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DOCUMENTING THE FIRST OCCURRENCE OF *FEIHYLA BALADIKA* (ANURA, RHACOPHORIDAE) IN EAST JAVA: ECOLOGY, GENETICS, AND HABITAT SUITABILITY

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Documenting the first ocurrence of *Feihyla baladika* (Anura, Rhacophoridae) in East Java: ecology, genetics, and habitat suitability. Rijalullah, M. A., Khanifan, N., Assiddiqy, M. F., Soeprijadi, Anandhika M.S.P., Fathoni, M., Nurrofik, A., Kurniawan, N. † & Septiadi, L. — Previously, *Feihyla baladika* (Riyanto and Kurniati, 2014) was known exclusively from Sumatra, Indonesia. This study reports a new record of this species from the eastern region of Java Island, within a lowland tropical rainforest close to Kondang Merak beach. Due to the absence of other findings in Java and some morphological differences along with a genetic distance of 2–3%, we cautiously refer to the specimens as *F.* cf. *baladika.*

Species distribution modeling using MaxEnt suggests that *F. baladika* may potentially occur in Sumatra, Java, and Bali, in areas characterized by relatively low precipitation during the wettest month, forest cover, and low temperature seasonality.

Key words: Amphibian, Indonesia, phylogeny, species distribution model

Introduction

Old World tree frogs (Anura, Rhacophoridae) is one of the most diverse families of amphibians in Asia (Chan et al., 2018), consisting of more than 400 species (Frost, 2024). The rapid and extensive diversification within the family, combined with a lack of distinctive shared morphological characteristics, frequently led to misunderstanding (e. g., Frost et al., 2006; Grosjean et al., 2008; Li et al., 2008; Biju et al., 2020; Chan et al., 2020; Chen et al., 2020). One of its genera, *Feihyla*, is noted for having the most diverse phylogenetic tree within the Rhacophoridae (Onn et al., 2018). Based on previous phylogenetic studies (Biju et al., 2020; Liu et al., 2023), *Feihyla* were clustered in to three groups: *F. palpebralis* group (2 members: *F. palpebralis* and *F. fuhua*), *F. vittiger* group (3 members: *F. inexpectata*, *F. kajau*, and *F. vittiger*), and *F. vittatus* group (5 members: *F. vittatus*, *F. baladika*, *F. hansenae*, *F. senapatiensis*, *F. shyamrupus*, and *F. wuguanfui*).

Feihyla baladika (Riyanto and Kurniati, 2014) is currently known exclusively on Sumatra Island (Riyanto and Kurniati, 2014; Biju et al., 2020) and no occurrences have previously been recorded on other island that were part of Sundaland, such as Java. This insular endemism has led to its classification as Near Threatened by the International Union for the Conservation of Nature (IUCN SSC Amphibian Specialist Group, 2018). In addition, occurrence data is unavailable in Global Biodiversity Information Facility (https://www.gbif.org) and limited to coordinates retrieved from literatures (Riyanto and Kurniati, 2014; Biju et al., 2020). The lack of records outside Sumatra has left its broader biogeographic pattern, habitat preferences, and conservation status uncertain.

The limited documentation regarding the distribution of *F. baladika* could be related to the rare encounter of this species during field surveys, due to challenges in monitoring and a limited comprehension of their habitat preferences. Elith and Graham (2009) argue that this issue can be resolved by the utilisation of species distribution models (SDMs). Several previous research indicates that species distribution models (SDMs) serve as valuable tools for exploring and predicting species distribution across various landscapes (e. g., Searcy & Shaffer, 2014; Fois et al., 2015; Kurniawan et al., 2024). MaxEnt (Kramer-Schadt et al., 2013) is a widely used SDM because it only requires presence data (Phillips et al., 2006), works well with small sample sizes (Wisz et al., 2008), and suitable for rare and narrowly endemic species (Rebelo and Jones, 2010; Rinnhofer et al., 2012).

In this study, we report the first confirmed occurrence of *F. baladika* in East Java using an integrative approach. We employed molecular and morphological analyses to verify species identity, assessed the ecological characteristics of the new locality, and applied species distribution modeling (SDM) to estimate potential habitats across Sumatra, Java, and Bali as a basis for future research. These islands, which were included in the model due to their ecological suitability, are believed to be evolutionarily connected and share biogeographic patterns among various taxa (Lohman et al., 2011). Our findings aim to refine understanding of the species' distributional limits, guide conservation priorities, and highlight the need for intensified biodiversity surveys in underexplored areas.

Material and Methods

Field Study and sampling

Field observation and sample collection were conducted in lowland forest near Kondang Merak Beach, Malang Regency, and East Java Province, Indonesia during rainy season (January–February 2024). Adult frogs, egg clutches, and habitat was photographed in the wild. The frog encounter's location was documented using GPS Garmin. Furthermore, detailed descriptions of the habitats were made, including the recording of various abiotic factors such as microclimate (temperature and relative humidity) and water (temperature, pH, dissolved oxygen, electric conductivity, total dissolved solid, turbidity) parameters. Prior to euthanizing the frogs by immersing them in a solution containing 0.5% tricaine methane sulfonate (MS-222), photographs were taken from different angles (dorsal, ventral, and lateral) of the frogs. Subsequently, the liver tissue was stored in a microtube containing 96% ethanol for molecular study. Whole frog specimens were fixed overnight in 10% formalin, subsequently kept in 70% ethanol. Indonesia. Depositories: NK — Non-type were deposited in Laboratory of Animal Diversity and Environmental Technology, Biology Department, Faculty of Sciences, Technology, and Mathematics, Brawijaya University, Indonesia. Coordinate data from our field study were mapped using QGIS v.3.22.5.

Molecular data and Phylogenetic analyses

Mitochondrial DNA was extracted from the liver tissue utilizing Quick-DNA™ Miniprep Plus kit following manufacturer's protocol (Zymo Research Corporation). DNA amplifications were performed using L1-L2 primer set (12S rRNA + tRNA^{val} + 16S rRNA) (Table 1) following Zhang et al. (2013). The amplicons were evaluated qualitatively using 2% agarose gel and quantitatively using NanoDrop 2000 spectrophotometer.

DNA sequences were deposited in Genbank (PV820714-PV820716) and subsequently aligned using ClustalW in MEGA 7 with default parameters (Kumar et al., 2016). Maximum Likelihood (ML) and Bayesian Interference (BI) were performed on a sequence with total 328 base pair. The most suitable nucleotide substitution model was determined using the Akaike Information Criterion (AIC) in jModelTest

Table 1. **Primer used for DNA amplification in this study**

Primer name	Sequence	References
L2 LX12SN	5'-TACACACCGGCCGTCA-3'	Kurniawan et al. (2023)
L2 LX16S1R	5'-GACCTGGATTACTCCGGTCTGAACTC-3'	Kurniawan et al. (2023)
L1 16S2000H	5'-GTGATTAYGCTACCTTTGCACGGT-3'	Kurniawan et al. (2023)
L1 12SAL	5'-AAACTGGGATTAGATACCCCACTAT-3'	Kurniawan et al. (2023)

(Posada, 2008). The General Time Reversible (GTR) model, with a proportion of invariant sites (+I) and gamma-distributed rate variation among sites (+G), was found to be the best fit nucleotide substitution model. Utilizing MrBayes software (Ronquist & Huelsenbeck, 2003), uniform priors and four Metropolis-Coupled Markov Chains Monte Carlo (MCMCMC) chains were used for 10 million generations of Bayesian analysis with tree sampling every 1000th generation. After discarding the first 25% of trees as burn-in, Bayesian posterior probabilities for the clades were summarized. Maximum Likelihood Clade Support (BS) was analysed using 10,000 comprehensive bootstrap replicates with the IQ-TREE web server (Trifinopoulos et al., 2016). Uncorrected pairwise genetic distances for the 16S rRNA were computed in PAUP using all sites (Swofford, 2002). Phylogenetic trees were visualized using FigTree v.1.3.1 (Rambaut, 2009).

Morphological Measurement and Analysis

The collected specimens undergo a total of 17 morphological character measurements and a description of their webbing characteristics in order to compare them with *F. baladika* from Sumatra in Riyanto & Kurniati (2014): SVL (snout-vent length), HL (head length), HW (head width), ELW (width of upper eyelid), ED (eye diameter), IND (internarial distance), IOD (interorbital distance), SNL (snout length), DNE (distance from the nostril to the eye), TD (tympanum diameter), FLL (forelimb length), HLT (hand length), THL (thigh length), TIL (tibia length), FL (proximal edge of the inner metatarsal tubercle to the tip of the fourth toe), 3FDW (width of the disk of the third finger), 4TDW (width of the disk of the fourth toe). The measurement accuracy level is approximately 0.1 mm. Our morphometric analysis was conducted by following the defensible framework by Chan and Grismer (2021). Measured data were pre-processed by applying allometric body size correction using the *GroupStruct* r package to account for ontogenetic variation (Chan and Grismer, 2022). Since the data did not follow normal distribution, the non-parametric Mann-Whitney U test was employed. Nevertheless, Principal Component Analysis (PCA) was still conducted to explore the data structure (Bispo & Marquez, 2023).

Species Distribution Model

We utilized Maximum Entropy (MaxEnt v.3.4.1) (Phillips et al., 2017) modeling for predicting potential distribution of *F. baladika*. Total of five occurrence data of *F. baladika* in Sumatera was obtained from literature (Riyanto & Kurniati, 2014; Biju et al., 2020) and an occurrence of *F.* cf. *baladika* in Java was obtained from our field study. The predictor variables were selected based on treefrog biology and ecology, which modified from Kurniawan et al. (2024). A total of 23 variables were generated using Google Earth Engine (https://code.earthengine.google.com) in 250x250 meter scale for Sumatra–Java–Bali area, including 19 bioclimatic variables from WorldClim v.2.1 (Fick and Hijmans, 2017), land cover from ESA WorldCover v.200 (Zanaga et al., 2022), tree cover from Hansen Global Forest Change v.1.10 (Hansen et al., 2013), NDVI (MOD13Q1) from MODIS (Didan, 2021), and elevation from NASA SRTM Digital Elevation 30m (Farr et al., 2007). All variables were resampled using r package *terra* (Hijmans, 2025) to address discrepancies in raster extent. Subsequently, continuous-type variables (excluding land cover) were assessed for multicollinearity using Variance Inflation Factor (VIF) analysis in r package *usdm* (Naimi et al., 2014). To develop the final species distribution model, two iterations were carried out using identical parameter settings. The first aimed to eliminate variables with zero contribution, while the second finalized the model based on the remaining predictors. Parameter were used in this study including: a subsample approach with 20% random test points, 1.5 regularization multiplier, 10 replicates, linear feature (L) only, 5000 maximum iteration, and other parameters were setting in default. Jackknife analysis was performed to evaluate predictor variables contribution in our model. The fitness of our model was evaluated based on area under the curve value (AUC) which depicted in receiver operating characteristic (ROC) curve. Our modelled species distribution map was visualized using QGIS v.3.22.5. We also utilized Geospatial Conservation Assessment Tool (GeoCAT) (http://www.kew.org) to evaluate the possible IUCN conservation status based on area of occupancy (AOO) and extent of occurrence (EOO) (4 km^2 cell size).

Results

Feihyla cf. *baladika*

Non-type. Indonesia: East Java Province: Malang Regency, Bantur District, lowland forest near Kondang Merak Beach [8°23'31.43" S 112°31'4.58" E], 20 m a. s. l., secondary lowland forest, temporary pond near vehicle road, 17.01.2024, 5 ♂, 3 ♀ (M. A. Rijalullah & M. F. Assiddiqy) (NK).

Identification. The collected specimens are morphologically aligned with the *Feihyla vittatus* group (also referred to as the *Rohanixalus* group by Biju et al., 2020), based on the following characteristics: (1) the presence of dorsolateral stripes — specifically, a pair of contrasting light-colored stripes that originate at the tip of the snout (with a darker line underneath), run over the upper eyelid margins, and terminate near the vent on both sides. This pattern differs from that of the *Feihyla palpebralis* group, which has a white streak along the upper lip margin extending from the snout tip or below the eye to the shoulder, and from the *Feihyla vittiger* group, which exhibits a narrow white streak starting from the snout tip and extending along the lateral surfaces of the head to the groin (without the darker line underneath), clearly separating the dorsal and lateral coloration; and (2) nest type — *F. vittatus* forms bubble-nests, in contrast to the jelly-nests observed in both the *F. palpebralis* and *F. vittiger* groups.

F. baladika is known only from North Sumatra and West Sumatra (Riyanto & Kurniati, 2014; Biju et al., 2020). It differs genetically from other closest congeners: *F. hansenae* from Thailand, Cambodia and Myanmar (Yodthong et al., 2014); *F. senapatiensis* from India (Manipur, Nagaland, Mizoram and Tripura) (Biju et al., 2020); *F. shyamrupus* from India (Arunachal Pradesh and Nagaland) and new record from China (southern Xizang) (Biju et al., 2020; Liu et al., 2023); *F. wuguanfui* from China (Cangyuan County, Lincang City, Jiangcheng County, Pu'er City and Ximeng County in southern Yunnan), western Myanmar and northern Laos (Liu et al., 2023); and *F. vittatus* from India, Bangladesh, Myanmar, Thailand, Laos, Cambodia, Vietnam and southern China (Aowphol et al., 2013; Biju et al., 2020).

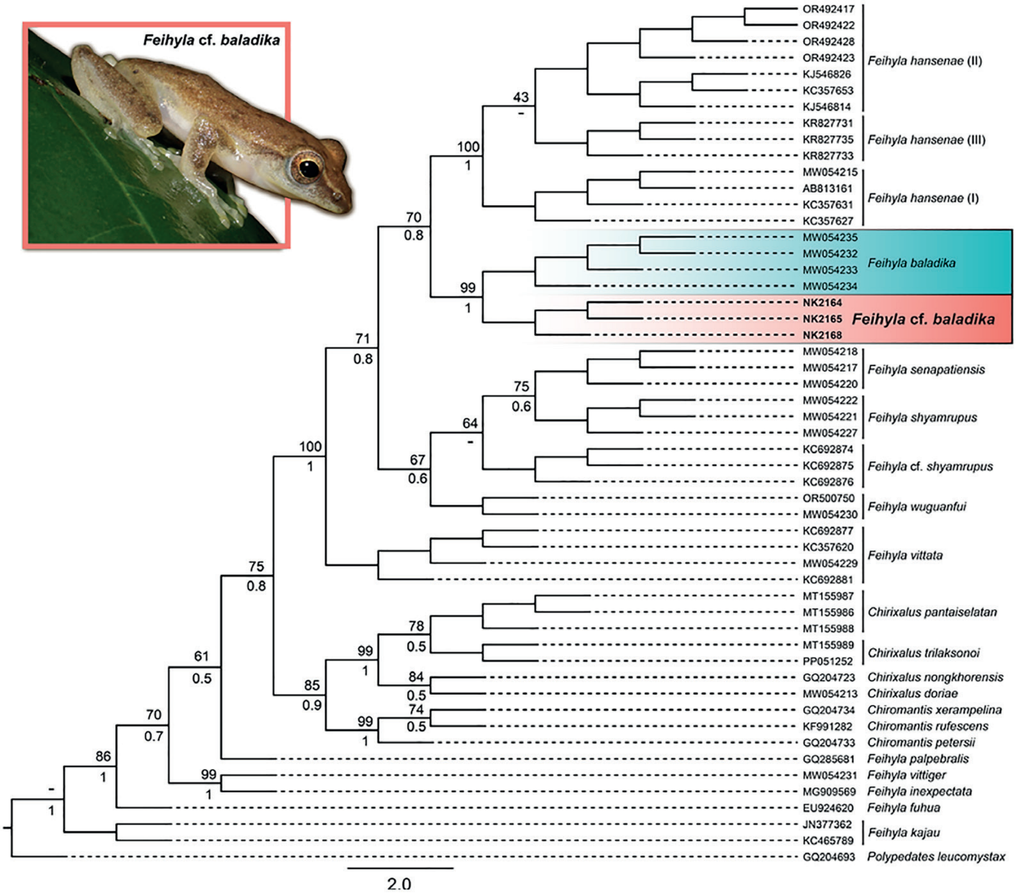

Fig. 1. Phylogenetic tree of Bayesian Inference and Maximum Likelihood analysis based on 328 bp of 16S rRNA of *F.* cf. *baladika* from East Java and other related species. Numbers on the branches represent the nodal supports for Maximum Likelihood Bootstrap (top) and Bayesian Posterior Probabilities (bottom)

Table 2. **Uncorrected pairwise sequence divergence among *F. baladika* 16S ribosomal RNA sequences of mtDNA**

No	Taxa	1	2	3	4	5	6	7
1	PV820714 (NK 2164) *F.* cf. *baladika* East Java							
2	PV820714 (NK 2165) *F.* cf. *baladika* East Java	0.00						
3	PV820714 (NK 2168) *F.* cf. *baladika* East Java	0.00	0.00					
4	MW054235 *F. baladika* Sumatera	0.03	0.03	0.03				
5	MW054232 *F. baladika* Sumatera	**0.03**	**0.03**	**0.03**	0.00			
6	MW054233 *F. baladika* Sumatera	**0.03**	**0.03**	**0.03**	0.00	0.00		
7	MW054234 *F. baladika* Sumatera	0.02	**0.02**	**0.02**	0.01	0.00	0.01	

Morphological characters of these specimens (*n* = 8; NK 2164–67, NK 2170–73) differ with other *Feihyla*, which includes: (1) lack of dark stripes on dorsum (vs. present in *F. shyamrupus*, and *F. vittatus*), (2) distinct tympanum (vs. indistinct in *F. marginis*, *F. punctatus* and some specimen of *F. vittatus*), (3) finger free of web (vs. present rudimentary in *F. shyamrupus*, *F. vittatus*, *F. punctatus*, *F. palpebralis* and *F. marginis*), (4) dorsal skin smooth (vs. dorsal skin sparsely granular in *F. vittatus*,

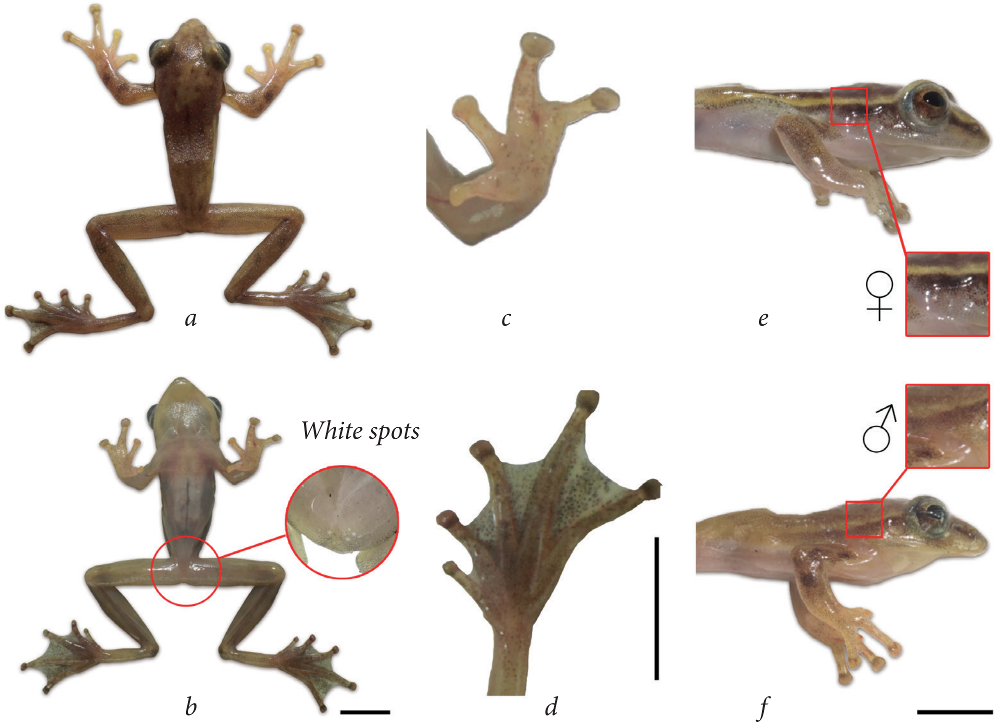

Fig. 2. Freshly preserved adult specimens (NK 2164 (♂), NK 2165 (♀)) from lowland forest near Kondang Merak Beach, Malang, East Java, Indonesia *a* — dorsal (♂); *b* — ventral (♂); *c* — ventral left hand (♂); *d*— ventral left foot (♂) of NK 2164. Sexual dimorphism could be distinguished by lateral yellow line prominence in adult (*e*) ♀ and (*f*) ♂. Scale bars 5 mm. Photos by M. F. Assiddiqy and A. M. S. P. Soeprijadi

F. nauli, *F. fuhua*, *F. inexpectata*, *F. kajau*, *F. palpebralis* and *F. vittiger*), (5) contrasting light coloured dorsolateral stripes (vs. absent in *F. palpebralis*, *F. fuhua*, *F. inexpectata*, *F. kajau* and *F. vittiger*).

Based on morphological characters and geographic distribution, our specimen closely related with *F. baladika*. However, several morphological characters in our specimen exhibit slight differences when compared to *F. baladika* (characters in parentheses) described by Riyanto & Kurniati (2014), including: (1) foot webbing moderate, webbing up to the first to second subarticular tubercle on either side of toe IV (vs. webbing up to the second subarticular tubercle on either side of toe IV); (2) prominent white spots around the cloaca (vs. not explained).

Phylogeny and genetic distance. Aligned sequence matrix of 16S rRNA (328 bp) comprises of 129 parsimony-informative, 155 variable sites, 26 singleton sites, and 173 conserved sites. Phylogenetic trees of both ML and BI demonstrated identical topologies and well-supported nodes and suggested these specimens were nested in the genus *Feihyla* and separated from Sumatran *F. baladika* lineage (MLBS = 99, BI = 1) (Fig. 1). The uncorrected *p*-distance of the 16s rRNA between *F. baladika* from Sumatra and East Java ranged 2–3% (Table 2). Therefore, we cautiously confer that these newly collected specimens are *F.* cf. *baladika*.

Description. Specimens (*n* = 8; NK 2164–67 and NK 2170–73) (Fig. 2) have a slender body and small sized adults (♂ SVL 23.3–24.8 mm, ♀ SVL 25.2–26.2 mm).

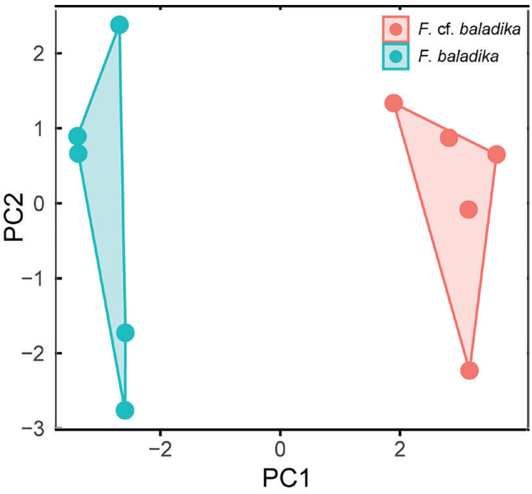

Fig. 3. *Plot of two principal components of F.* cf. *baladika* from East Java and *F. baladika* from Sumatra, using 17 allometric body-size correction characters

Head wider than long (HL/HW = 0.77–0.96); snout pointed and elongated (SL/HL = 0.43–0.60); nostril ovoid and closer to tip of snout than eye; canthus rostralis rounded, distinct; loreal region concave; interorbital space concave, narrower to broader than upper eyelid (IOD/ELW = 0.85–1.71), and exceeds internarial distance (IND/IOD = 0.72–0.96); eye large (ED/HL = 0.43–0.48), eye diameter similar to snout length (ED/SL = 0.77–1.03), pupil horizontally elongated to rounded; tympanum distinct, rounded, smaller than eye diameter (TD/ED = 0.23–0.4). Single median vocal sac; tongue attached anteriorly, deeply notched posteriorly with prominent U-shaped.

Forelimbs slender (FLL/SVL = 0.37–0.52); fingers free of web, relative length I < II < IV < III, well-developed disks on tip; third disk width approximately equal to tympanum width (3FDW/TD = 0.5–1.86); subarticular tubercles well developed, oval; inner surface nuptial pad at the base of first finger present.

Hindlimbs slender, tibia averaging slightly less than to over half snout-vent length (TIL/SVL = 0.41–0.59), thigh length approximately equal to tibia length (THL/TIL = 0.76–1.19); toes webbed moderately with varying formula (Table 4), relative length I < II < III < V < IV; developed disks on tip of toes, smaller to broader than finger (4TDW/3FDW = 0.38–1.50); subarticular tubercles well developed, oval; inner metatarsal tubercle distinct; outer metatarsal tubercle absent.

Skin texture on dorsal surface smooth; ventral surface smooth, thighs and belly surface composed of granules.

Coloration in life; Dorsal surface varies from creamy, pale brown to reddish brown with blotches ranging from faint dark to darker brown, some blotches slightly clumped; yellow lateral line runs from the tip of the snout to vent, tiny black speckles start at the loreal region and extends to dorsoventral; belly and ventral head are white, with yellowish coloration on the tip of the snout, tiny black speckles present on hindlimbs (thigh to toes) and forelimbs (palm), prominent white spots on vent; pupil dark, iris gold.

Coloration in preservation; Dorsal surface light to darker brown, finger I and II lighter than III and IV; light yellow lateral line running from tip of snout to vent, tiny black speckles present on dorsoventral and loreal region, white blotch in the middle of dorsoventral; ventral surface white, white spots on vent absent; pupil dark; iris yellow to gold.

Morphometric analysis and variations. According to our PCA analysis (Fig. 3) (*n* = 10; see Appendix Table A1, Table 4), PC1 had the eigenvalue of 9.76 indicating that most variation (57%) is contributed by the X-axis (PC1). Along the PC1, *F.* cf. *baladika* from East Java is separated from Sumatran *F. baladika.* The Y-axis (PC2) had the

Table 3. **Morphometric comparison of *F.* cf. *baladika* from East Java and *F. baladika* from Sumatra**

Character	Population		
	East Java (this study)		Sumatra(Riyanto & Kurniati, 2014)
Sexes	♂ (*n* = 5)	♀ (*n* =3)	♂ (*n* = 5)
SVL	24.0 ± 0.7 (23.3–24.8)	25.8 ± 0.5 (25.2–26.2)	21.4 ± 0.3 (21.1–21.8)
HL	6.8 ± 0.2 (6.5–7)	7.0 ± 0.0 (7.0)	7.9 ± 0.3 (7.4–8.2)
HW	7.5 ± 0.1 (7.4–7.6)	8.3 ± 0.1 (8. 2–8.4)	7.4 ± 0.3 (7.1–7.8)
ELW	2.2 ± 0.4 (1.7–2.6)	1.9 ± 0.1 (1.8–1.9)	1.0 ± 0.1 (0.9–1.1)
ED	3.0 ± 0.0 (3.0)	3.1 ± 0.1 (3.0–3.1)	3.4 ± 0.2 (3.1–3.6)
IND	2.2 ± 0.1 (2.1–2.3)	2.2 ± 0.0 (2.2)	2.2 ± 0.1 (2.1–2.4)
IOD	2.5 ± 0.2 (2.2–2.7)	2.9 ± 0.1 (2.8–2.9)	2.7 ± 0.2 (2.4–3)
SNL	3.2 ± 0.1 (3.0–3.4)	3.7 ± 0.2 (3.5–3.9)	3.7 ± 0.2 (3.5–4)
DNE	1.7 ± 0.2 (1.5–1.9)	1.9 ± 0.2 (1.7–2.1)	1.9 ± 0.2 (1.6–2)
TD	0.9 ± 0.2 (0.7–1.2)	0.9 ± 0.2 (0.8–1.2)	1.1 ± 0.1 (1–1.2)
FLL	10.3 ± 0.5 (9.7–10.8)	11.5 ± 0.7 (10.7–12)	9.7 ± 0.3 (9.4–10.1)
HLT	7.2 ± 1.1 (5.6–8.3)	8.4 ± 0.3 (8.2–8.8)	6.8 ± 0.3 (6.3–7.1)
THL	11.2 ± 0.6 (10.5–11.7)	12.7 ± 0.2 (12.6–12.9)	10.2 ± 0.6 (9.8–11.2)
TIL	11.8 ± 0.7 (10.8–12.4)	13.4 ± 0.6 (12.8–13.8)	10.7 ± 0.5 (10.2–11.3)
FL	9.8 ± 0.5 (9.1–10.4)	10.7 ± 1.0 (9.8–11.8)	9.4 ± 0.3 (9–9.8)
3FDW	0.7 ± 0.1 (0.6–0.9)	1.0 ± 0.3 (0.7–1.3)	1.4 ± 0.2 (1.2–1.6)
4TDW	0.6 ± 0.1 (0.5–0.7)	0.8 ± 0.1 (0.8–0.9)	1.1 ± 0.1 (0.9–1.3)

Note. See Material and Methods for abbreviations.

Table 4. Toe webbing variations of *F.* cf. *baladika* from East Java between sexes

Voucher ID	Sex	Toe Webbing Formula
NK 2164	♂	I 1–2 II 1–2 III 1–2 IV 1–1 V
NK 2167		I 1–2 II 1–2 III 1–2 IV 1 - 1 V
NK 2171		I 1–2 II 1–2 III 1–2 IV 2 - 1 V
NK 2172		I 1–2 II 1–2 III 1–2 IV 2 - 1 V
NK 2173		I 1–1 ½ II 1–2 III 1–2 IV 1–1 V
NK 2165	♀	I 1–1 ½II 1–2 III 1–2 IV 1–1 V
NK 2166		I 1–1 ½II 1–2 III 1–2 IV 1–1 V
NK 2170		I 1–2 II 1–2 III 1–2 IV 2–1 V

eigenvalue of 2.83 indicating that the variation (17%) also contributed to further separate *F.* cf. *baladika* and *F. baladika*. PCA loading for PC1 ranged from –0.30 to 0.31 with heavier loading on ELW (0.31), SVL (0.30), and FLL (0.29). The Mann–Whitney U test showed that the *F.* cf. *baladika* and *F. baladika* are significantly different ($p < 0.05$) in 10 assessed characters: SVL, HL, ELW, ED, SNL, FLL, THL, TIL, 3FDW, and 4TDW.

Sexual dimorphism (Table 3) is observed in seven morphometric characters of adults ♂ ($n = 5$) and ♀ ($n = 3$). SVL in adults ♂ (Mean ± SD = 24.0 ± 0.7) is shorter than in adults ♀ (25.8 ± 0.5), HW in adults ♂ (7.5 ± 0.1) is shorter than in adults

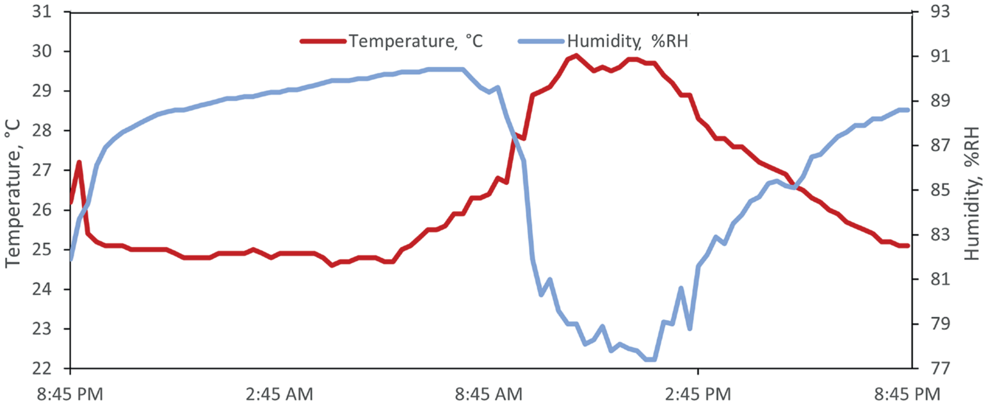

Fig. 4. The 24-hours microclimatic fluctuation (temperature and relative humidity) at encountered breeding site of *F.* cf. *baladika* from East Java

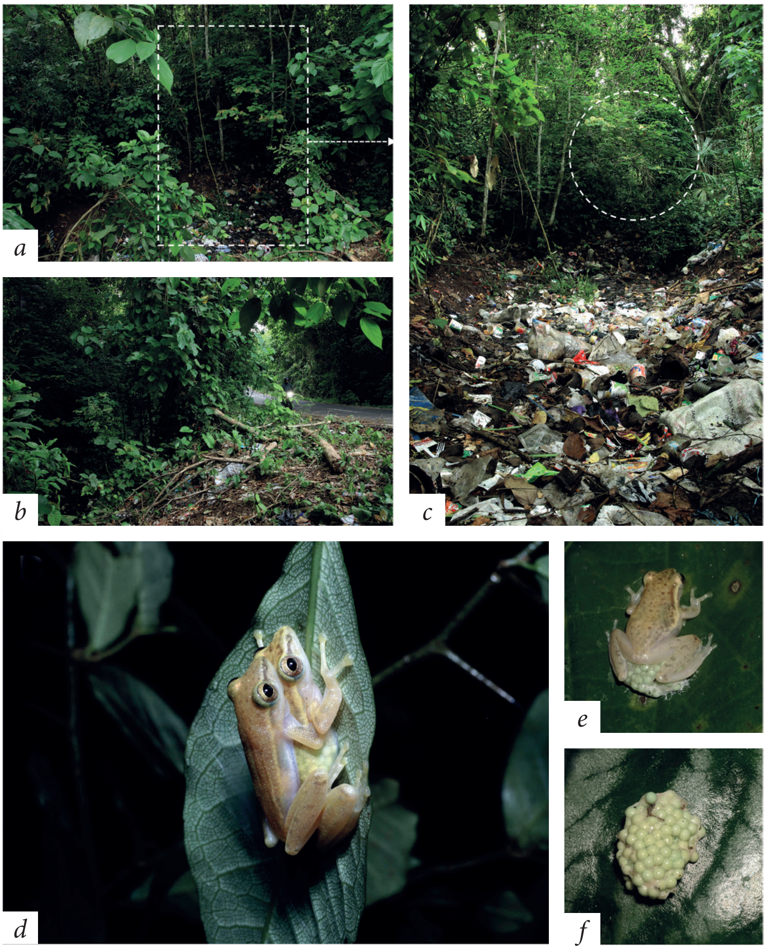

Fig. 5. Documentation of *F.* cf. *baladika* (NK 2164 (♂), NK 2165 (♀)) from lowland forest area near Kondang Merak beach, Malang, East Java, Indonesia: *a* — breeding site view from paved road with dashed line rectangle indicating the habitat site; *b* — paved road view from breeding site; *c*— pond in dry condition, with dashed lined circle indicating the position of the frog: *d* — amplecting pairs, *e* — oviposition, and *f* — bubble nest filled with egg of *F.* cf. *baladika*. Photographed by M. A. Rijalullah and A. M. S. P. Soeprijadi

♀ (8.3 ± 0.1), IOD in adults ♂ (2.5 ± 0.2) is shorter than in adults ♀ (2.9 ± 0.1), SNL in adults ♂ (3.2 ± 0.1) is shorter than in adults ♀ (3.7 ± 0.2), THL in adults ♂ (11.2 ± 0.6) is shorter than in adults ♀ (12.7 ± 0.2), TIL in adults ♂ (11.8 ± 0.7) is shorter than in adults ♀ (13.4 ± 0.6), 4TDW in adults ♂ (0.6 ± 0.1) is shorter than in adults ♀ (0.8 ± 0.1). Based on toe webbing formula examination (Table 4), most ♂ have toe II webbing that is II 1–2 III, while most ♀ have toe II webbing that is II 1½–2 III, indicating a tendency regarding sexual dimorphism. However, this characteristic is not definite sexual dimorphism diagnostic, as evidenced by the exceptions in NK 2173 (♂) and NK 2170 (♀), Table 4.

Habitat and natural history. The first two individuals found were a pair that was spawning (♂: NK 2164, ♀: NK 2165) and followed by oviposition by the ♀ (NK 2165) who was seen laying her bubble nest in the foliage overhanging the temporary pond (abiotic parameters of pond water can be seen in Table 5) surrounded by dense vegetation and close to the paved road (Fig. 4). The discovery occurred at night at 8.45 pm, during the rainy season. Temperature and relative humidity measurements recorded 24 hours after the discovery showed a temperature range of 24.6–29.9 °C (Mean ± SD = 26.4 ± 1.8) and relative humidity of 77.4–90.4% (86.1± 4.2) (Fig. 5). Other anuran species found in the same habitat included *Rhacophorus reinwardtii*, *Microhyla palmipes*, and *Hylarana chalconota*.

Distribution. *F. baladika* is distributed in lowland area within 15–273 m a.s.l. in Sumatra and Java (Fig. 6). This species is currently known from the following areas:

- North Sumatra: Tapanuli (Biju et al., 2020: MZB Amph 23920, 23951) and Berastagi, Karo (Biju et al., 2020: MZB Amph 31928).
- West Sumatra: Solok Selatan (Riyanto & Kurniati, 2014: MZB Amph 17935–17939).
- Bengkulu: Rejang Lebong (Biju et al., 2020: MZB Amph 26114).
- East Java: Malang (this study: NK 2164–2167 and NK 2170–2173).

Based on the current known distribution data, the extent of occurrence (EOO) of *F. baladika* is estimated 28,186,778.3 ha, while the area of occupancy (AOO) is 2,400 ha.

Species distribution model using MaxEnt. Our species distribution model for *Feihyla baladika* resulted an acceptable performance (AUC = 0.801) (Fig. 7). The most influential predictor variables (Fig. 8) were precipitation of the wettest month (Bio13, 81.2%), land cover (8.4%), and temperature seasonality (Bio04, 4.8%). According to the model, suitable habitats for *F. baladika* are charac-

Table 5. **Microclimatic parameters measured at temporary pond at encountered breeding site of *F.* cf. *baladika* from East Java**

Parameter	Mean (Range)
Temperature (°C)	27.0 (26.8–27.1)
pH	6.8 (6.7–6.8)
TDS (ppm)	324.8 (317–330)
EC (µS)	650 (434–660)
DO (mg/L)	2.4 (2.3–2.5)
Turbidity (NTU)	30 (29.5–30.8)

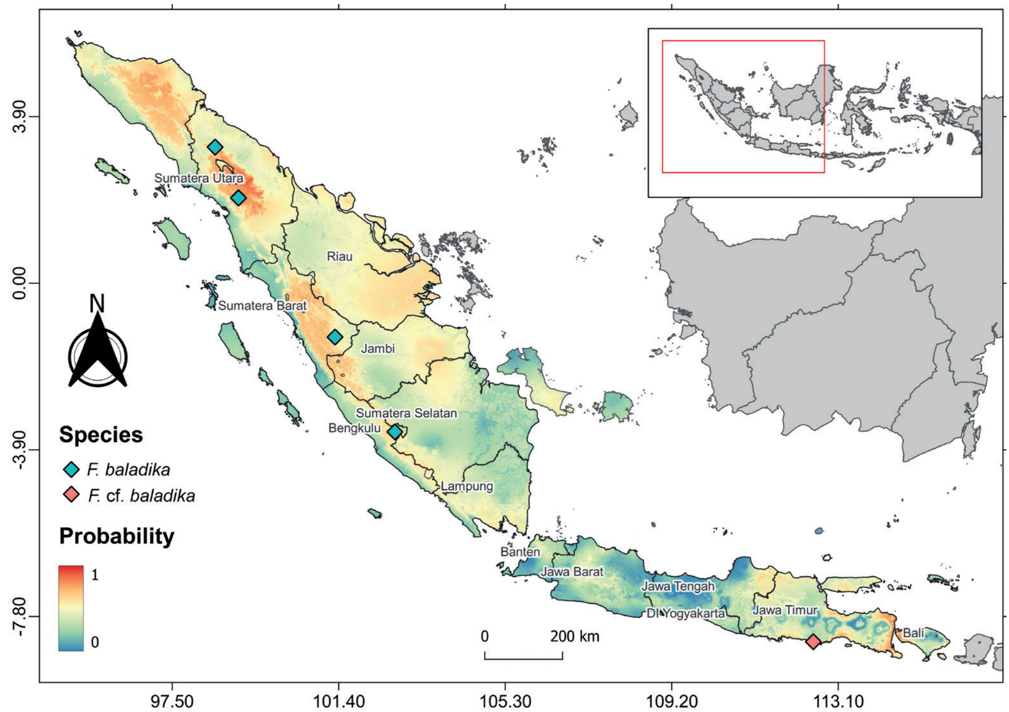

Fig. 6. Geographic distribution of *F. baladika* and *F.* cf. *baladika* (this study) in Sumatra, Java and Bali. Distribution probability was established using Maximum Entropy modeling

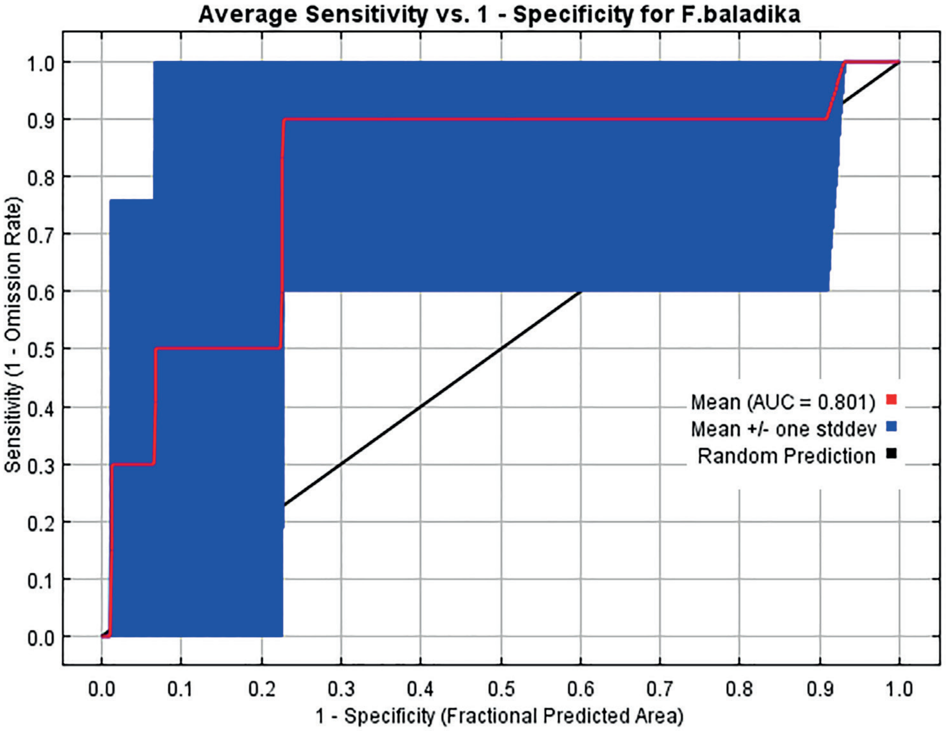

Fig. 7. Receiver Operating Characteristic (ROC) curve based on Maximum Entropy modeling for *F. baladika*

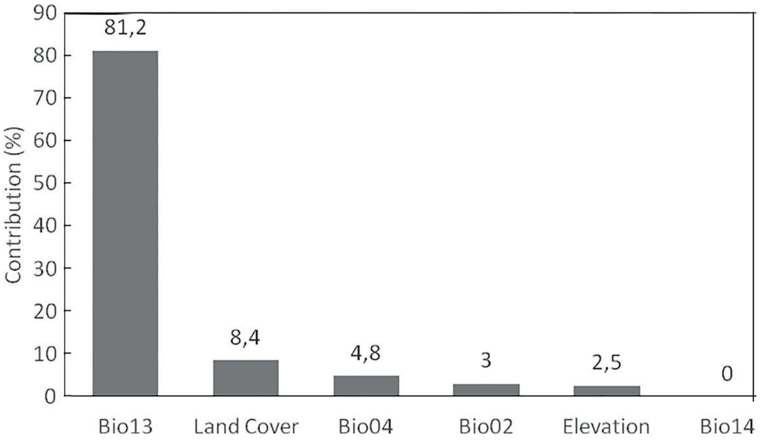

Fig. 8. Environmental variables contribution based on Maximum Entropy modeling for *F. baladika*

terized by precipitation of 145–233 mm during the wettest month, areas with tree cover, and low temperature seasonality.

Discussion

Our findings from East Java contribute valuable data regarding the current distribution, habitat, and morphological characteristics of *F.* cf. *baladika*. Morphological analysis revealed that the population from East Java exhibits significant differences from the *F. baladika* specimens originating from Sumatra, with 10 morphometric characters depicting significant differences. In comparison with other congener cryptic species (*F. hansenae* vs. *F.* cf. *hansenae* = 5.2–5.7%, *F. shyamrupus* vs. *F.* cf. *shyamrupus* = 2.8%) (Biju et al., 2020), genetic distance analysis (ranging from 2–3%) supports the possibility that Javan *F.* cf. *baladika* may represent a cryptic species from Sumatran *F. baladika*. However, given the lack of comparative data from the central to western regions of Java Island, this justification should be interpreted with caution. In addition, we are also unable to compare our female specimen with Sumatran *F. baladika* due to the absence of sample (Riyanto & Kurniati, 2014; Biju et al., 2020). Therefore, further specimens from central and western Java, as well as female samples of *F. baladika* from Sumatra, are essential to conclusively assess the taxonomic status of *F.* cf. *baladika*.

The distribution, ecology, and systematics of *F. baladika* populations remain poorly understood outside of Sumatra. In Java, the species has only been recorded at our study site in East Java, although the taxonomic status of this population remains uncertain and is therefore referred to as *F.* cf. *baladika*. Our species distribution model suggests that *F. baladika* may also occur in other forested areas characterized by low precipitation and minimal temperature fluctuation. Among the environmental predictors, precipitation (Bio13) was the most influential variable, accounting for 81.2% of the model's contribution. This result aligns with regional climatic data from Avia (2019), which reported that East Java receives less rainfall than the western and central regions of the island during the rainy season. Supporting this hypothesis, a recent observation of *F. baladika* at the Way Canguk Research Station in Lampung, Sumatra (Septiadi, pers. comm., 2025), also indicates the species' preference for areas with relatively low precipitation. Such environmental variation may be a key factor limiting the species' occurrence in the wetter western and central parts of Java. However, further field surveys in those regions are necessary to validate our model predictions.

The habitat occupied by *F.* cf. *baladika* in East Java appears similar to that of *F. baladika* in Sumatra, as both are found in disturbed lowland forests affected by anthropogenic activities, such as vehicle-accessible forest roads in East Java and palm oil monocultures in Sumatra (IUCN SSC Amphibian Specialist Group, 2018). These habitat conditions (Figure 4) underscore the need to initiate in-situ conservation efforts. Although *F. cf. baladika* exhibits ecological traits similar to *F. baladika*, including tolerance of disturbed habitats and association with temporary ponds (Riyanto & Kurniati, 2014; Frost et al., 2015; Biju et al., 2020), the sustainability of its habitat near Kondang Merak Beach in East Java remains a concern. Targeted measures, such as improved waste management to reduce water pollution and further surveys to explore the feasibility of artificial ponds, are recommended. This urgency is further supported by the dense vegetation surrounding the temporary ponds, which also serve as important breeding sites for other rhacophorids, including *Polypedates pseudotilophus*, *P. leucomystax*, and *Rhacophorus reinwardtii* (Kadafi et al., 2019; Kurniawan et al., 2023; Kurniawan et al., 2024).

The disjunct distribution of *F. baladika* highlights the importance of refined assessments of species range and conservation status. Although the extent of occurrence (EOO) may suggest a broader distribution consistent with a Least Concern (LC) classification under IUCN criteria, the area of occupancy (AOO) may place the species closer to the threshold for Endangered (EN) status. Recent records of *Polypedates pseudotilophus* (Kurniawan et al., 2023) and *Nyctixalus margaritifer* (Hanifa et al., 2023) from East Java, both previously unrecorded in this region, suggest that amphibian diversity in East Java has been historically underestimated. Furthermore, the deforestation that has occurred on this island since the 1950s (Haryadi and Andarwati, 2019), which currently makes East Java the region with the highest deforestation rate on the island of Java (Prasetyo et al., 2009), deserves concern. These findings highlight the urgent need for intensive and long-term monitoring in East Java to inform more accurate conservation assessments and support the preservation of enigmatic biodiversity.

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REFERENCES

Aowphol, A., Rujirawan A., Taksintum W., Arsirapot S. & McLeod, D. S. 2013. Re-evaluating the taxonomic status of *Chiromantis* in Thailand using multiple lines of evidence (Amphibia: Anura: Rhacophoridae). *Zootaxa*, **3702** (2), 101–123. https://doi.org/10.11646/zootaxa.3702.2.1

Biju, S. D., Garg, S., Gokulakrishnan, G., Chandrakasan, S., Thammachoti, P., Ren, J., Gopika, C., Bisht, K., Hamidy, A. & Shouche, Y. 2020. New insights on the systematics and reproductive behaviour in tree frogs of the genus *Feihyla*, with description of a new related genus from Asia (Anura, Rhacophoridae). *Zootaxa*, **4878** (1), 1–55. https://doi.org/10.11646/zootaxa.4878.1.1

Bispo, R. & Marques, F. 2023. Stability of principal components under normal and non-normal parent populations and different covariance structures scenarios. *Journal of Statistical Computation and Simulation*, **93** (7), 1060–1076. https://doi.org/10.1080/00949655.2022.2125971

Chan, K. O. & Grismer, L. L. 2022. GroupStruct: An R Package for Allometric Size Correction. *Zootaxa*, **5124** (4), 471-482. https://doi.org/10.11646/zootaxa.5124.4.4

Chan, K. O., Grismer, L. L., Brown, R. M. 2018. Comprehensive multi-locus phylogeny of Old World tree frogs (Anura, Rhacophoridae) reveals taxonomic uncertainties and potential cases of over- and underesti-mation of species diversity. *Molecular Phylogenetics and Evolution*, **127**, 1010–1019. https://doi.org/10.1016/j.ympev.2018.07.005

Chan, K. O., Hutter, C.R., Wood, Jr. P. L., Grismer, L. L. & Brown, R. M. 2020. Target-capture phylogenomics provide insights on gene and species tree discordances in Old World treefrogs (Anura: Rhacophoridae). *Proceedings of The Royal Society*, **287** (1940), 1–9. https://doi.org/10.1098/rspb.2020.2102

Chen, J. M., Prendini, E., Wu, Y. H., Zhang, B. L., Suwannapoom, C., Chen, H. M., Jin, J. Q., Lemmon, E. M., Lemmon, A. R., Stuart, B. L., Raxworthy, C. J., Murphy, R. W., Yuan, Z. Y. & Che, J. 2020. An integrative phylogenomic approach illuminates the evolutionary history of Old World tree frogs (Anura: Rhacophoridae). *Molecular Phylogenetics and Evolution*, **145**, 106724. https://doi.org/10.1016/j.ympev.2019.106724

Didan, K. (2021). *MODIS/Terra Vegetation Indices 16-Day L3 Global 250m SIN Grid V061* [Data set]. NASA EOSDIS Land Processes Distributed Active Archive Center. https://doi.org/10.5067/MODIS/MOD13Q1.061. Accessed on 15 June 2025.

Elith, J. & Graham, C. H. 2009. Do they? How do they? Why do they differ? On finding reasons for differing performances of species distribution models. Ecography, 32, 66–77. https://doi.org/10.1111/j.1600-0587.2008.05505.x

Farr, T. G., Rosen, P. A., Caro, E., Crippen, R., Duren, R., Hensley, S., Kobrick, M., Paller, M., Rodriguez, E., Roth, L., Seal, D., Shaffer, S., Shimada, J., Umland, J., Werner, M., Oskin, M., Burbank, D. & Alsdorf, D. E. 2007. The Shuttle Radar Topography Mission. *Reviews of Geophysics*, **45** (2). https://doi.org/10.1029/2005RG000183

Fick, S. E. & Hijmans, R. J. 2017. WorldClim 2: new 1km spatial resolution climate surfaces for global land areas. *International Journal of Climatology*, **37** (12), 4302-4315. https://doi.org/10.1002/joc.5086

Fois, M., Fenu, G., Cuena Lombraña, A., Cogoni, D. & Bacchetta, G. 2015. A practical method to speed up the discovery of unknown populations using species distribution models. *Journal for Nature Conservation*, 24, 42–48. https://doi.org/10.1016/j.jnc.2015.02.001

Frost, D. R. 2015. *Amphibian Species of the World: an Online Reference. Version 6.0 (14 January 2016)*. New York, USA. Available at: http://research.amnh.org/herpetology/amphibia/index.html. Accessed on 31 May 2025.

Frost, D. R. 2024. *Amphibian Species of the World, an Online Reference. Version 6.2. Electronic Database*. American Museum of Natural History, New York. https://amphibiansoftheworld.amnh.org/. Accessed on 31 May 2025.

Frost, D. R., Grant, T., Faivovich, J. N., Bain, R. H., Haas, A., Haddad, C. F. B., De Sá, R., Channing, A., Wilkinson, M., Donnellan, S. C., Raxworthy, C. J., Camp-bell, J. A., Blotto, B. L., Moler, P., Drewes, R. C., Nussbaum, R. A., Lynch, J. D., Green, D. M. & Wheler, R. C. 2006. The amphibian tree of life. *Bulletin of the American Museum of Natural History*, **2006** (297), 1–291. https://doi.org/10.1206/0003-0090(2006)297[0001:TATOL]2.0.CO;2

Grosjean, S., Delorme, M., Dubois, A. & Ohler, A. 2008. Evolution of reproduction in the Rhacophoridae (Amphibia, Anura). *Journal of Zoological Systematics and Evolutionary Research*, **46** (2), 169–176. https://doi.org/10.1111/j.1439-0469.2007.00451.x

Hanifa, B. F., Septiadi, L., Hasyim, M. A., Fathoni, M., Prabasari, K., Erfanda, M. P., Rahmadana, M., Widjanarko, H. & Kurniawan, N. 2023. New data on and the easternmost record of the Javan endemic Pearly Tree Frog, *Nyctixalus margaritifer* Boulenger, 1882 (Anura, Rhacophoridae). *Check List*, **19** (6), 971–982. https://doi.org/10.15560/19.6.971

Hansen, M. C., Potapov, P. V., Moore, R., Hancher, M., Turubanova, S. A., Tyukavina, A., Thau, D., Stehman, S. V., Goetz, S. J., Loveland, T. R., Kommareddy, A., Egorov, A., Chini, L., Justice, C. O. & Townshend, J. R. G. 2013. High-Resolution Global Maps of 21st-Century Forest Cover Change. *Science*, **342** (6160), 850–853. http://dx.doi.org/10.1126/science.1244693. Data available on-line from: https://glad.earthengine.app/view/global-forest-change.

Haryadi, F. T., Andarwati, S. 2019. The roles of religion in participatory development communication in the environmental issues in Indonesia. *J Agric Environ Int Dev (JAEID)*, **113** (2), 171–180. https://doi.org/10.12895/jaeid.20192.887

Hijmans, R. 2025. *terra: Spatial Data Analysis*. R package version 1.8-29. https://CRAN.R-project.org/package=terra. Accessed on 15 June 2025.

IUCN SSC Amphibian Specialist Group. 2018. *Chiromantis baladika*. The IUCN Red List of Threatened Species 2018: e.T89187134A95509827. https://dx.doi.org/10.2305/IUCN.UK.2018-1.RLTS.T89187134A95509827.en. Accessed on 06 June 2025.

Kadafi, A. M., Fathoni, M., Fauzi, M. A., Firmansyah, R., Priambodo, B. & Kurniawan, N. 2019. Study of species richness and structure community of herpetofauna on Kondang Merak Forest, Malang, Indonesia. In *Proceedings of the 6th International Conference on Advanced Molecular Bioscience and Biomedical Engineering (ICAMBBE 2019)*, SCITEPRESS, (pp. 89–95). https://doi.org/10.5220/0009586100890095

Kramer-Schadt, S., Niedballa, J., Pilgrim, J. D., Schröder, B., Lindenborn, J., Reinfelder, V., Stillfried, M., Heckmann, I., Scharf, A. K., Augeri, D. M., Cheyne, S. M., Hearn, A. J., Ross, J., Macdonald, D. W., Mathai, J., Eaton, J., Marshall, A. J., Semiadi, G., Rustam, R., Bernard, H., Alfred, R., Samejima, H., Duckworth, J. W., Breitenmoser-Wuersten, C., Belant, J. L., Hofer, H. & Wilting, A. 2013. The importance of correcting for sampling bias in MaxEnt species distribution models. *Diversity and Distributions*, 19, 1366–1379. https://doi.org/10.1111/ddi.12096

Kumar, S., Stecher, G. & Tamura, K. 2016. MEGA7: Molecular Evolutionary Genetics Analysis Version 7.0 for Bigger Datasets. *Molecular Biology and Evolution*, **33** (7), 1870–1874. https://doi.org/10.1093/molbev/msw054

Kurniawan, N., Fathoni, M., Assiddiqy, M. F., Septiadi, L., Rijalullah, M. A. 2024. Habitat suitability modelling of *Rhacophorus reinwardtii* (Schlegel, 1840) in Java, with notes on habitat characteristics from Malang Region–East Java. *Journal of Tropical Biodiversity and Biotechnology*, **9** (2), 1-16. https://doi.org/10.22146/jtbb.84459

Kurniawan, N., Kadafi, A. M., Fathoni, M., Firmansyah, R., Prabasari, K. & Fauzi, M. A. 2023. A new distribution record of *Polypedates pseudotilophus* (Anura: Rhacophoridae) from East Java, based on morphology and molecular evidence. *Russian Journal of Herpetology*, **30** (3), 167–174. https://doi.org/10.30906/1026-2296-2023-30-3-167-174

Li, J. T., Che, J., Bain, R. H., Zhao, E. M. & Zhang, Y. P. 2008. Molecular phylogeny of Rhacophoridae (Anura): A framework of taxonomic reassignment of species within the genera Aquixalus, Chiromantis, Rhacophorus, and Philautus. *Molecular Phylogenetics and Evolution*, **48** (1), 302–312. https://doi.org/10.1016/j.ympev.2008.03.023

Liu, X. L., Huang, J. K., Stuart, B. L., Ai, R. D., Bernstein, J. M., Suwannapoom, C., Chomdej, S., Che, J. & Yuan, Z. Y. 2023. Taxonomic revision of genus *Rohanixalus* (Anura: Rhacophoridae) in China with description of one new species. *Zoological Research*, **44** (6), 1146–1151. https://doi.org/10.24272/j.issn.2095-8137.2023.179

Lohman, D. J., de Bruyn, M., Page, T., von Rintelen, K., Hall, R., Ng, P. K. L., Shih, H.-T., Carvalho, G. R., & von Rintelen, T. 2011. Indo-Australian biogeography in the Sunda Arc. *Annual Review of Ecology, Evolution, and Systematics*, **42**, 205–226. https://doi.org/10.1146/annurev-ecolsys-102710-145001

Naimi, B., Hamm, N. A. S., Groen, T. A., Skidmore, A. K. & Toxopeus, A. G. 2014. Where is positional uncertainty a problem for species distribution modelling?. *Ecography*, **37**, 191–203. https://doi.org/10.1111/j.1600-0587.2013.00205.x

Phillips, S. J. 2017. *A Brief Tutorial on Maxent*. http://biodiversityinformatics.amnh.org/open_source/maxent/. Accessed on 15 June 2025.

Phillips, S. J., Anderson, R. P. & Schapire, R. E. 2006. Maximum entropy modeling of species geographic distributions. *Ecological Modelling*, **190** (3–4), 231–259. https://doi.org/10.1016/j.ecolmodel.2005.03.026

Posada, D. 2008. jModelTest: Phylogenetic Model Averaging. *Molecular Biology and Evolution*, **25** (7), 1253–1256. https://doi.org/10.1093/molbev/msn083

Prasetyo, L. B., Kartodihardjo, H., Adiwibowo, S., Okarda, B. & Setiawan, Y. 2009. *Journal of Integrated Field Science*, 6, 37–44

Rambaut, A. 2009. Molecular evolution, phylogenetics and epidemiology: FigTree. *World Wide Web electronic publication*. **7** (2018), 396-412. http://tree.bio.ed.ac.uk/software/figtree

Rebelo, H. & Jones, G. 2010. Ground validation of presence-only modelling with rare species: a case study on barbastelles *Barbastella barbastellus* (Chiroptera: Vespertilionidae). *Journal of Applied Ecology*, 47, 410–420. https://doi.org/10.1111/j.1365-2664.2009.01765.x

Rinnhofer, L. J., Roura-Pascual, N., Arthofer, W., Dejaco, T., Thaler-Knoflach, B., Wachter, G. A., Christian, E., Steiner, F. M. & Schlick-Steiner, B. C. 2012. Iterative species distribution modelling and ground validation in endemism research: an Alpine jumping bristletail example. *Biodiversity and Conservation*, 21, 2845–2863. https://doi.org/10.1007/s10531-012-0341-z

Riyanto, A. & Kurniati, H. 2014. Three new species of *Chiromantis* Peters 1854 (Anura: Rhacophoridae) from Indonesia. *Russian Journal of Herpetology*, **21** (1), 65–73. https://www.researchgate.net/publication/26121638

Ronquist, F. & Huelsenbeck, J. P. 2003. MrBayes 3: Bayesian phylogenetic inference under mixed models. *Bioinformatics*, **19** (12), 1572-1574. https://doi.org/10.1093/bioinformatics/btg180

Searcy, C. A. & Shaffer, H. B. 2014. Field validation supports novel niche modeling strategies in a cryptic endangered amphibian. Ecography, 37, 983–992. https://doi.org/10.1111/ecog.00733

Swofford, D. L. 2002. PAUP *. Phylogenetic analysis using parsimony (* and other methods). Ver. 4, Sinauer Associates, Sunderland

Trifinopoulos, J., Nguyen, L. T., von Haeseler, A. & Minh, B. Q. 2016. W-IQ-TREE: a fast online phylogenetic tool for maximum likelihood analysis. *Nucleic acids research*, **44** (W1), W232–W235. https://doi.org/10.1093/nar/gkw256

Wisz, M. S., Hijmans, R. J., Li, J., Peterson, A. T., Graham, C. H. & Guisan, A. 2008. Effects of sample size on the performance of species distribution models. *Diversity and Distributions*, 14, 763–773. https://doi.org/10.1111/j.1472-4642.2008.00482.x

Yodthong, S., Siler, C. D., Prasankok, P. & Aowphol, A. 2014. Phylogenetic patterns of the Southeast Asian tree frog *Chiromantis hansenae* in Thailand. *Asian Herpetological Research*, **5** (3), 179–196. https://doi.org/10.3724/SP.J.1245.2014.00179

Zanaga, D. Van De Kerchove, R., Daems, D., De Keersmaecker, W., Brockmann, C., Kirches, G., Wevers, J., Cartus, O., Santoro, M., Fritz, S., Lesiv, M., Herold, M., Tsendbazar, N. E., Xu, P., Ramoino, F. & Arino, O. 2022. *ESA WorldCover 10 m 2021 v200*. Zenodo. https://doi.org/10.5281/zenodo.7254221. Accessed on 15 June 2025.

Zhang, P., Liang, D., Mao, R. L., Hillis D. M., Wake D. B., Cannatella D. C. 2013. Efficient sequencing of anuran mtDNAs and a mitogenomic exploration of the phylogeny and evolution of frogs. *Mol Biol Evol*, **30** (8), 1899–1915.

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Appendix

Table A1. **Summary statistics and loading for the PCA analysis of *F. baladika* from Sumatra and *F.* cf. *baladika* from East Java, using 17 allometric body-size correction characters**

Parameter	PC1	PC2	PC3	PC4	PC5	PC6	PC7
Standard deviation	3.12	1.68	1.24	1.06	0.92	0.73	0.54
Proportion of variance	0.57	0.17	0.09	0.07	0.05	0.03	0.02
Cumulative proportion	0.57	0.74	0.83	0.9	0.95	0.98	0.99
Eigenvalue	9.76	2.83	1.53	1.13	0.84	0.53	0.29
SVL	0.3	0.04	-0.02	0.07	-0.11	-0.1	0.12
HL	-0.3	-0.16	-0.13	0.07	-0.07	-0.07	0.11
HW	0.11	-0.34	-0.41	0.1	0.51	-0.05	0.45
ELW	0.31	0.03	0.12	0.08	-0.06	0.07	-0.05
ED	-0.27	0.01	-0.01	0.23	0.18	0.56	-0.4
IND	-0.08	0.47	0.27	0.07	0.48	-0.06	-0.08
IOD	-0.16	-0.27	0.11	0.63	-0.13	-0.29	-0.23
SNL	-0.27	-0.21	0.14	-0.3	-0.07	-0.14	-0.18
DNE	-0.21	-0.1	-0.53	-0.16	-0.21	-0.12	-0.35
TD	-0.21	-0.25	0.42	0.27	0.17	-0.17	0.09
FLL	0.29	-0.02	-0.13	-0.04	0.34	0.11	-0.38
HLT	0.13	-0.33	0.46	-0.38	-0.16	0.16	0.05
THL	0.26	-0.28	0.02	0.24	-0.06	0.35	0.07
TIL	0.27	-0.29	-0.02	0.08	-0.1	0.26	-0.21
FL	0.2	-0.33	0.08	-0.2	0.35	-0.44	-0.34
3FDW	-0.3	-0.18	-0.01	-0.06	0.05	0.21	0.27
4TDW	-0.27	-0.19	0.05	-0.27	0.29	0.23	-0.01

Table A2. **List of sequence utilized for phylogenetic analysis**

Species	Locality	Country	GenBank accession	Reference
Feihyla hansenae (Clade I)	Nong Khor, Si Racha District, Chonburi Prov.	Thailand	MW054215	Biju et al. (2020)
Feihyla hansenae (Clade I)	Nam Tok Hongkaew Prov.	Thailand	AB813161	Matsui et al. (2014)
Feihyla hansenae (Clade I)	Wang Nam Khieo district, Nakhon Ratchasima Prov.	Thailand	KC357631	Aowphol et al. (2013)
Feihyla hansenae (Clade I)	Ban Ta Khun district, Surat Thani Prov.	Thailand	KC357627	Aowphol et al. (2013)
Feihyla hansenae (Clade II)	Longzhou, Guangxi	China	OR492417	Liu et al. (2023)
Feihyla hansenae (Clade II)	Shiwan Mountain, Guangxi	China	OR492422	Liu et al. (2023)
Feihyla hansenae (Clade II)	Wuzhishan, Hainan	China	OR492428	Liu et al. (2023)
Feihyla hansenae (Clade II)	Hekou, Yuannan	China	OR492423	Liu et al. (2023)
Feihyla hansenae (Clade II)	Mae Hong son Prov	Thailand	KJ546826	Yodthong et al. (2014)
Feihyla hansenae (Clade II)	Mueang district, Mae Hong Son Prov.	Thailand	KC357653	Aowphol et al. (2013)
Feihyla hansenae (Clade II)	Mae Sod district, Tak Province	Thailand	KJ546814	Aowphol et al. (2013)
Feihyla hansenae (Clade III)	Phu Hin Rong Kla NP, Phitsanulok Prov.	Thailand	KR827731	Grosjean et al. (2015)
Feihyla hansenae (Clade III)	Thung Salaeng Luang NP, Phetchabun Prov.	Thailand	KR827735	Grosjean et al. (2015)
Feihyla hansenae (Clade III)	Thung Salaeng Luang NP, Phetchabun Prov. Sama koordinate	Thailand	KR827733	Grosjean et al. (2015)
Feihyla baladika	Berastagi, North Sumatra	Indonesia	MW054235	Biju et al. (2020)
Feihyla baladika	Tapanuli, North Sumatra	Indonesia	MW054232	Biju et al. (2020)
Feihyla baladika	Tapanuli, North Sumatra	Indonesia	MW054233	Biju et al. (2020)
Feihyla baladika	Rejanglebong, Bengkulu	Indonesia	MW054234	Biju et al. (2020)
Feihyla cf. *baladika*	Malang, East Java	Indonesia	PV820714	This study
Feihyla cf. *baladika*	Malang, East Java	Indonesia	PV820715	This study
Feihyla cf. *baladika*	Malang, East Java	Indonesia	PV820716	This study
Feihyla senapatiensis	Nagaland	India	MW054218	Biju et al. (2020)
Feihyla senapatiensis	Manipur	India	MW054217	Biju et al. (2020)
Feihyla senapatiensis	Manipur	India	MW054220	Biju et al. (2020)
Feihyla shyamrupus	Arunachal Pradesh	India	MW054222	Biju et al. (2020)
Feihyla shyamrupus	Manipur	India	MW054221	Biju et al. (2020)
Feihyla shyamrupus	Nagaland	India	MW054227	Biju et al. (2020)
Feihyla cf. *shyamrupus*	Putao District, Kachin State	Myanmar	KC692874	Aowphol et al. (2013)
Feihyla cf. *shyamrupus*	Putao District, Kachin State	Myanmar	KC692875	Aowphol et al. (2013)
Feihyla cf. *shyamrupus*	Putao District, Kachin State	Myanmar	KC692876	Aowphol et al. (2013)

The end Table A2

Species	Locality	Country	GenBank accession	Reference
Feihyla wuguanfui	Kham, Xiengkhouang	Laos	OR500750	Liu et al. (2023)
Feihyla wuguanfui	Naung Layan, Loi Mwe WS, Kyaitong Township	Myanmar	MW054230	Biju et al. (2020)
Feihyla vittata	Dewei District, Tanintharyi Division	Myanmar	KC692877	Aowphol et al. (2013)
Feihyla vittata	Sangkhla Buri district, Kanchanaburi Prov.	Thailand	KC357620	Aowphol et al. (2013)
Feihyla vittata	Rangat, Middle Andaman, Andaman and Nicobar Islands	India	MW054229	Biju et al. (2020)
Feihyla vittata	Myitkyina District, Kachin state	Myanmar	KC692881	Aowphol et al. (2013)
Feihyla palpebralis	Lang Bian, Lam Dong	Vietnam	GQ285681	Li et al. (2009)
Feihyla vittiger	Pengalengan, West Java	Indonesia	MW054231	Biju et al. (2020)
Feihyla inexpectata	Camel Trophy field station, Maliau Basin Conservation Area, Sandakan Division, Sabah	Malaysia	MG909569	Haas et al. (2018)
Feihyla fuhua	Pingbian, Yunnan	China	EU924620	Yu et al. (2009)
Feihyla kajau	Camp 1, Gunung Mulu N.P., Sarawak, Borneo	Malaysia	JN377362	Haas et al. (2012)
Feihyla kajau	Bintulu Division, Sarawak, Borneo	Malaysia	KC465789	Li et al. (2013)
Chirixalus pantaiselatan	Leuweung Sancang Nature Reserve, Sancang, Cibalong District, Garut Regency, West Java	Indonesia	MT155987	Munir et al. (2021)
Chirixalus pantaiselatan	Leuweung Sancang Nature Reserve, Sancang, Cibalong District, Garut Regency, West Java	Indonesia	MT155986	Munir et al. (2021)
Chirixalus pantaiselatan	Leuweung Sancang Nature Reserve, Sancang, Cibalong District, Garut Regency, West Java	Indonesia	MT155988	Munir et al. (2021)
Chirixalus trilaksonoi	Jasinga, Bogor, West Java	Indonesia	MT155989	Munir et al. (2021)
Chirixalus trilaksonoi	Bukit Baru, Ilir Barat I District, Palembang, South Sumatra	Indonesia	PP051252	Herlambang et al. (2023)
Chirixalus nongkhorensis	Laos (Vientiane and Champasak)	Laos	GQ204723	Meegaskumbura et al. (2010)
Chirixalus doriae	Kyaiphaung to Win Bo village, Kyaitong Township	Myanmar	MW054213	Biju et al. (2020)
Chiromantis xerampelina	Africa	Africa	GQ204734	Meegaskumbura et al. (2010)
Chiromantis rufescens	Cameroon	Cameroon	KF991282	Barej et al. (2014)
Chiromantis petersii	Africa	Africa	GQ204733	Meegaskumbura et al. (2010)
Polypedates leucomystax	Java	Indonesia	GQ204693	Meegaskumbura et al. (2010)