumaran et al., 2006) and the riparian skinks *Sphenomorphus sungaicolus* Sumarli, Grismer, Wood, Amirrundin, Syed, Lukman, Nur Amalina, Norhayati & Linkem, 2016 and *Lipinia surda* (Boulenger, 1900) and *L. sekayuensis* Grismer, Ismail, Awang, Rizal & Ahmad, 2014a (Grismer et al., 2016b); for other lizards species see the distribution maps in Grismer (2011). We fully expect that new or existing species within the swamp clade will eventually be found farther north on both sides of the Banjaran Titiwangsa.

The discovery of a plethora of new species in montane and island ecosystems in Peninsular Malaysia has dominated discussions of herpetological diversity and conservation over the last 13 years (see Grismer et al., 2011, 2016a, 2017 for discussions and references). Left out of these discussions, however, is the growing importance of swamplands to the herpetological diversity of Singapore and Peninsular Malaysia. Das & Lim (2001) and Sukumaran et al. (2006) reported on *Ingerophrynus kumquat* Das & Lim, 2001 from peat swamps in Selangor and Pahang and Grismer (2007b) reported *I. gollum* Grismer, 2007 from a swamp in Endau-Rompin, Johor. Grismer et al. (2014b) reported on five unique Bent-toed Geckos (*Cyrtodactylus*) constituting a swamp clade from Singapore and Peninsular Malaysia which has been augmented with three additional species from Sumatra and Natuna Besar, Indonesia (Riyanto et al., 2015; Harvey et al., 2015). With the description of *Tytthoscincus temasekensis* sp. nov., an established swamp clade of skinks is now recognised to occur in Singapore and Peninsular Malaysia. As swamplands are explored further, it is likely additional new species of amphibians and reptiles will be discovered and the important role that these distinctive environments have to play in herpetological biodiversity and conservation will begin to emerge.

ACKNOWLEDGEMENTS

The authors wish to thank Nick Baker and Noel Thomas for the use of their photographs and Nick Baker for discussions over the years concerning the natural history of *Tytthoscincus temasekensis* sp. nov. Funding for LLG came from grants from the College of Arts and Sciences at La Sierra University and from a National Geographic Society Explorers Grant (9277-15).

MATERIAL EXAMINED

- Tytthoscincus bukitensis*. West Malaysia, Pahang, Fraser's Hill, Telecom Loop (LSUHC 11655, 11771), Jeriau (LSUHC 12226, 12686–87), Bishops's Trail (ZRC 2.6245 [holotype]). West Malaysia, Pahang, Genting Highlands, Awana Road (LSUHC 12237, 12750).
- Tytthoscincus butleri*. West Malaysia: Kedah, Pulau Langkawi, Gunung Raya; LSUHC 6790, 11152, 11784–87, 11840–41, LRCUKM 143, 148. West Malaysia: Kedah, Pulau Singa Besar; DWNP 3032. West Malaysia: Perak, Bukit Larut; LSUHC 9043, 9204–06, 12429, 12432–33. West Malaysia: Penang, Penang Island, Air Hitam Dam (LSUHC 11275, 11802) and Penang Hill (LSUHC 12071).
- Tytthoscincus ishaki*. West Malaysia: Pahang, Pulau Tioman, Gunung Kajang LSUHC 4429, 12582, ZRC 2.6157 (holotype), 2.6158–59 (paratypes).
- Tytthoscincus jaripendek* West Malaysia: Pahang, Cameron Highlands, Robinson Falls LSUHC 11679, 11681, 11987 (paratypes), 11680 (holotype).
- Tytthoscincus kakikecil* West Malaysia: Pahang, Fraser's Hill, Richmond Road (LSUHC 11769 [holotype]), Telecom Loop (LSUHC 11770, 11772). West Malaysia: Pahang, Genting Highlands, Ulu Kali LSUHC 12754, FMNH 199945. West Malaysia: Pahang, Cameron Highlands, Telom Valley ZRC 2.5944.
- Tytthoscincus martaе* West Malaysia: Pahang, Fraser's Hill, Hindu Temple LSUHC 12688 (holotype), ZRC 3.6246 (paratype). West Malaysia, Pahang, Genting Highlands, Awana Road LSUHC 12517–18, 12749, 12751 (paratypes), 12072.
- Tytthoscincus perhentianensis*. West Malaysia: Terengganu, Pulau Perhentian Besar LSUHC 8075 (holotype).
- Tytthoscincus temengorensis*. West Malaysia: Perak, Royal Belum Park DWNP 5018 (holotype). West Malaysia: Perak, Temengor Forest Reserve, Gibbon Trail LSUHC 5650 (paratype).

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