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A new species of tree frog (Amphibia, Anura, Rhacophoridae) from Central Java, Indonesia

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Abstract. A new species of tree frog of the genus *Zhangixalus* from Central Java, Indonesia, which was previously confused with *Z. prominanus*, is described based on molecular and morphological evidence. *Zhangixalus faritsalhadii*, new species, is distinguishable from its congeners by having a genetic distance of more than 3.1% of 16s rRNA gene and the combination of morphological characters. The discovery of this new species provides the latest information on the amphibian species in Java and encourages conservation efforts in protecting the habitats of amphibians on this island.

Key words. new species, *Zhangixalus faritsalhadii*, 16S rRNA, morphology, Java, Indonesia

INTRODUCTION

Within the family Rhacophoridae, the genus *Zhangixalus* Li, Jiang, Ren & Jiang, 2019, currently consists of 43 species, of which 40 are distributed in eastern Asia and northern Indochina, ranging from northeastern India, Nepal, Bhutan, southern China, Myanmar, northern Thailand, Laos, northern Vietnam, Taiwan, and Japan (Jiang et al., 2019; Frost, 2024). The other three species—*Z. prominanus* (Smith, 1924), *Z. achantharrhena* (Harvey, Pemberton & Smith, 2002), and *Z. dulitensis* (Boulenger, 1892)—are from the Sunda region, including Malaysia, Brunei, and Indonesia (Chan et al., 2018; O'Connell et al., 2018; Jiang et al., 2019; Chan et al., 2020; Chen et al., 2020; Dufresnes et al., 2022). This Sunda population forms a basal clade in relation to the clade comprising Asian mainland species that diversified in the early Miocene (~20 Mya) (Jiang et al., 2019; Dufresnes et al., 2022).

The jade tree frog, *Zhangixalus prominanus*, was originally described from Jor, Batang Padang, Perak, Peninsular Malaysia (Smith, 1924). Compared to *Z. dulitensis* and *Z. achantharrhena*, which have restricted distributions within Borneo and Sumatra, respectively (Dehling & Dehling, 2013; O'Connell et al., 2018; Ujang et al., 2021; Dufresnes et al., 2022), *Z. prominanus* occurs outside of Peninsular Malaysia and is considered to have a wide distribution in the Sunda region, covering Sumatra (Harvey et al., 2002; O'Connell et al., 2018; Dufresnes et al., 2022) and Peninsular Thailand (Thong-aree et al., 2011). Recent molecular studies confirmed that *Zhangixalus* species from the Sunda region (*Z. dulitensis, Z. prominanus*, and *Z. achantharrhena*) form a monophyletic group (Chan et al., 2018; O'Connell et al., 2018; Dufresnes et al., 2022).

The first photograph of a living specimen that morphologically resembles *Zhangixalus prominanus* from Mount Slamet, Central Java, was presented by Alhadi et al. (2021). However, they temporarily identified it as *Rhacophorus* sp. The specimen depicted by the photographs was sent to and deposited at the Museum Zoologicum Bogoriense (MZB Amph 32890). The status of the specimen MZB Amph 32890 was unclear and required further investigation. Therefore, we conducted an additional survey in July 2022 and collected five additional specimens in the same locality. From the inspections and further genetic analyses of these specimens, distinct morphological characters as well as molecular genetic differences were observed, differentiating this from other species of *Zhangixalus* from Sundaland. Thus, we describe it here as a new species.

MATERIAL AND METHODS

Field surveys. Field surveys were conducted on 10 February 2020 and 4 July 2022 in Mount Slamet, Central Java,

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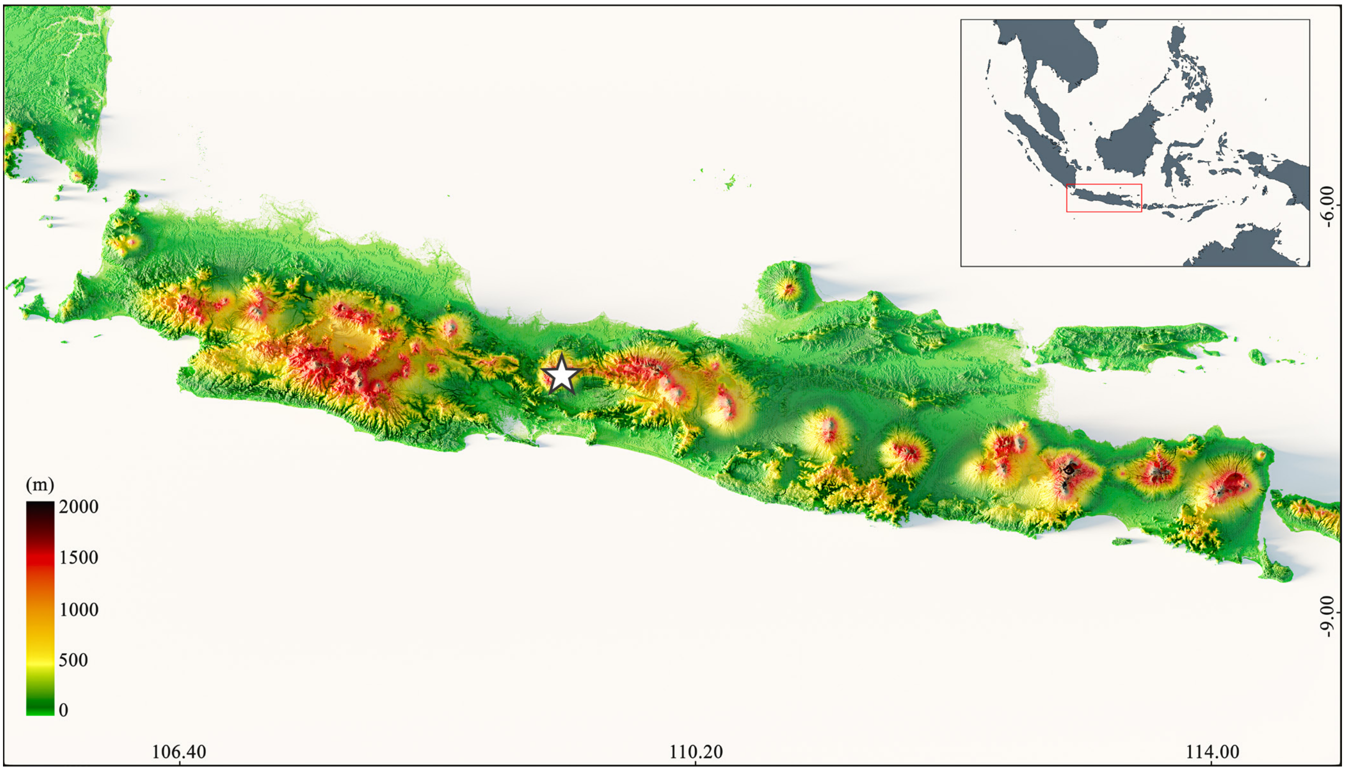

Fig. 1. Map showing *Zhangixalus* sp. (star) type locality at the slope of Mount Slamet, Central Java, Indonesia. Land topography was generated with the SRTM 90 m database from CGIAR CSL (https://srtm.csi.cgiar.org), which was created using QGIS 3.22 Białowieża, and then visualised using Blender 3.6.2 (Blender Community, 2023).

Indonesia (Fig. 1). The sampling, collection, storage, and transportation of samples to the lab followed the ethical guidelines for the use of animals in research and was performed with minimal disturbance to both the habitats and animals, with utmost focus on animal welfare (McDiarmid, 1994). Frogs were first euthanised by immersion in diluted chloretone. Tissue samples were then collected from the liver and stored in 96% ethanol. The specimens were then fixed in 10% formalin, preserved in 70% ethanol, and deposited at the Museum of Zoologicum Bogoriense (MZB), Directorate of Scientific Collection Management, National Research and Innovation Agency, Cibinong, West Java, Indonesia.

Molecular analyses. Whole genomic DNA from the liver samples were extracted using the Qiagen DNEasy kit (Qiagen®, Valencia, California, USA), according to the manufacturer's protocol. The extracted DNA product was amplified from partial DNA sequences of the mitochondrial 16s rRNA gene, following Hamidy et al. (2018), using the primers H3056 5′–CTCCGGTCTGAACTCAGATCACGTAGG–3′ and L2606 5′– CTGACCGTGCAAAGGTAGCGTAATCACT–3′, with an approximate span of 500 bp (Hedges et al., 1993). PCR products were sequenced using the same primers. Four sequences of *Zhangixalus* sp. from Java and *Z. achantharrhena* from Sumatra, respectively, were assembled and checked manually using Chromas Pro v.1.34 (Technelysum Pty Ltd., Brisbane, Australia) and then deposited in GenBank.

We obtained 40 additional sequences (Supplementary Table S1) from GenBank, including eight sequences of *Zhangixalus prominanus,* nine sequences of *Z. achantharrhena,* three sequences of *Z. dulittensis*, and one sequence each of *Z. omeimontis* (Stejneger, 1924); *Z. smaragdinus* (Blyth, 1852); *Z. dugritei* (David, 1872); *Z. schlegelii* (Günther, 1858); *Z. nigropunctatus* (Liu, Hu & Yang, 1962); *Z. feae* (Boulenger, 1893); *Leptomantis belalongensis* (Dehling & Grafe, 2008); *L. gauni* (Inger, 1966); *L. gadingensis* (Das & Haas, 2005); *L. angulirostris* (Ahl, 1927); *Rhacophorus bengkuluensis* Streicher, Hamidy, Harvey, Anders, Shaney, Kurniawan & Smith, 2014; *R. margaritifer* (Schlegel, 1837); *R. barisani* Harvey, Pemberton & Smith, 2002; *R. catamitus* Harvey, Pemberton & Smith, 2002; *R. indonesiensis* Hamidy & Kurniati, 2015; *R. baluensis* Inger, 1954; *R. nigropalmatus* Boulenger, 1895; *R. reinwardtii* (Schlegel, 1840); and *Kurixalus appendiculatus* (Günther, 1858) and *Buergeria oxycephala* (Boulenger, 1900) as outgroups (not shown in our phylogenetic tree).

A total of 48 sequences (GenBank and newly sequenced materials) were aligned using MAAFT v7.480 (Katoh & Standley, 2003) using the default settings. Phylogenetic trees were constructed using Maximum Likelihood (ML) and Bayesian Inference (BI) analyses. The evolutionary model was calculated using the Kakusan 4 software (Tanabe, 2011), and GTR+G+I substitution models were selected for each analysis using the Akaike Information Criterion (AIC). The ML analysis was conducted using the RAxML programme (Stamatakis, 2014) with 1,000 bootstraps. The BI analysis was conducted using MrBayes 3.2.7a (Ronquist et al., 2012). Two simultaneous runs were performed with four chains, each analysis replicated up to 10 million generations, sampled every 100 generations using Markov Chain Monte Carlo (MCMC) and 25% burn-in. The convergence of the MCMC runs was verified using the TRACER v1.6 software (Rambaut et al., 2014). Nodes with ≥ 70% bootstrap values (BS) (Huelsenbeck & Hillis, 1993) and ≥ 0.95 posterior probability (PP) values (Leaché & Reeder, 2002) were highly supported. Genetic distance was calculated using the pairwise distance method in MEGA 11 (Tamura et al., 2021).

Morphological analyses. We examined three male and three female *Zhangixalus* species from Java. For morphological comparisons, we examined ten specimens of *Z. prominanus,* 19 specimens of *Z. achantharrhena* from Sumatra, and 11 specimens of *Z. dulitensis* from Borneo. All specimens were deposited at the MZB (Appendix 1). We measured 34 morphological characters (see Matsui, 1984; Matsui et al., 2013) to the nearest 0.1 mm using digital callipers: (1) snout-vent length (SVL), tip of the snout to the vent; (2) head length (HL), posterior margin of the lower jaw to tip of the snout; (3) head width (HW), widest distance of the head; (4) snout length (SL), from the anterior angle of the eye to the tip of the snout along the canthus rostralis; (5) snout-nostril length (S-NL), from the anterior edge of the nostril to the tip of the snout; (6) nostril-eye length (N-EL), from the posterior edge of the nostril to the anterior edge of the eye; (7) eye diameter (ED), horizontal distance between the anterior and posterior corners of the eye; (8) tympanum diameter (TD), widest horizontal width of the tympanum; (9) internarial distance (IND), shortest distance between the nostrils; (10) intercanthal distance (ICD), shortest distance between the anterior corner of the eyes; (11) interorbital distance (IOD), shortest distance across the top of the head between the medial margins of the orbits; (12) upper eyelid width (UEW), from the base of the upper eyelid to the tip of eyelid; (13) brachium length (BL), length of a flexed elbow, from the axilla to the joint between the elbow and forearm; (14) lower arm length (LAL), from the elbow to the tip of the fourth finger; (15) first finger length (Fin1L); (16) second finger length (Fin2L); (17) third finger length (Fin3L); (18) fourth finger length (Fin4L); (19) first finger disc width (Fin1DW); (20) third finger disc width (Fin3DW); (21) inner palmar tubercle length (IPTL), longest length from the anterior to posterior of the inner palmar tubercle; (22) femur length (FML), longest length of the femur; (23) tibia length (TL), longest length of the tibia; (24) tarsus length (TSL), the tibio-tarsal articulation to the inner metatarsal; (25) foot length (FL), longest length from the base of the inner metatarsal to the tip of fourth toe; (26) first toe length (Toe1L); (27) second toe length (Toe2L); (28) third toe length (Toe3L); (29) fourth toe length (Toe4L); (30) fifth toe length (Toe5L); (31) first toe disc width (Toe1DW), longest length of the first toe disc; (32) third toe disc width (Toe3DW), longest length of the third toe disc; (33) fourth toe disc width (4TDW), longest length of the fourth toe disc; (34) inner metatarsal tubercle length (IMTL), longest length of the inner metatarsal tubercle. Sex and maturity were determined based on the presence of nuptial pads in males and eggs or oviducts in females. The webbing formula follows Savage & Heyer (1967, 1997).

For morphological analysis, each character was scaled to the same size—to eliminate biases caused by ontogenetic variations—using an allometric equation implemented in the R package "GroupStruct" (Chan & Grismer, 2022): $X_{adj} = \log(X) - \beta[\log(SVL) - \log(SVL_{mean})]$, where X_{adj} is the adjusted value, X is the measured value, β is the unstandardised regression coefficient of each population, and SVL_{mean} is the overall average SVL of all samples (Thorpe, 1983; Lleonart et al., 2000). Principal Component Analysis (PCA) was conducted to determine the optimal low-dimensional space for morphological clustering in the built-in R function "prcomp" (R Core Team, 2020). Eigenvalues > 1 were retained according to Kaiser's criterion (Kaiser, 1960). The "Factoextra" package was used to visualise the PCA plot (Kassambara & Mundt, 2020). In the univariate analysis, we normalised each character with Log^{10} and conducted a Student's t-test for differences in mean values between *Zhangixalus* sp. from Java and its closer congeners. P-values ≤ 0.05 imply statistical significance. All statistical analyses were performed in R Core Team (2020).

RESULTS

Phylogenetic analyses showed ML and BI trees in alignment with a total of 455 bp with essentially the same topology as the genus *Zhangixalus* (Fig. 2). In the genus *Zhangixalus*, there were two clades (PP = 0.99, BS = 68), Clades A and B. Clade A consisted of Sundaland species that included three species with our putative new species (*Zhangixalus* sp., *Z. prominanus*, *Z. achantharrhena*, and *Z. dulitensis*). The genetic distance (Table 1) among Clade A ranged from 2.6% to 5.8%. Clade B consisted of Asian mainland species (see Fig. 2). Our putative new species *Zhangixalus* sp. from Java exhibited a distinct monophyletic group (PP = 1.00, BS = 100), which aligns closely with *Z. prominanus* (PP = 0.98, BS = 72). *Zhangixalus* sp. shows a genetic distance ranging from 3.1% to 3.3% compared to *Z. prominanus*, 4.6% to 5.8% compared to *Z. achantharrhena*, and 4.6% to 4.9% compared to *Z. dulitensis*.

The PCA results of our putative new species showed significant morphometric differences from other species of *Zhangixalus* from Sundaland (*Z. prominanus*, *Z. achantharrhena*, and *Z. dulitensis*) in the scatter plots of the first two components (Fig. 3). In males, the first four components accounted for 85.6% of total variance (Supplementary Table S2). The first Principal Component (PC1) accounted for 32.2% of the variance and showed significant contribution values in SVL, HL, ICD, IOD, UEW, TL, FL, and Toe5L, while PC2 accounted for 26.5% of the variance and showed significant contribution values in SL, SNL, IND, Fin4L, Fin3DW, IPTL, FML, TSL, Toe3DW, and Toe4DW. In females, the first three components accounted for 94.7% of total variance (Supplementary Table S2). PC1 accounted for 49.2% of the variance. Significant values were shown in HL, HW, SNL, TD, BH, LAL, Fin1L, Fin2L, Fin3L, Fin4L, Fin1DW, FML, Toe1L, Toe3L, and Toe1DW, while PC2 accounted for 25.7% of the variance

Table 1. Uncorrected p-distance of the partial 16s rRNA gene of *Zhangixalus faritsalhadii*, new species, and its congeners.

Species	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**
Zhangixalus faritsalhadii, new species	0.0									
Zhangixalus prominanus	3.1–3.3	0.0–0.4								
Zhangixalus achantharrhena	4.6–5.8	3.5–5.3	0.0–1.7							
Zhangixalus dulitensis	4.6–4.9	2.6–3.1	3.0–4.4	0.0–0.7						
Zhangixalus omeimontis	6.7	5.8–6.2	5.7–8.1	6.4–6.6	0.0					
Zhangixalus smaragdinus	10.6	8.6–9.1	8.6–10.1	8.6–8.8	8.0	0.0				
Zhangixalus dugritei	6.9	6.7–6.9	6.8–8.4	6.2–6.9	3.5	8.8	0.0			
Zhangixalus schlegelii	8.4	8.6–9.1	8.6–10.1	8.2–8.9	5.1	8.8	4.9	0.0		
Zhangixalus nigropunctatus	7.1	6.6–7.1	6.6–8.8	6.2–6.9	3.3	8.0	5.1	5.3	0.0	
Zhangixalus feae	6.2	5.5–6.0	5.7–7.7	5.3–6.0	4.2	6.2	4.7	5.1	4.0	0.0

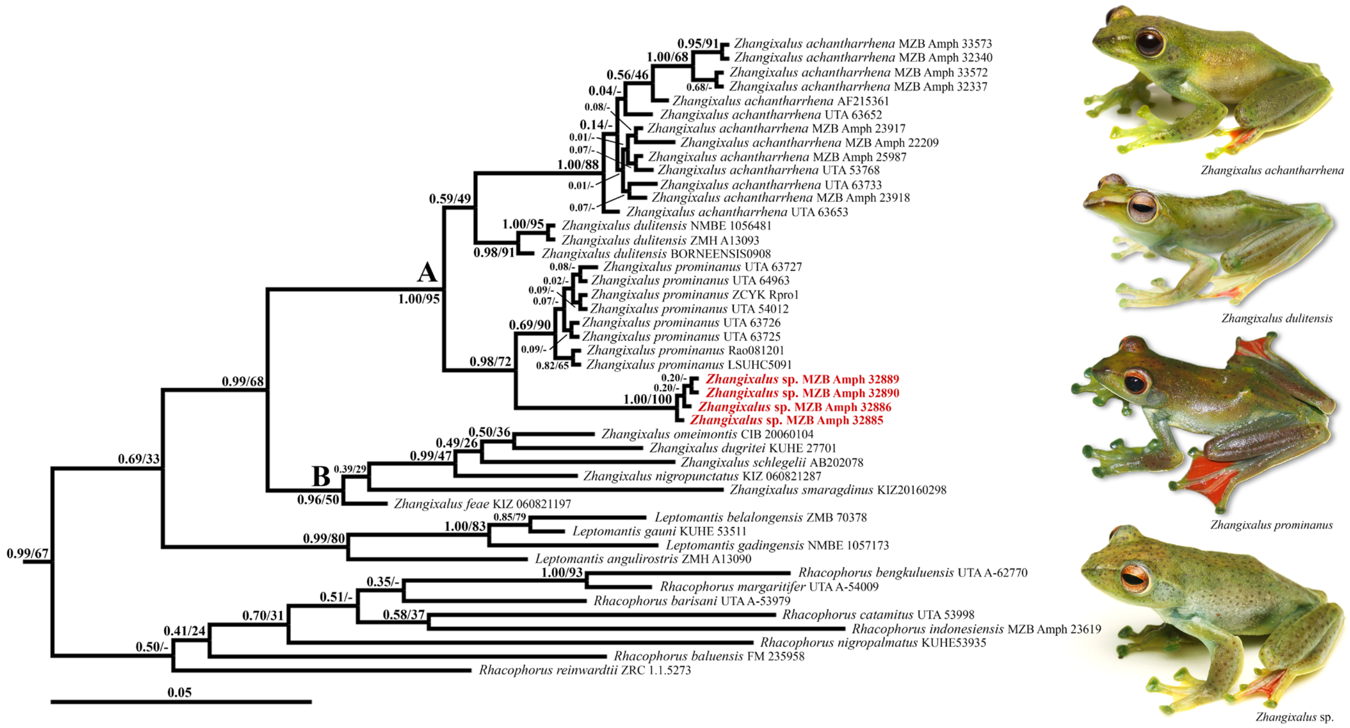

Fig. 2. Bayesian phylogenetic tree based on 455 bp of partial 16s rRNA gene, values above or below branches represent posterior probabilities (PP) and bootstrap values (BS). Photographs by Misbahul Munir (*Zhangixalus achantharrhena* and *Z. faritsalhadii*, new species), Eric N. Smith (*Z. prominanus*), and Chien Lee (*Z. dulitensis*).

and showed significant values in SVL, ICD, IOD, Toe2L, Toe4L, Toe5L, Toe3DW, and IMTL. In the univariate analysis (Table 2), we compared *Zhangixalus* sp. from Java with *Z. prominanus* and detected differences between these species in several morphological characteristics. There were sex-specific differences in morphometric characters in this comparison (see Table 2).

Based on the results of both molecular and morphological approaches, we conclude that *Zhangixalus* sp. from Java is a distinct species. Herein we describe the species.

Table 2. Morphometric variation of selected characters of *Zhanigxalus faritsalhadii*, new species, with other Sundaland species of *Zhangixalus* in ratios (R) values, with T-test values. ZF: *Zhangixalus faritsalhadii*, new species; ZP: *Zhangixalus prominanus*.

Characters	***Zhangixalus faritsalhadii*, new species**				***Zhangixalus prominanus***				**T-test p-value**	
	Males (n = 3)		**Females (n = 3)**		**Males (n = 7)**		**Females (n = 3)**		**ZF vs. ZP**	
	Mean ± SD	**Range**	**Mean ± SD**	**Range**	**Mean ± SD**	**Range**	**Mean ± SD**	**Range**	**Males**	**Females**
SVL	39.6 ± 1.7	37.6–40.7	53.1 ± 2.0	50.7–54.5	52.4 ± 4.5	44.4–58.5	64.6 ± 5.4	60.5–70.7	0.000*	0.034*
RHL	32.6 ± 0.7	33.4–34.8	32.6 ± 0.7	31.8–33.2	32.7 ± 0.7	31.6–33.7	32.4 ± 0.4	32.1–32.9	0.634	0.013*
RHW	31.9 ± 0.3	32.2–33.8	31.9 ± 0.3	31.5–32.2	30.4 ± 0.9	29.2–31.7	30.7 ± 0.9	30.1–31.8	0.528	0.000*
RSL	15.3 ± 0.3	15.2–15.9	15.3 ± 0.3	15.0–15.8	16.1 ± 0.4	15.5–16.7	15.6 ± 0.3	15.2–15.9	0.014*	0.553
RSNL	6.1 ± 0.2	7.4–7.6	6.1 ± 0.2	5.8–6.2	6.7 ± 0.2	6.3–7.2	5.7 ± 0.0	5.7–5.8	0.000*	0.895
RNEL	7.5 ± 0.0	7.8–7.9	7.5 ± 0.0	7.4–7.6	7.6 ± 0.1	7.4–7.8	7.7 ± 0.2	7.5–7.9	0.716	0.014*
RED	8.7 ± 0.0	10.2–10.7	8.7 ± 0.0	8.7–8.8	10.3 ± 0.3	9.8–10.7	9.2 ± 0.0	9.1–9.2	0.000*	0.004*
RTD	7.7 ± 0.1	8.7–9.8	7.7 ± 0.1	7.5–7.9	7.8 ± 0.1	7.5–7.9	7.5 ± 0.1	7.3–7.6	0.013*	0.027*
RIND	10.0 ± 0.3	10.5–10.6	10.0 ± 0.3	9.7–10.3	9.1 ± 0.2	8.7–9.3	9.8 ± 0.3	9.5–10.2	0.000*	0.019*
RICD	19.1 ± 0.1	18.8–19.1	19.1 ± 0.1	19.0–19.2	18.9 ± 0.3	18.3–19.4	18.7 ± 0.1	18.6–18.9	0.665	0.101
RIOD	13.4 ± 0.3	12.9–12.9	13.4 ± 0.3	13.0–13.7	12 .0 ± 0.1	11.8–12.2	12.2 ± 0.4	11.9–12.7	0.002*	0.004*
RUEW	6.7 ± 0.2	7.3–7.7	6.7 ± 0.2	6.5–7.0	7.7 ± 0.1	7.6–8.0	7.2 ± 0.1	7.1–7.3	0.118	0.001*
RBH	18.3 ± 0.4	15.0–15.5	18.3 ± 0.4	17.8–18.6	19.4 ± 0.8	18.4–20.7	18.2 ± 0.4	17.9–18.7	0.000*	0.014*
RLAL	47.8 ± 1.4	44.9–47.5	47.8 ± 1.4	46.2–49.0	46.8 ± 1.1	45.6–48.2	47.0 ± 0.6	46.4–47.7	0.136	0.000*
RFin1L	8.3 ± 0.3	8.2–8.4	8.3 ± 0.3	8.0–8.7	7.6 ± 0.4	7.1–8.3	8.5 ± 0.1	8.4–8.7	0.046*	0.015*
RFin3L	18.3 ± 0.2	15.5–16.2	18.3 ± 0.2	18.1–18.5	17.5 ± 0.6	16.6–18.5	17.6 ± 0.4	17.2–18.0	0.002*	0.000*
RFin3DW	7.5 ± 0.6	5.7–5.9	7.5 ± 0.6	6.8–8.1	6.7 ± 0.6	5.6–7.6	6.6 ± 0.4	6.2–7.1	0.150	0.000*
RIPTL	5.4 ± 0.0	6.2–6.2	5.4 ± 0.0	5.4–5.5	6.2 ± 0.3	5.8–6.7	6.2 ± 0.0	6.1–6.3	0.423	0.000*
RFML	48.7 ± 2.0	44.5–47.4	48.7 ± 2.0	46.4–49.9	49.9 ± 0.9	48.3–51.1	49.2 ± 1.1	47.9–49.9	0.018*	0.000*
RTL	51.0 ± 2.2	46.7–51.4	51.0 ± 2.2	48.4–52.6	52.0 ± 1.2	50.0–53.1	51.9 ± 2.4	49.3–54.2	0.031*	0.000*
RTSL	25.8 ± 0.8	25.1–25.4	25.8 ± 0.8	25.0–26.6	25.9 ± 0.6	24.7–26.7	26.4 ± 0.4	26.1–26.9	0.001*	0.002*
RFL	46.5 ± 2.8	40.0–42.5	46.5 ± 2.8	43.2–48.3	47.6 ± 0.8	46.2–48.4	48.4 ± 0.1	48.1–48.5	0.000*	0.000*
RToe1L	7.8 ± 0.4	6.6–7.9	7.8 ± 0.4	7.4–8.3	8.2 ± 0.3	7.8–8.7	8.3 ± 0.2	8.2–8.6	0.283	0.105
RToe4L	27.3 ± 0.6	22.6–23.4	27.3 ± 0.6	26.6–27.7	26.6 ± 0.4	26.2–27.2	28.6 ± 0.2	28.4–28.8	0.000*	0.000*
RToe1DW	3.5 ± 0.1	2.9–3.4	3.5 ± 0.1	3.4–3.7	3.4 ± 0.3	3.1–4.0	3.0 ± 0.3	2.8–3.5	0.010*	0.022*
RToe3DW	4.7 ± 0.6	3.5–4.1	4.7 ± 0.6	4.1–5.3	4.9 ± 0.5	4.0–5.6	4.2 ± 0.1	4.1–4.4	0.253	0.601
RToe4DW	5.1 ± 0.6	4.1–4.4	5.1 ± 0.6	4.5–5.7	5.2 ± 0.5	4.2–5.9	5.3 ± 0.3	5.0–5.6	0.365	0.017*
RIMTL	3.2 ± 0.2	3.9–4.1	3.2 ± 0.2	2.9–3.3	2.9 ± 0.1	2.8–3.2	2.6 ± 0.0	2.6–2.7	0.000*	0.009*

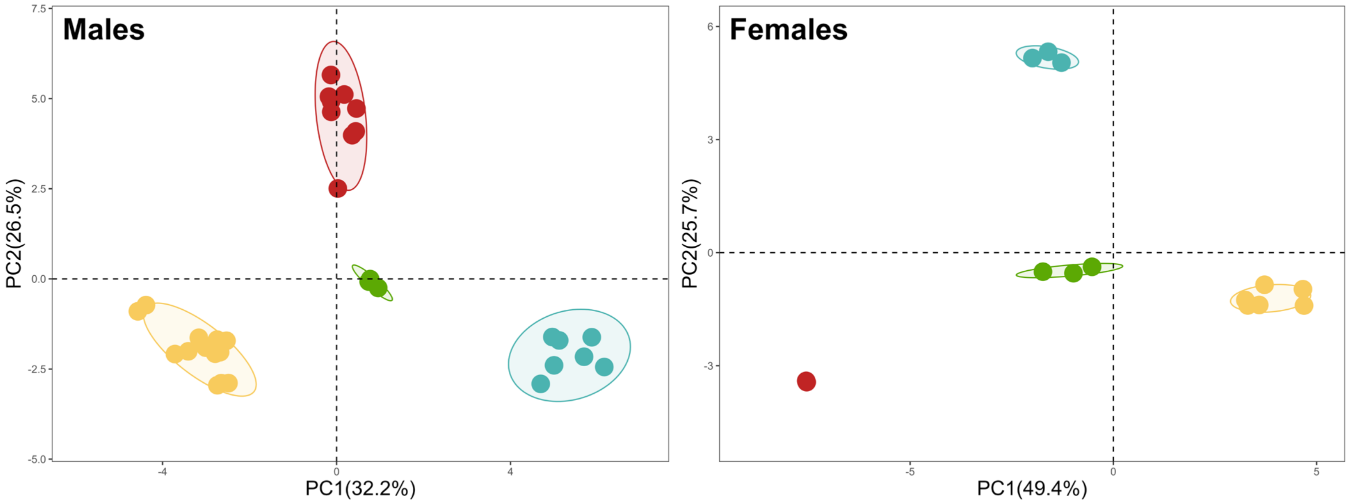

Fig. 3. Scatterplots of the first two principal component analyses within four populations of *Zhangixalus* sp. (green), *Z. prominanus* (blue), *Z. achantharrhena* (yellow), and *Z. dulitensis* (red) based on size-adjusted morphometric data, with confidence ellipses for emphasis.

TAXONOMY AND SYSTEMATICS

Family Rhacophoridae Hoffman, 1932

Zhangixalus Li, Jiang, Ren & Jiang, 2019 in Jiang et al. (2019)

Zhangixalus faritsalhadii, new species

(Figs. 4, 5)

Rhacophorus sp.: Alhadi et al. (2021)

Holotype. MZB Amph 32885, an adult male collected from Mt. Slamet, Kalipagu, Ketenger Village, Baturaden District, Banyumas Regency, Central Java Province, Indonesia (7°19′05.33″S, 109°12′17.46″E; elevation 773 m a.s.l) collected by Fajar Kaprawi, Eki Abdul Kholik, and Tarwo on 4 July 2022.

Paratypes. A total of five specimens: one adult male (MZB Amph 32886) and three adult females (MZB Amph 32887–89) collected by the same collectors and from the same locality as the holotype; and one male (MZB Amph 32890) collected by Farits Alhadi, Fajar Kaprawi, Jarian Permana, and Karso on 10 February 2020 from the same locality as the holotype.

Etymology. The specific epithet "*faritsalhadii*" is an eponym, dedicated to the deceased Farits Alhadi, a herpetologist in Indonesia who collected the first known specimen of this species that is now part of the type series and the first to discover that it could possibly be a new undescribed species on Java.

Suggested English common name. Farits Alhadi's tree frog.

Suggested Indonesian common name. Katak-pohon Farits Alhadi.

Diagnosis. Based on the molecular analyses, the new species is nested within the clade of the genus *Zhangixalus*. *Zhangixalus faritsalhadii*, new species, can be differentiated from its congeners using the following combination of morphological characters: (1) relatively medium-sized body (SVL 37.6–40.7 mm in males; SVL 50.7–54.5 mm in females); (2) yellowish-green dorsum colouration with numerous dark spot and irregular blotches cream; (3) surfaces of dorsum smooth, covered with small and low spicules; (4) snout in lateral view slope with blunt edge; (5) fringes of skin along limbs and tarsal projection; (6) extensive webbing of toes; (7) finger webbing in males between first to second fingers, and that between second to third fingers reduced, only reaching the distal subarticular tubercle, whereas that in females much more extensive, reaching the base of the disc; (8) webbing between third to fifth toes red; (9) well-developed bilobed supracloacal dermal ridge and tarsal dermal ridge; (10) presence of vomerine teeth; (11) and absence of vocal sac opening.

Description of holotype. MZB Amph 32885 (Figs. 4A, 5A–F), an adult male SVL 40.7 mm; head longer (HL 14.2 mm, 34.8 % SVL) than wider (HW 13.8 mm, 33.9 % SVL); snout longer (SL 6.5 mm, 15.9 % SVL) than eye distance (ED 4.4 mm, 10.7 % SVL), laterally sloped with blunt edge, and projecting over lower jaw; canthus rostralis distinct; lore oblique, concave; nostril slightly protuberant, without flap of skin, closer to the tip of the snout (SNL 3.1 mm, 7.6 % SVL) than to the eye (NEL 3.2 mm, 7.8 % SVL); internarial distance (IND 4.4 mm, 10.7 % SVL) smaller than interorbital distance (IOD 5.3 mm, 12.9 % SVL); interorbital distance wider than the eyelid (UEW 3.1 mm, 7.7 % SVL); pineal spot absent; pupil of eye horizontal; tympanum distinct, circular, diameter (TD 3.8 mm, 9.4 % SVL) approximately half eye length; choanae circular; vomerine teeth in straight transverse in two series between the choanae and on a level with their anterior borders, not touching the choanae and separated from each other by about two individual ridges; and vocal sac opening absent.

Forelimb slender; relative finger length I < II < IV < III, second finger (Fin2L 4.2 mm, 10.2 % SVL) longer than the first finger (Fin1L 3.4 mm, 8.4 % SVL); tips of fingers

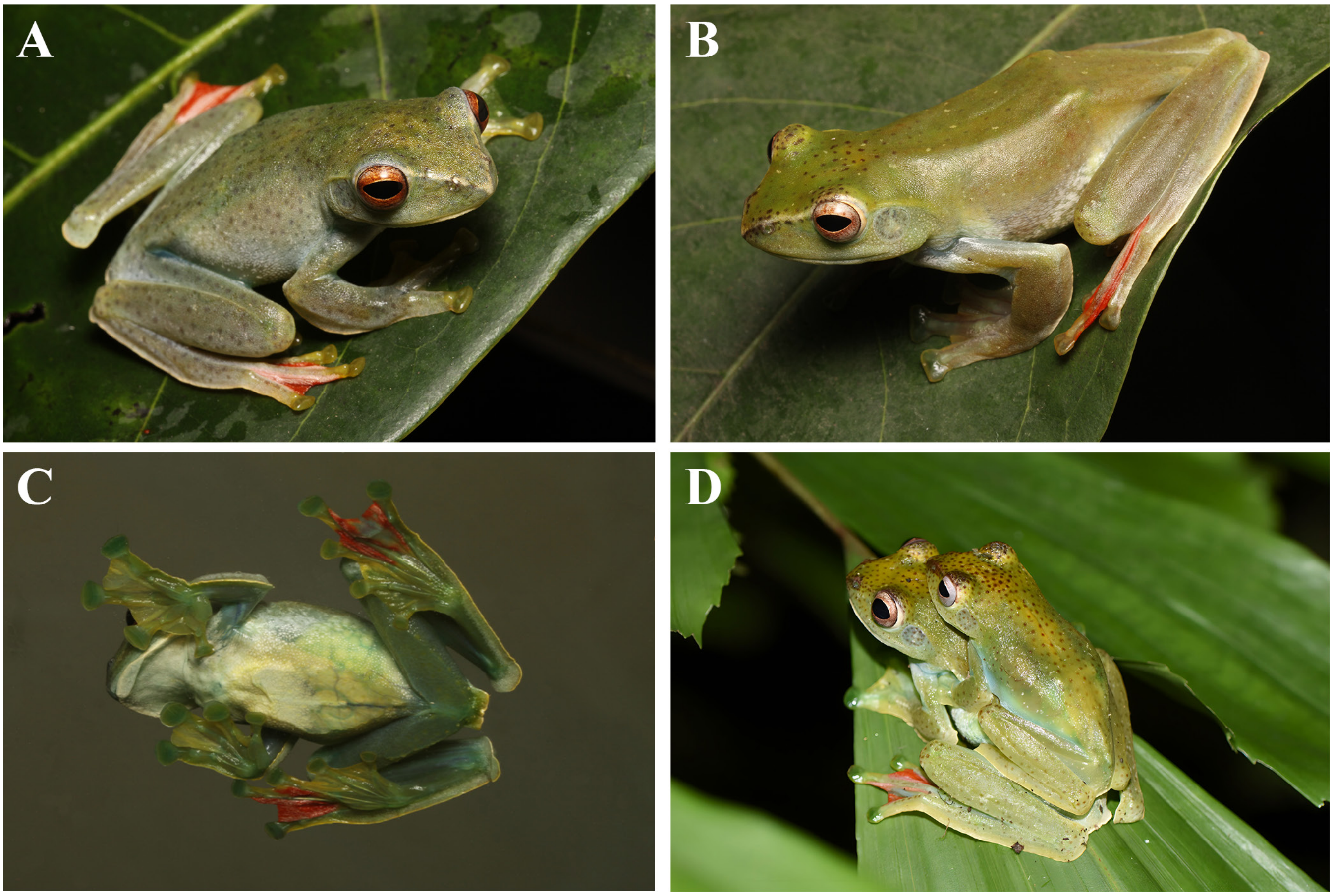

Fig. 4. A, *Zhangixalus faritsalhadii*, new species, male holotype in life, MZB Amph 32885; B, female paratype, MZB Amph 32887; C, MZB Amph 32889, female paratype in ventral view; D, MZB Amph 32886 and MZB Amph 32889 in amplexus. Photographs by Misbahul Munir (A–C) and Fajar Kaprawi (D).

expanded into large discs (3FDW 2.3 mm, 5.7 % SVL) with circummarginal and transverse ventral grooves; fingers incomplete webbing, webbing between first and second fingers reduced, it only reaches distal subarticular tubercle on both fingers, webbing formula I 2–2 II 1–2 III 1–1 IV; nuptial excrescences on first finger, from the base of the first finger to the level of the subarticular tubercle; supernumerary tubercles present, but indistinct; prepollex absent; inner palmar tubercle oval (IPTL 2.6 mm, 6.3 % SVL), middle palmar tubercle indistinct, and outer palmar tubercle oval.

Hindlimb slender; relative length of toes I < II < III < V < IV, tibiotarsal articulation of adpressed limb reaching eye; thigh (FML 18.1 mm, 44.5 % SVL) shorter than tibia (TL 19.1 mm, 46.8 % SVL); foot (FL 16.3 mm, 40.1 % SVL) shorter than tibia; tips of toes expanded into a round disc with circummarginal grooves (4TDW 1.8 mm, 4.5 % SVL), smaller than disc of fingers; toe webbing more extensive, toe webbing formula I 1–1 II 1–1 III 1–1 IV 1–1 V; subarticular tubercles well-developed, rounded; supernumerary tubercles indistinct; inner metatarsal tubercles (IMTL 1.6 mm, 4.0 % SVL) oval and low, length more than half length of first toe (Toe1L 2.7 mm, 6.7 % SVL); outer metatarsal tubercles absent.

Dorsum smooth, covered with small and low spicules, also occurs on eyelid and densely in head; abdomen, chest, throat, thigh, cloaca, and flank prominently granular; flanks wrinkled; an oblique thickened skin forms a low supratympanic fold, from the eye and indistinctly ending above arm insertion, slightly touching the tympanic annulus; dorsolateral fold absent; fringe of skin present along the edge of forearm and the outer edge of fifth to tibiotarsal articulation; dermal ridge at tibiotarsal curved, and supracloaca bilobed.

Colour. In life, dorsum yellowish-green with numerous dark spots and irregular cream blotches, dark spots prominent in eyelid, head, and nostril regions; lower lips cream; from the anterior eye to above the nostril, extending to the tip of the snout with a cream line; limbs without crossbars; abdomen, thighs, ventral of tarsus, tibia, lower arms, and upper arms translucent; throat, flanks, elbows, and knees covered with white spot covering the granular; eyes with black periphery, white sclera, dark pupils, and thin pale yellowish network of iris; webbing between third to fifth toes red, yellowish-green on remaining toes; tips of fingers and toes bluish-green; inguinal region, ventral elbows and knees bluish. In preservative, dorsum green fading to cream and cream blotches become faded, but dark spots remain unchanged; red webbing on toes fading to light red and eyelids turn black.

Variations. The morphometric variations are listed in Table 2. Males had larger RHL, RHW, RSNL, RNEL, RED, RTD, RIND, RUEW, RIPTL, and RIMTL than females, while females had larger SVL, RIOD, RBL, RLAL, Rfin1L,

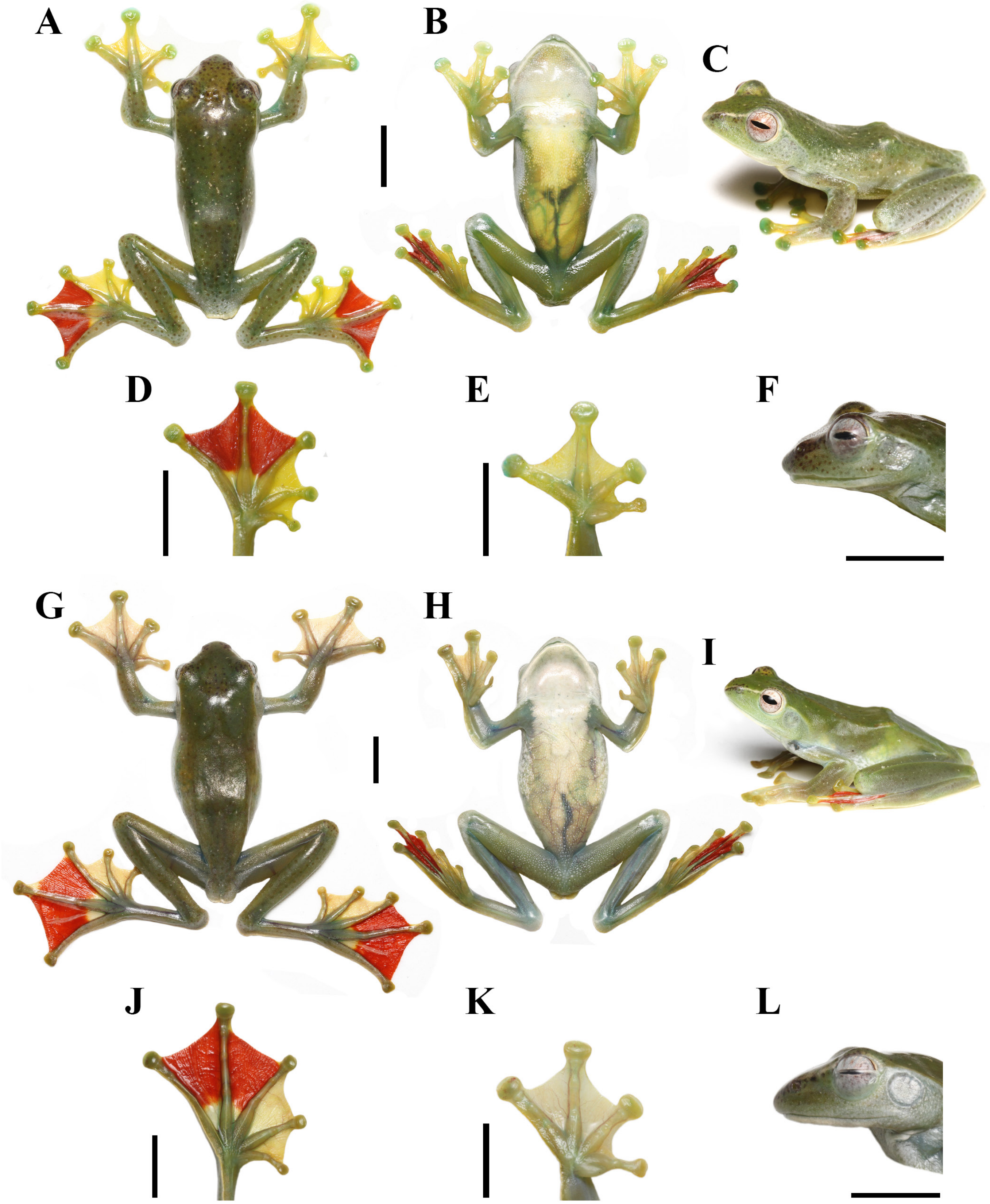

Fig. 5. *Zhangixalus faritsalhadii*, new species, from Mount Slamet, Java, Indonesia. A–F, an adult male holotype, MZB Amph 32885; G–L, an adult female paratype, MZB Amph 32887. Scale bar = 10 mm. Photographs by Misbahul Munir.

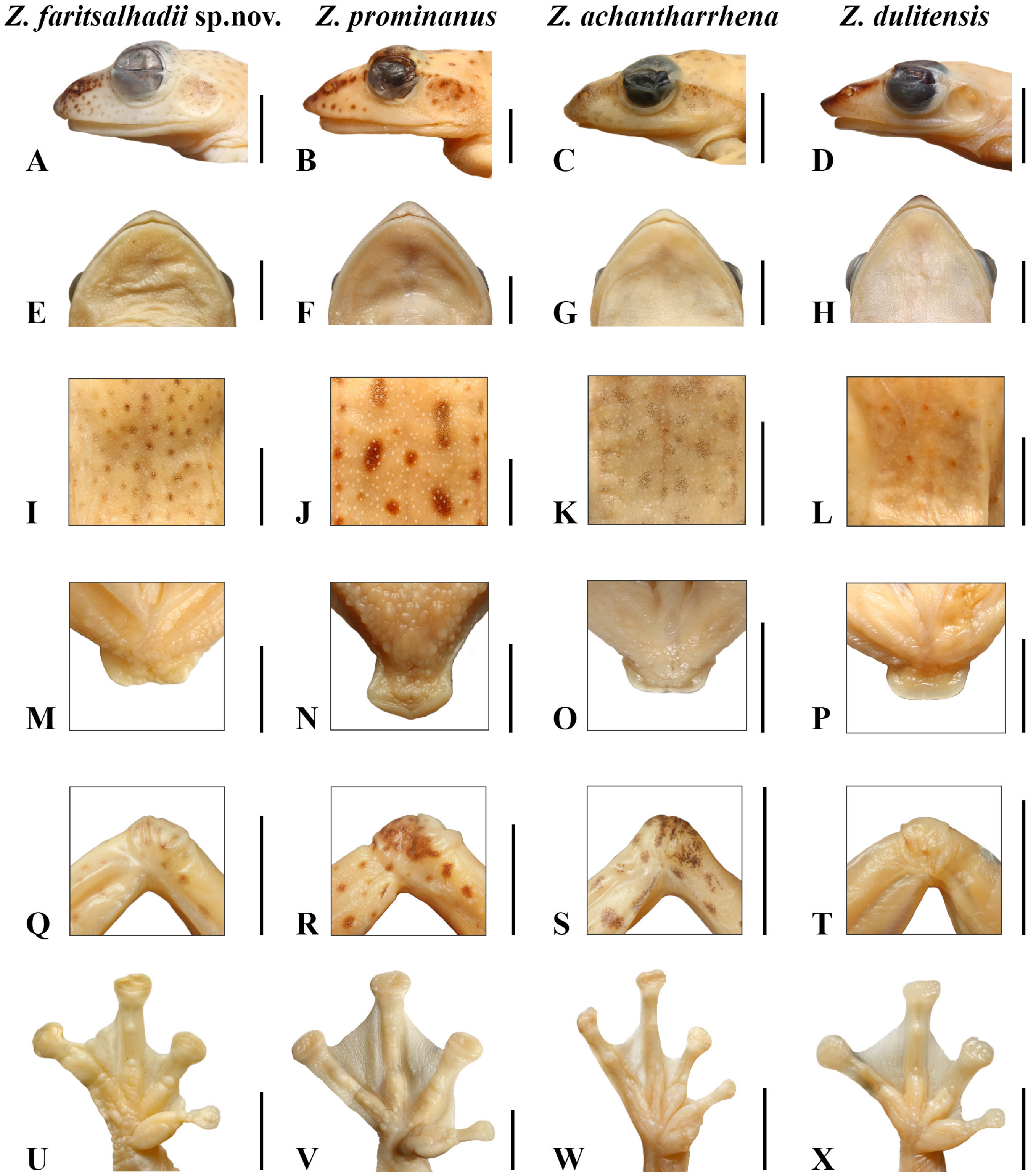

Fig. 6. Comparison of morphological characters between male species of *Zhangixalus* from Sundaland. Scale bar = 5 mm. Photographs by Ade Damara Gonggoli.

Rfin2L, Rfin3L, Rfin4L, RFin1DW, RToe3DW, RFML, RTL, RTSL, RFL, RToe1L, RToe2L, RToe3L, RToe4L, RToe5L, RToe1WD, RToe3DW, and RToe4DW than males. A male paratype (MZB Amph 32890) had a smaller body than others. All types of females had a smoother dorsum with no spicules compared to males. In females, webbing on first to second and second to third fingers was more extensive than that for males. Finger webbing formula for females: I 2–1 II 1–1 III 1–1 IV (Fig. 5K). The tibiotarsal articulation varies among females, but does not exceed the nose and eyes; that for MZB Amph 32887 reaches the nose, that for MZB Amph 32888 reaches between the nose and eyes, and that for MZB Amph 32889 reaches the eyes.

Comparisons. Based on the phylogenetic tree and geographical proximity that separated Sundaland species (*Z.*

Table 3. Morphometric variation of selected characters of *Zhangixalus achantharrhena* and *Zhangixalus dulitensis*.

Characters	***Zhangixalus achantharrhena***				***Zhangixalus dulitensis***			
	Males (n = 13)		**Females (n = 6)**		**Males (n = 9)**		**Females (n = 2)**	
	Males	**Females**	**Mean ± SD**	**Range**	**Mean ± SD**	**Range**	**Mean ± SD**	**Range**
SVL	35.0 ± 1.1	33.5–37.9	43.3 ± 1.8	39.6–44.6	35.9 ± 1.6	33.6–38.7	46.4 ± 0.6	46.0–46.9
RHL	33.7 ± 1.1	31.4–35.5	33.5 ± 0.4	32.9–34.0	32.5 ± 0.5	31.5–32.9	32.8 ± 0.3	32.6–33.0
RHW	33.2 ± 0.6	32.0–34.5	32.6 ± 0.4	32.1–33.2	29.7 ± 0.4	29.0–30.1	29.5 ± 0.3	29.2–29.7
RSL	14.7 ± 0.4	14.3–15.9	15.1 ± 0.1	14.9–15.4	13.9 ± 0.1	13.7–14.2	15.2 ± 0.0	15.1–15.2
RSNL	6.2 ± 0.2	5.7–6.5	5.9 ± 0.2	5.7–6.1	5.9 ± 0.4	5.4–6.4	5.9 ± 0.1	5.8–6.0
RNEL	7.5 ± 0.3	6.9–8.0	8.8 ± 0.5	7.8–9.2	7.3 ± 0.3	6.8–7.8	8.2 ± 0.0	8.2–8.3
RED	11.7 ± 0.4	11.3–12.7	11.8 ± 0.1	11.5–12.0	12.7 ± 0.1	12.4–12.9	12.3 ± 0.2	12.1–12.5
RTD	8.0 ± 0.2	7.4–8.1	8.0 ± 0.2	7.7–8.3	7.5 ± 0.2	7.1–7.9	7.4 ± 0.4	7.1–7.7
RIND	10.3 ± 0.4	9.5–10.9	9.8 ± 0.2	9.6–10.2	11.1 ± 0.3	10.6–11.5	10.8 ± 0.2	10.7–11.0
RICD	19.4 ± 1.0	17.6–20.7	19.2 ± 0.4	18.5–19.6	19.7 ± 0.5	18.5–20.3	21.0 ± 0.0	21.0
RIOD	13.9 ± 0.4	12.9–15.0	14.2 ± 0.5	13.1–14.8	12.3 ± 0.3	12.0–12.8	13.3 ± 0.0	13.3–13.4
RUEW	7.8 ± 0.5	7.1–8.9	7.5 ± 0.2	7.3–8.0	8.1 ± 0.2	7.6–8.3	7.9 ± 0.1	7.7–8.0
RBH	21.3 ± 0.6	20.3–22.4	21.2 ± 0.4	20.5–21.7	20.8 ± 0.4	20.0–21.3	18.8 ± 0.4	18.5–19.1
RLAL	50.5 ± 0.8	49.1–51.9	51.2 ± 0.3	50.7–51.6	46.4 ± 0.9	44.7–47.9	46.9 ± 0.5	46.5–47.3
RFin1L	8.0 ± 0.3	7.3–8.8	9.1 ± 0.5	8.1–9.6	8.0 ± 0.3	7.5–8.6	8.6 ± 0.2	8.5–8.8
RFin3L	17.5 ± 0.3	16.9–18.0	18.6 ± 0.3	17.9–18.9	16.8 ± 0.2	16.4–17.2	17.6 ± 0.1	17.5–17.6
RFin3DW	5.7 ± 0.3	5.2–6.3	6.7 ± 0.2	6.4–7.0	6.6 ± 0.2	6.3–7.0	6.0 ± 0.1	5.9–6.1
RIPTL	4.4 ± 0.2	4.1–4.8	5.4 ± 0.2	5.0–5.6	6.4 ± 0.1	6.1–6.7	6.0 ± 0.0	5.9–6.0
RFML	50.7 ± 1.3	48.6–53.5	49.4 ± 1.5	47.7–51.7	48.0 ± 2.0	44.8–50.9	52.2 ± 0.7	51.7–52.7
RTL	52.7 ± 1.4	50.8–55.0	52.8 ± 0.9	51.8–54.4	51.0 ± 1.8	48.2–53.9	54.4 ± 0.3	54.2–54.7
RTSL	28.7 ± 0.7	27.2–29.9	28.3 ± 0.4	27.9–29.3	26.4 ± 0.5	25.4–27.2	28.2 ± 0.8	27.6–28.8
RFL	43.4 ± 1.0	40.8–45.0	47.0 ± 0.3	46.6–47.4	44.1 ± 1.0	42.9–46.2	49.2 ± 0.4	48.9–49.5
RToe1L	7.7 ± 0.2	7.4–8.1	8.3 ± 0.2	8.0–8.7	7.7 ± 0.3	7.0–8.3	8.0 ± 0.0	7.9–8.0
RToe4L	24.4 ± 0.5	23.6–25.3	26.1 ± 0.3	25.6–26.7	24.7 ± 0.5	24.0–25.6	27.2 ± 0.5	26.8–27.6
RToe1DW	3.1 ± 0.1	3.0–3.4	3.6 ± 0.1	3.4–3.7	2.9 ± 0.1	2.7–3.0	2.6 ± 0.1	2.4–2.7
RToe3DW	3.7 ± 0.2	3.3–4.1	4.9 ± 0.0	4.8–5.0	4.1 ± 0.3	3.8–4.9	3.8 ± 0.0	3.7–3.8
RToe4DW	4.3 ± 0.2	3.9–4.7	5.2 ± 0.1	5.0–5.4	5.0 ± 0.5	4.0–5.5	4.4 ± 0.0	4.4–4.5
RIMTL	3.9 ± 0.3	3.4–4.3	3.8 ± 0.0	3.7–4.0	2.9 ± 0.2	2.6–3.2	4.0 ± 0.1	3.9–4.1

faritsalhadii, new species, *Z. prominanus*, *Z. achantharrhena*, and *Z. dulitensis*) from Asian mainland species, we only compared *Z. faritsalhadii*, new species, with the other three Sundaland species. Morphologically, *Z. faritsalhadii*, new species, is more similar to *Z. prominanus*, but can be distinguished from the latter with its smaller body (SVL 37.6–40.7 mm vs. 44.4–58.5 mm in males; SVL 50.7–54.5 mm vs. 60.5–70.5 mm in females); dorsum with low spicules which are not prominent in males (vs. appears prominently and elevated; Figs. 6I, J); males snout slope with blunt edge in lateral view (vs. slope with pointed edge; Figs. 6A, B); supracloaca dermal ridge broader and shorter (vs. longer and narrower; Figs. 6M, N); less distribution of melanophores at kness (vs. dense; Figs. 6Q, R); males with reduced webbing on second to third fingers (vs. extensive web finger; Figs. 6U, V).

Zhangixalus faritsalhadii, new species, differs from *Z. achantharrhena* by having a larger body size (SVL 37.6–40.7 mm vs. 33.5–37.9 mm in males; SVL 50.7–54.5 mm vs. 39.6–44.6 mm in females; see Table 3); more developed webbing on fingers (vs. reduced; Figs. 6U, W); vocal sac opening absent (vs. present); dorsum with small spicules (vs. relatively large; Figs. 6I, K); less distributed melanophores on knees (vs. dense; Figs. 6Q, S); dark spots on dorsum scattered (vs. relatively dense).

Zhangixalus faritsalhadii, new species, differs from *Z. dulitensis* by having a larger body size (SVL 37.6–40.7 mm vs. 33.6–38.7 mm in males; 50.7–54.5 mm vs. 46.0–46.9 mm in females; see Table 3); web colouration between third to fifth toes red (vs. only between fourth to fifth toes); vocal sac opening absent (vs. present); shorter supracloaca dermal ridge (vs. longer; Figs. 6M, P); males snout slope with blunt edge in lateral view (vs. slope with sharply pointed edge; Figs. 6A, D); well-developed fringe of skin along the edge of the forearm and the outer edge of fifth to tibiotarsal articulation (vs. less developed).

Range and natural history. The type series of *Zhangixalus faritsalhadii*, new species, is so far known only from the highlands of Mount Slamet. The type series was found in Rasamala (*Altingia excelsa*) forest near swamps, approximately 10 m from the main river (Fig. 7). A male paratype (MZB Amph 32890) was collected while it was calling from a palm tree, approximately 15 m above ground, during rainy season in February 2020. During the transition season from the dry to the rainy season in July 2022, two pairs of amplectants of the type series were found on a rattan plant (MZB Amph 32886 and MZB Amph 32889; Fig. 4D) and on tree leaves (MZB Amph 32885 and MZB Amph 32888), while one female (MZB Amph 32889) not far from the same locality was also found. The habitat was surrounded by small puddles formed from water running off the slope. This new species may be in other lowland areas of Mount Slamet. A record dated 18 February 2020 appeared in a citizen science database at the exact location (Khafizh, 2020). Tadpole and acoustic information are unknown. The following frog species are sympatric with the new species: *Polypedates leucomystax* (Gravenhorst, 1829); *Philautus aurifasciatus* (Schlegel, 1837); *Limnonectes microdiscus* (Boettger, 1892); *Rhacophorus reinwardtii*; *Leptobrachium hasseltii* Tschudi, 1838; and *Microhyla achatina* Tschudi, 1838.

Fig. 7. Natural habitat of *Zhangixalus faritsalhadii*, new species, at the type locality. Photograph by Fajar Kaprawi.

DISCUSSION

Our phylogenetic tree is concordant with previous studies, in which Sundaland species of *Zhangixalus* formed a sister clade to Asian mainland species (Jiang et al., 2019; Dufresnes et al., 2022; Brakels et al., 2023). Generally, Sundaland species can be distinguished from Asian mainland species by having a well-developed supracloacal dermal ridge (Jiang et al., 2019), except for *Z. pachyproctus* Yu, Hui, Hou, Wu, Rao & Yang, 2019. Our morphological observations show that Sundaland species are characterised by the relatively yellowish-green body colouration and distinct red-marking on the foot webbing, while that of Asian mainland species appear mostly green (Jiang et al., 2019) and have variable colour markings on the foot webbing, e.g., tangerine in *Z. pinglongensis* Mo, Chen, Liao & Zhou, 2016; orange in *Z. jodiae* Nguyen, Ninh, Orlov, Nguyen & Ziegler, 2020; cream in *Z. melanoleucus* Brakels, Nguyen, Pawangkhanant, Idiiatullina, Lorphengsy, Suwannapoom & Poyarkov, 2023; greyish brown in *Z. franki* Nguyen, Ninh, Orlov, Nguyen & Ziegler, 2020; and pale green in *Z. pachyproctus*. In addition, Asian mainland species have large dark blotches (e.g., *Z. jodiae* and *Z. pinglongensis*; Pan et al., 2017) or white lines (e.g., *Z. pachyproctus* and *Z. smaragdinus* (Blyth, 1852); Yu et al., 2019) on the flanks, while such colour patterns in Sundaland species are absent. Thus, Sundaland species are molecularly and morphologically distinct from Asian mainland species.

Among the Sundaland species, *Zhangixalus faritsalhadii*, new species, morphologically resembles *Z. prominanus*. These species are allopatric and inhabit different islands. *Z. prominanus* is distributed in the Thai Peninsula, Malay Peninsula, and Sumatra, whereas *Z. faritsalhadii*, new species, is possibly restricted to Java (or even Mt. Slamet) based on current knowledge. According to data collected from the MZB specimens, both *Z. prominanus* and Z. *achantharrhena* are found in the Bukit Barisan Selatan Mountain range which spans across Sumatra. They are found at different elevations, with *Z. prominanus* primarily inhabiting lowlands at below 1,000 m a.s.l, while *Z. achantharrhena* is found above 1,000 m a.s.l (Harvey et al., 2002). *Z. faritsalhadii*, new species, has only been found, so far, specifically in Rasamala (*Altingia excelsa*) vegetation type within mountainous forest, but may also occur in other vegetation types. Although *Z. prominanus* and *Z. faritsalhadii*, new species, are different molecularly (genetic distance from 3.1% to 3.3%) and can be distinguished based on meristic traits, the sample size used for the morphometric analysis was relatively small, which could affect the statistics of the analyses (Chan & Grismer, 2021). Further studies using larger samples, multiple gene analyses, and additional information on larval, acoustic, and behavioral characteristics are needed to better understand this new species.

Java, the most densely populated island in Indonesia with a total human population of 1,542 million (BPS, 2022), has experienced one of the highest rates of forest conversion (Prasetyo et al., 2009; Devenish et al., 2021; Santoro et al., 2023). It is also worth noting that the type locality of the new species, Mount Slamet, is not currently included in Indonesia's system of protected areas, making the new species fragile and vulnerable to exploitation. Another possible threat is exploitation for trade and habitat alteration for touristic purposes. The unique and colourful appearance of this new species makes it an attractive target for the exotic pet market and may draw more tourists to the type locality, raising concerns about unsustainable collection practices, and the potential transformation of its natural habitat. The type locality is situated in close proximity to a camping ground, a leisure activity that has become more popular in Indonesia in the past years. In addition, there is a looming threat of volcanic eruptions of Mount Slamet. According to the Indonesian National Disaster Management Agency's eruption range for Mt. Slamet (BNPB, 2015), we predict that the population of the new species at the type locality could be severely impacted. Ultimately, all of these threats cumulatively place this new species at risk. Conservation efforts and a well-structured conservation management plan involving collaboration among stakeholders and local communities are needed. This collaborative approach is essential in ensuring the success of conservation efforts for this new species.

Since 1822 when the first amphibian species (*Megophrys montana* Kuhl & Van Hasselt, 1822) was described from Java, numerous new species have been described. In the last decade alone, four species have been described, with three being from the family Rhacophoridae: *Chirixalus trilaksonoi* (Riyanto & Kurniati, 2014); *Leptophryne javanica* Hamidy, Munir, Mumpuni, Rahmania & Kholik, 2018; *Chirixalus pantaiselatan* Munir, Hamidy, Kusrini, Kennedi, Ridha, Qayyim, Rafsanzani & Nishikawa, 2021; and *Theloderma pseudohorridum* Kurniawan, Septiadi, Kadafi, Fathoni, Prabasari & Thammachoti, 2023b. Although the island of Java has been explored for many years, there are probably more amphibian species to be discovered on the island. Finally, the discovery and description of *Zhangixalus faritsalhadii*, new species, has contributed to the overall amphibian species count in Java, bringing the total number of species to 47 (Alhadi et al., 2021; Sabinhaliduna et al., 2022; Kurniawan et al., 2023a).

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APPENDIX 1. SPECIMENS EXAMINED

Zhangixalus achantharrhena (n = 19): Batahan Street, Pagar Gunung, Kotanopan District, Mandailing Natal Regency, North Sumatra Province, Sumatra, Indonesia [one male (MZB Amph 32191)]; Mt. Burnitelong, Hutan Bukit, Bukit District, Bener Meriah Regency, Aceh Province, Sumatra, Indonesia [one male (MZB Amph 32337)]; Mt. Kerinci, Kersik Tulo, Kayu Ayu District, Kerinci Regency, Jambi Province, West Sumatra Province, Sumatra, Indonesia [one male (MZB Amph 22208)]; Mt. Merapi, Aie Angek, Sepuluh Koto District, Tanah Datar Regency, West Sumatra Province, Sumatra, Indonesia [one male (MZB Amph 26074)]; Mt. Singgalang, Balingka, IV Koto District, Agam Regency, West Sumatra Regency, Sumatra, Indonesia [six male (MZB Amph 32338–32341, 33574–33575) and two females (MZB Amph 33572–33573)]; Mt. Tujuh, Kerinci Seblat National Park, Jambi Province, Sumatra, Indonesia [three females (MZB Amph 14816, 14818–14819)]; Mt. Ulubelu, Hutan District, Tanggamus Regency, Lampung Province, Sumatra, Indonesia [one male (MZB Amph 22209)]; Kampung Telege Atu, Kebayakan District, Aceh Tengah Regency, North Sumatra Province, Sumatra, Indonesia [one male (MZB Amph 26071)]; Sopotinjak, Batang Natal District, Mandailing Natal Regency, North Sumatra Province, Sumatra, Indonesia [one male (MZB Amph 32193) and one female (MZB Amph 32194)].

Zhangixalus dulitensis (n = 11): Kelay Subdistrict, Berau Barat Regency, East Kalimantan Province, Borneo, Indonesia [nine males (MZB Amph 31600–31609) and two females (MZB Amph 31599, 31609)].

Zhangixalus prominanus (n = 10): Pondok Durian Sipurak, Kerinci Seblat National Park, Jambi Province, Sumatra, Indonesia [five males (MZB Amph 14786–14790) and one female (MZB Amph 33576)]; Tanjung Dalam, Merangin Regency, Jambi Province, Sumatra, Indonesia [one male (MZB Amph 21849)]; Sibuali, Tapanulis Selatan Regency, North Sumatra Province, Sumatra, Indonesia [one male (MZB Amph 26189)]; Mt. Dempo, Pagar Alam, South Sumatra Province, Sumatra, Indonesia [one female (MZB Amph 25921)]; Pemerian, Bukit Barisan Selatan National Park, Lampung Province, Sumatra, Indonesia [one female (MZB Amph 3465)].

SUPPLEMENTARY MATERIAL

The following data are available online:

Supplementary Table S1. Samples used for phylogenetic analysis with the information on museum voucher, GenBank accession number, locality, and reference. (https://figshare.com/articles/dataset/Supplementary_Material_1_xlsx/26393887/1)

Supplementary Table S2. The first five principal component analyses of *Zhangixalus faritsalhadii*, new species, with the other Sundaland species of *Zhangixalus*, with the summary statistics and loading scores. (https://figshare.com/articles/dataset/Supplementary_Material_2_xlsx/26393884)

Supplementary Table S3. Measurements of *Zhangixalus faritsalhadii*, new species, *Zhangixalus prominanus*, *Zhangixalus achantharrhena*, and *Zhangixalus dulitensis* (in mm). (https://figshare.com/articles/dataset/Supplementary_Material_3_xlsx/26393881)