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The occurrence of the very rare species *Gekko* cf. *brooksii* (Squamata, Gekkonidae) in West Sumatra, Indonesia, based on molecular and morphological evidence

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Abstract. *Chatri M, Ahda Y, Zulyusri, Septiadi L, Riyanto A, Nugraha FAD. 2024. The occurrence of the very rare species* Gekko *cf.* brooksii *(Squamata, Gekkonidae) in West Sumatra, Indonesia, based on molecular and morphological evidence. Biodiversitas 25: 3369-3379.* Sumatra, Indonesia is a region of vast, rich and diverse flora and fauna, yet knowledge of herpetology in Sumatra is limited. One such group is the genus *Gekko*, which is poorly known, morphologically diverse and taxonomically problematic, especially for canopy-dwelling geckos. During our recent fieldwork in the Barisan Mountains of West Sumatra, we found an unidentified camouflaged gecko and used molecular and morphological approaches to confirm its identity. Based on molecular (NADH dehydrogenase 2 [ND2] and flanking tRNA genes) and morphological comparisons (31 characters), we confirmed a new record and an expansion range of *Gekko* cf. *brooksii* to West Sumatra; we also reported several morphological characters that have not been reported in previous studies. The individual was found on the leaves of a young breadfruit plant (*Artocarpus communis* J.R.Forst. & G.Forst.) located about 1 meter from the hiking trail, where the surrounding vegetation consisted of several tall trees and was mostly dominated by herbaceous plants that did not exceed 1 meter in height. It conclusion, despite a long history of exploration, the herpetofauna of Sumatra continues to yield new discoveries and records. As the geckos inhabiting the higher canopy layers of tropical rainforests in Sumatra remain largely unknown, further intensive surveys for canopy-dwelling geckos are needed to further elucidate the complete taxonomic composition of Sumatra's herpetofauna.

Keywords: Barisan mountain range, fringe *Gecko*, molecular phylogeny, ND2, range extension

INTRODUCTION

Sumatra, Indonesia is the westernmost and largest island in the Greater Sunda Islands. As one of the largest islands in Indonesia, which contains the Bukit Barisan Mountains (a mountain range that stretches around 1,700 km from the north to the south), Sumatra are area with vast, rich, and biodiverse flora and fauna (Kiew 2002). This is true for amphibians than reptiles, however, previous studies indicate that knowledge of herpetology in Sumatra is far from satisfactory (Harvey et al. 2002; Inger and Iskandar 2005), which is relatively underestimated compared to Borneo and Java. Most herpetological publications relevant to the island are quite dated, having been published since the late 19th century, where collections made in Sumatra are scarce (de Lang 2003; Inger and Iskandar 2005).

Despite extensive historical exploration, the herpetofauna of Sumatra continues to yield novel discoveries. Over the past 6 years, we have seen the discovery of new species in Sumatra, these includes amphibian, e.g., *Megophrys selatanensis* Munir, Nishikawa, Hamidy and Smith 2021, *Megophrys acehensis* Munir, Nishikawa, Hamidy and Smith 2021 (Munir et al. 2021), *Megophrys lancip* Munir, Hamidy, Farajallah and Smith 2018 (Munir et al. 2018), *Microhyla sriwijaya* (Eprilurahman et al. 2021), *Microhyla gadjahmadai* Atmaja, Hamidy, Arisuryanti, Matsui and Smith, 2018 (Atmaja et al. 2019), *Micryletta sumatrana* Munir, Hamidy, Matsui, Kusrini and Nishikawa 2020 (Munir et al. 2020), *Sigalegalephrynus burnitelongensis* Sarker, Wostl, Thammachoti, Sidik, Hamidy, Kurniawan and Smith 2019, *Sigalegalephrynus gayoluesensis Sar*ker, Wostl, Thammachoti, Sidik, Hamidy, Kurniawan and Smith 2019, *Sigalegalephrynus harveyi* Sarker, Wostl, Thammachoti, Sidik, Hamidy, Kurniawan and Smith 2019 (Sarker et al. 2019), *Hylarana fantastica* Arifin, Cahyadi, Smart, Jankowski, and Haas 2018 (Arifin et al. 2018a), *Sumaterana montana* Arifin, Smart, Hertwig, Smith, Iskandar and Haas 2018, and *Sumaterana dabulescens* Arifin, Smart, Hertwig, Smith, Iskandar and Haas 2018 (Arifin et al. 2018b); and reptiles, e.g., *Gonocephalus inauris* Harvey, Sarkar, Sidik, Kurniawan and Smith 2023 (Harvey et al. 2023), *Gonocephalus pyrius* Harvey, Rech, Riyanto, Kurniawan and Smith 2021 (Harvey et al. 2021), *Lophocalotes achlios* Harvey, Scrivani, Shaney, Hamidy, Kurniawan and Smith 2018 (Harvey et al. 2018), *Cyrtodactylus gonjong* Nugraha, Ahda, Tjong, Kurniawan, Riyanto, Fauzi and Lin 2023 (Nugraha et al. 2023), *Cyrtodactylus awalriyantoi* Ahda, Nugraha, Hon Tjong, Kurniawan, Amardi, Fauzi and Lin 2023 (Ahda et al. 2023), *Trimeresurus calamitas* Vogel, David and Sidik 2022, *Trimeresurus kirscheyi* Ogel, David and Sidik 2022, and *Trimeresurus whitteni* Vogel, David and Sidik 2022 (Vogel et al. 2022). These findings underscore the island's exceptional biodiversity and illuminate the significant knowledge gaps that persist. This ongoing process of species discovery necessitates sustained field expeditions and rigorous investigation to further elucidate the complete taxonomic composition of Sumatran herpetofaunas.

The family Gekkonidae is one of the largest families in Squamata, comprising more than 1,200 species and with more than 60 genera (Wood et al. 2020; Uetz et al. 2023). Until now, the diversity of gecko species in tropical regions is still far from comprehensively explored. Among these, canopy-dwelling geckos represent an extreme circumstance where their specialization in inhabiting microhabitats high in the tree canopy makes them almost invisible to non-arboreal sampling efforts. An example of such canopy-dwelling species is the camouflage geckos, previously known as members of the polyphyletic genus *Luperosaurus* Gray 1845 sensu lato (Wood et al. 2020). With extremely low detectability even during extensive and dedicated fieldwork, they are regarded as some of the world’s rarest gekkonid lizards, with poor investigations into their biology (Brown et al. 1997, 2000; Brown and Diesmos 2000).

Indonesia represents a country which harbours a high potential diversity of undiscovered gekkonids. In previous studies, there were three camouflage geckos recorded in Indonesia, i.e., *Gekko brooksii* Boulenger 1920 in Sumatra (Boulenger 1920), *Gekko iskandari* Brown, Supriatna and Ota, 2000 from Sulawesi (Brown et al. 2000), and *Luperosaurus yasumai* Ota, Sengoku and Hikida 1996 in Kalimantan (Ota et al. 1996). Previously, all these species were described based on a single specimen, but Wood et al. (2020) later collected additional data and analyzed their phylogenetic relationships to resolve their taxonomy. Based on phylogenomic data, the results proposed moving *Luperosaurus brooksii* and *Luperosaurus iskandari* to genus *Gekko* (subgenus *Lomatodactylus*) and present a new classification emphasizing the most inclusive gekkonid taxonomy arranged into seven subgenera (i.e., *Gekko, Japonigekko, Ptychozoon, Rhacogekko, Lomatodactylus, Balawangekko*, and *Archipelagekko*) under genus *Gekko* (Wood et al. 2020).

During our recent fieldwork in the Barisan mountain range of West Sumatra, we found an unidentified camouflaged gecko. By employing molecular and morphological methods, we were able to identify and confirm the identity of this elusive camouflage gecko through newly collected specimen. We provide morphological and genetic data, as well as updated information on the geographic distribution of this species and its congeners. We also discussed the need for extensive surveys targeting canopy-dwelling species in Sumatran rainforests.

MATERIALS AND METHODS

Field survey and collection

A field survey was conducted on May 31, 2022, from approximately 7 to 9 PM in Barisan mountain range of West Sumatra, Indonesia. We carefully examined all potential, but reachable, herpetofauna habitats (terrestrial and arboreal), including brushing through the weeds, pulling high leaves, peering into cracks in the bushes, and inspected high stem trees. These surveys resulted in numerous herpetofauna collections, including a specimen of gekkonid lizard with an unknown identity. These individuals were captured by hand, put into transparent plastic bags that were temporarily provided with sufficient air space, then placed in plastic square cages with air circulation, and quickly transferred to the laboratory for examination. We also took information of the specimens, e.g., habitat, natural history, elevation, and coordinates.

In the laboratory, these individuals were euthanized using benzocaine and fixed with 10% formalin following standard ethical guidelines in animal preservation (Simmons 2014, 2015; Dodd 2016). A series of photographs of the specimens were taken before and immediately after euthanasia. The collected specimens were deposited at the Laboratory of Ecology, Department of Biology, Universitas Negeri Padang (UNP) under voucher specimen number UNP 111. A tissue sample from the liver was stored in a 1.5 ml tube containing 95% ethanol for molecular analysis. The gekkonid lizard with unknown identity was then investigated based on molecular and morphological analyses.

Molecular analysis

Total genomic DNA was extracted from liver stored in 95% ethanol using the Qiagen DNeasy™ tissue kit (Valencia, CA, USA) following the standard protocol for animal tissue. The Natrium Dehydrogenase Subunit 2 (ND2) and partial flanking tRNAs genes were amplified using Polymerase Chain Reaction (PCR) under the following conditions: 9 min at 94°C, followed by 35 cycles of 45 s at 94°C, 45 s at 60°C, and 1 min at 72°C, with a final extension step of 6 min at 72°C. Amplifications were carried out in a 25-µL volume consisting of 2.5 µL genomic DNA (approximately 100 ng), 0.4 µM each primer, and 1x MyTaq™ HS Red Mix (Bioline, Meridian Bioscience). The primers used in this study followed Oliver et al. (2012), i.e., M112F (5’-AAGCTTTCGGGGCCCATACC-3’) and M1123R (5’-GCTTAATTAAAGTGTYTGAGTTGC-3’). The PCR product and the previously used primers were sent for sequencing using Sanger method to the service provider 1st BASE (www.base-asia.com/) through PT. Genetika Science Indonesia.

Our derived sequence was assembled and edited in DNA Sequence Assembler v.4, Heracle BioSoft (www.dnabaser.com) and deposited in GenBank (OP554816). We aligned this sequence with other gekkonids distributed in Sundaland and other locality as ingroup, and *Gehyra mutilata* as outgroup (Table 1), based on a recent phylogenetic study of geckos by Wood et al. (2020), using MAFFT v.7 online service (Katoh et al. 2019; www.mafft.cbrc.jp/alignment/server/). Uncorrected *p*-distance was calculated in MEGA v.7 (Kumar et al. 2016) for the ND2 gene.

Table 1. Sample used in the molecular analyses including localities and GenBank accession numbers of the mitochondrial NADH dehydrogenase subunit 2 and flanking tRNA genes. An asterisk (*) indicates the species name was modified (following Wood et al. 2020) from that provided in the GenBank accession due to taxonomic revision at the time of download

Species	Locality	GenBank number	Reference
Gekko athymus	Barangay Mainit, Municipality of Brooke's Point, Palawan Province, Palawan Island, Philippines	JQ173403	Siler et al. 2012
Gekko auriverrucosus	Yuncheng, Shanxi, China	JN019062	Rösler et al. 2011
Gekko badenii	Captive	JN019065	Rösler et al. 2011
Gekko chinensis	Wuzhi Shan, Hainan Island, China	JQ173409	Siler et al. 2012
Gekko crombota	Barangay Babuyan Claro, Municipality of Calayan, Cagayan Province, Babuyan Claro Island, Philippines	JQ173410	Siler et al. 2012
Gekko gecko	1.5 km E. of Aural Village, Kampong Speu Province, Cambodia	JQ173416	Siler et al. 2012
Gekko grossmanni	Captive	JN019064	Rösler et al. 2011
Gekko hokouensis	Lanyu Township, Orchid Island, China	JQ173422	Siler et al. 2012
Gekko japonicus	Ryukyu Islands, Japan	JQ173424	Siler et al. 2012
Gekko mindorensis	Barangay Formon, Municipality of Bongabong, Oriental Mindoro Province, Mindoro Island, Philippines	JN710490	Brown et al. 2011
Gekko monarchus	Municipality of Brooke's Point, Mt. Mantalingajan, Palawan Province, Palawan Island, Philippines	JQ173501	Siler et al. 2012
Gekko petricolus	Captive	JN019066	Rösler et al. 2011
Gekko romblon	Barangay Balogo, Municipality of Calatrava, Romblon Province, Tablas Island, Philippines	JN710497	Brown et al. 2011
Gekko smithii	Pekan, Pahang, Peninsular Malaysia	JQ173534	Siler et al. 2012
Gekko subpalmatus	Chengdu, Szechuan, China	JN019063	Rösler et al. 2011
Gekko swinhonis	Boai, Henan, China	JN019061	Rösler et al. 2011
Gekko vittatus	Pet trade, reportedly from eastern Indonesia	JQ437899	Brown et al. 2012
Gekko vittatus	Luesalo, Santa Cruz Island, Temotu, Solomon Islands	JN019073	Rösler et al. 2011
*Gekko iskandari**	Mt. Tompotika, Sulawesi Tengah Province, Indonesia	JQ437906	Brown et al. 2012
*Gekko kuhli**	Tekek-Juara Trail, Tioman Island, Pahang, West Malaysia	JQ437918	Brown et al. 2012
*Gekko lionotum**	Khao Luang National Park, Nakhon Si Thammarat, Thailand	JQ437914	Brown et al. 2012
*Gekko rhacophorus**	Gunung Penrissen, Sarawak, East Malaysia	JQ437913	Brown et al. 2012
Gekko* cf. *brooksii	**Near Sarasah Uwak Waterfall, Limau Manis, Padang City, West Sumatra, Indonesia**	**OP554816**	***This study***
Lepidodactylus herrei	Municipality of Baybay, Leyte Islands, Philippines	JQ173539	Siler et al. 2012
Lepidodactylus moestus	Ngerur Island, Palau	JN019079	Rösler et al. 2011
Luperosaurus angliit	Barangay Zabali, Municipality of Baler, Aurora Province, Luzon Island, Philippines	JQ437903	Brown et al. 2012
Luperosaurus cumingii	Mt. Malinao, Municipality of Tiwi, Luzon Island, Philippines	JQ437902	Brown et al. 2012
Luperosaurus joloensis	Barangay Pasanonca, Zamboanga City, Mindanao Island, Philippines	JQ437900	Brown et al. 2012
Luperosaurus macgregori	Barangay Babuyan Claro, Municipality of Calayan, Cagayan Province, Babuyan, Claro Island, Philippines	JQ437904	Brown et al. 2012
Luperosaurus macgregori	Municipality of Calayan, Cagayan Province, Calayan Island, Philippines	JQ437905	Brown et al. 2012
Luperosaurus sp.	Barangay San Antonio, Municipality of Basco, Batanes Province, Batanes Island, Philippines	JQ437901	Brown et al. 2012
Pseudogekko compressicorpus	Barangay Danicop, Municipality of Sierra Bullones, Bohol Province, Bohol Island, Philippines	JQ437898	Brown et al. 2012
Pseudogekko smaragdinus	Barangay Pinaglubayan, Municipality of Polillo, Quezon Province, Polillo Island, Philippines	JQ437897	Brown et al. 2012
Gehyra mutilata	Nimalawa, Sri Lanka	JN019082	Rösler et al. 2011

Using JMODELTEST2 (Darriba et al. 2012), the nucleotide substitution model was estimated. Maximum Likelihood (ML) and Bayesian Inference (BI) of the ND2 alignment were found to be best fitted by the GTR substitution model. With 1,000 Ultrafast Bootstrap (UFB) replicates for branch support evaluation (Hoang et al. 2018), IQ-TREE (Nguyen et al. 2015) was used to estimate phylogenetic inferences based on the ML. MRBAYES v.3.2.7a (Ronquist et al. 2012) was employed for BI, where Bayesian posterior probability (BPP) were used for branch support evaluation. According to Kurniawan et al. (2023), relationships with UFB ≥95 and BPP ≥0.95 are considered to be well-supported. Both were examined using CIPRES Science Gateway (Miller et al. 2010; www.phylo.org/). The trees were then visualized and edited using FIGTREE v.1.3.1 (Rambaut 2009).

Morphological examination

For the morphological analyses, the specimen was compared to the previously known gekkonid distributed in Indonesia and neighboring countries, these includes examination data from literatures, i.e., *G. brooksii* (Boulenger 1920; BMNH 1920.1.16.2), *Gekko browni* (Russel 1979: FMNH 185106), and *G. iskandari* (Brown et al. 2000; MZB Lace. 2114); and selected diagnostic characters of several *Gekko* species reported in Brown et al.

2000 (Table 2). We also compared our specimen to *G. browni* specimen collected from Gombak, Selangor, Malaysia (LSUHC 15106), available from La Sierra University Herpetological Collection, La Sierra University, Riverside, California, USA. We visualized the geographic distributions of our specimen and other previously collected specimen in Indonesia.

Morphometric and mensural data from two specimens (UNP 111 and LSUHC 15106) was recorded for the 21 measurements following Brown et al. (2011): SVL=snout-vent length; HL=head length; HW=head width; HD=head depth; SL=snout length; ED=eye diameter; EN=eye-nostril distance; IN=internarial distance; IO=interorbital distance; AG=axilla-groin distance; FL=femur length; TL=tibia length; TaL=tail length; TaD=tail depth; Supr=number of supralabials; Infr=number of infralabials; SAL=snout-arm length; PFP=precloacal and femoral pores; PVT=subdigital lamellae on fingers and toes, paravertebral tubercles; DTR=transverse midbody tubercles; PCT=post-cloacal tubercles. We also counted the postmental scale; observed the presence or absence of tubercles on feet, arm, and subrictal region; and the shape of auricular opening and penultimate scansors. Scales were both counted directly on the preserved specimen and confirmed on the close-up images, coloration was based on the images taken before euthanization. Sex was identified by checking the posterior part of hemipenis pocket.

RESULTS AND DISCUSSION

Phylogeny and genetic distance

The aligned sequence matrix of the ND2 and flanking tRNA genes (589 bp) comprises 421 parsimony-informative sites, 460 variable sites, 39 singleton sites, and 126 conserved sites. The BI phylogenetic tree (Figure 1) indicates that our specimen is nested within the genus *Gekko* clades, specifically within the subgenera *Lomatodactylus, Rhacogekko,* and *Ptychozoon* subclades, with strongly supported nodes. Collectively, they form the sister subclades which includes other subgenera, i.e., *Japonigekko, Gekko,* and *Archipelagekko.*

Based on the ND2 gene (578 bp), by incorporating our specimen and subgenera *Lomatodactylus, Rhacogekko,* and *Ptychozoon* subclades (Figure 1; excluding *G. iskandari* due to high number of missing data), the uncorrected *p*-distance ranged from 7.4-58.2, whereas genetic distance between specimen from West Sumatra to *G. badenii* were 36.2%, and *G. vittatus* were 42.0-42.6% (Table 2). Unfortunately, the ND2 gene sequence of *G. browni* and *G. brooksii* was not available, and we could not compare to these species. Therefore, morphological comparisons are conducted to confirm the identity of our specimen.

Identification

We compared our specimen (UNP 111) to available measurement data of *G. iskandari*, *G. brooksii*, and *G. browni*. Our specimen can be distinguished from *G. iskandari* (Brown et al. 2000: MZB Lace. 2114) by having different ear opening shape (oval oblique vs elliptical, vertical, narrow), no subrictal tubercles (absence vs presence), smaller HL/HW (1.2 vs 1.6), greater TD/TW (0.95 vs 0.77), fewer supralabial (13-14 vs 16) and infralabial (12-15 vs 17), higher number of preanofemoral pores (36 vs 10), fewer number of anteriormost chin scales (1 vs 2), presence of lateral tail tubercles (present vs absent), no lateral denticulate lobe along tail (absent vs present).

Our specimen differs from *G. brooksii* (Boulenger 1920: BMNH 1920.1.16.2) by having different ear opening shape (oval oblique vs round), smaller HL/HW (1.2 vs 1.7), greater TD/TW (0.95 vs 0.72), higher number of supralabials (13-14 vs 11) and infralabials (12-15 vs 10-11), different shape of penultimate subdigital lamellae (bowed vs notched-divided), fewer number of pre-anofemoral pores (36 vs 40), posterior forelimb extension skin (present vs absent), and different color of body ventrum (yellow vs white).

Our specimen differs from *G. browni* (LSUHC 15106; Russel 1979: FMNH 185106) by having smaller HL/HW (1.2 vs 1.6-1.7), greater TD/TW (0.95 vs 0.56-0.80), higher number of continuous pores on pre-anal and femoral (36 vs 28-32), fewer number of minimum of subdigital lamellae on toe I (10 vs 11), fewer number of anteriormost chin scales (1 vs 2), higher number of gular scales in contact with 1st, 3rd, and 4th infralabials (respectively 3, 3, 3 vs 2, 2, 2), no tubercles on subrictal region (absent vs present). The detailed morphometric and mensural data comparing our specimen (UNP 111) to *G. browni* (LSUHC 15106) is shown in Table 3.

Table 2. Uncorrected *p*-distances (in percentage) of the ND2 and its flanking tRNA genes (578 bp) of our specimen from West Sumatra, Indonesia and associated taxa

Species	1	2	3	4	5	6	7	8	9
JN019065 *Gekko badenii*	0.0								
JQ437899 *G. vittatus*	41.3	0.0							
JN019073 *G. vittatus*	42.6	7.4	0.0						
OP554816 *G.* cf. *brooksii*	36.2	42.0	42.6	0.0					
JN019066 *G. petricolus*	46.5	45.7	49.0	47.0	0.0				
JQ437918 *G. kuhli*	46.5	44.2	43.0	50.9	58.2	0.0			
JQ437913 *G. rhacophorus*	45.4	49.3	47.2	46.7	53.3	48.1	0.0		
JN019064 *G. grossmanni*	41.1	51.3	49.8	48.0	49.4	55.7	54.0	0.0	
JQ437914 *G. lionotum*	43.1	48.7	50.4	44.6	55.5	49.2	52.5	48.1	0.0

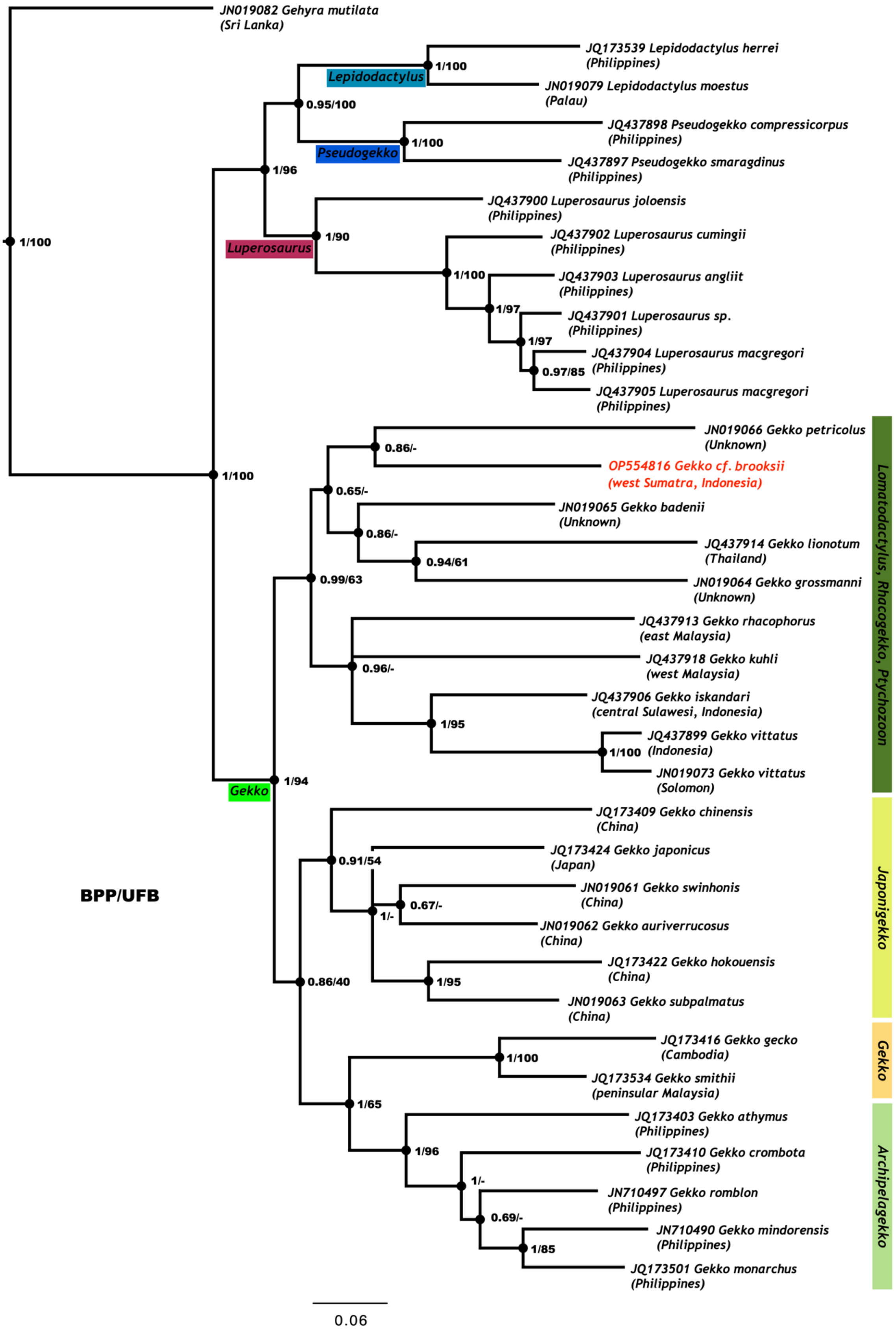

Figure 1. Bayesian Inference (BI) tree from the alignment of the ND2 and its flanking tRNA genes (589 bp) showing the phylogenetic position of our specimen from West Sumatra, Indonesia (OP554816). Values next to nodes indicate bootstrap support for Bayesian Posterior Probability (BPP) and Ultrafast Bootstrap (UFB). The genus clade is highlighted below the node and the subgenus *Gekko* subclade is presented on the right side

Our specimen from West Sumatra (UNP 111) has characteristics that are relatively intermediate between *G. browni* and *G. brooksii*, e.g., the number of pre-cloacal and femoral pores (36) is closer to *G. brooksii* (36) than *G. browni* (28-32), the number of supralabials (13-14) is closer to *G. browni* (15) than *G. brooksii* (11), and the number of infralabials (13-14) is closer to *G. browni* (15) than *G. brooksii* (11). Given that observations of *G. brooksii* and *G. browni* are only based on a very limited number of specimens, it is likely that there are still variations in characteristics that remain unknown. Morphological and genetic evidence from other samples is needed to resolve the identity of our specimen. Considering the closer location of the specimen to the type locality of *G. brooksii* (Lebong Tandai, Bengkulu Province; distance ±290 km), our specimen (UNP 111) is provisionally identified as *G.* cf. *brooksii*.

Description

An adult male and medium-sized *Gekko* cf. *brooksii* (UNP 111); habitus slender, elongated, not depressed; dorsal tubercles small, rounded; head width approximately same as trunk; snout rounded at tip; rostral rectangular, without dorsomedian groove, height half of width, in contact with internasal scales, nostril, and first supralabial; nostril opening rather oval; nostril opening in contact with five scales: with rostral scale anteroventrally, with first supralabial ventrally, with crescent-shaped scale posteriorly, with enlarged scale (internasal scale) and smaller scale anterodorsally; three internasal scales, similar in size, middle one in contact with three significantly smaller scales posteriorly; scales on snout juxtaposed, larger than on frontal, parietal, occipital and temporal of head; scales in venter of head circular and oval in shape; ear opening small and oval in shape, oblique, with single tubercle above; mental somewhat triangular in shape, in contact with one anteriormost gular scale; gular scales gradually reducing in size posteriorly, then starting to enlarge at neck and become gradually larger posteriorly to vent region; 1^{st}, 3^{rd}, and 4^{th} supralabials (right and left) in contact with three gular scales; indistinct ventrolateral fold; ventral scales flat, enlarged, sub-imbricate, oval in shape, larger than dorsal scales; dorsal lateral scales small, juxtaposed, interspersed with small tubercles; tubercles on dorsum rounded and low, smaller and lower than lateral tubercles (Figures 2 and 3).

Limbs well developed, bordered with cutaneous extension posteriorly, narrow at forelimbs, broader at hindlimbs; all fingers but first clawed, the same pattern for toes; digits well dilated, webbed reaching proximal tip of dilated portion; scales on dorsal surface of limbs as large as on body dorsum in general; scales on anteroventral surface of thigh larger than that on trunk ventrum; scales on posteroventral of thigh (after pre-cloacal pores row) much smaller than body ventrum scales; enlarged scales after pre-cloacal femoral pores present; post-cloacal swelling distinct; single enlarged and distinct tubercle on each posterior side of hemipenis pocket (Figures. 2, 4, and 5).

Table 3. Morphometric (in mm) and mensural data comparing our specimen (UNP 111) and *G. browni* (LSUHC 15106)

Abbrev	Characters	*Gekko* cf. *brooksii* (UNP 111)	*Gekko browni* (LSUHC 15106)
SVL	Snout-vent length	56.69	59.47
TaL	Tail length	42.97	41.02
HL	Head length	9.19	13.27
HW	Head width	7.82	8.02
HD	Head depth	5.01	5.3
SL	Snout length	4.38	5.93
ED	Eye diameter	2.95	4.26
EN	Eye-narial distance	4.17	4.45
IN	Internarial distance	2.08	2.45
IO	Interorbital distance	5.74	6.2
AG	Axilla-groin distance	30.05	29.9
FL	Femur length	6.80	8.88
TL	Tibia length	4.10	6.68
TaW	Tail width	4.92	4.76
TaD	Tail depth	4.70	2.68
SAL	Snout-arm length	17.78	19.96
Supr	Supralabial (L/R)	13/14	15/15
Infr	Infralabial (L/R)	12/15	12/12
PFP	Pre-cloacal and femoral pores	36	30
	Subdigital lamellae fingers I, II, III, IV, V	L: 10,12,15,17,12; R: 10,11,14,18,13	L:8,12,16,18,13; R: 8,12,16,18,13
	Subdigital lamellae toes I, II, III, IV, V	L: 10,14,17,14,14; R: 12,13,18,17,12	L:13,15,14,14,11; R: 13,15,14,14,11
DTR	Dorsal tubercle	7	6
PVT	Paravertebral tubercle	12	11
	Tubercles on feet and arms	absent	absent
PCT	Post-cloacal tubercles (L/R)	2/1	1/1
	Subrictal tubercles	absent	absent
	Auricular opening	oval, oblique	oval, square
	Penultimate scansors	bowed	bowed
	Post-mental scale	1	2

Tail subcylindrical, dorsally convex but flattened on ventral side; scales on tail dorsum as large as on body dorsum; scales on subcaudal larger than on body ventrum, as large as scales on pre- and post-cloacal pores; line in middle of tail separating two enlarge subcaudal scales distinct in posterior half of tail, two scales along midline larger than neighbouring scales laterally; spinous tubercles present on ventrolateral tail preceded by two or three smaller spinous tubercles that gradually decrease in size anteriorly (Figure 2).

Coloration of dorsal ground of head, forelimbs and hindlimbs, limbs cutaneous expansion, trunk and tail pale grey, irregular brown minute spots on the scales making the overall colour of the dorsum and lateral a combination of pale grey, and brown; five indistinct vertebral, fairly light yellow, on mid dorsum longitudinally from the neck to the region on hindlimbs insertion to the trunk; fairly light yellow flecks on each supraorbital region; indistinct yellow strip behind the eyes and in the lateral part of neck and the insertion part of forelimbs to the trunk; yellow spots on the posterior of brachium, dorsum fingers and toes, yellow indistinct transverse line on 5th finger; transverse brown on the trunk to the tip of tail; body ventrum yellow from the insertion part of forelimbs-body to the posterior of hemipenis pocket, the colour yellow gradually stronger posteriorly; yellow on limbs ventrum, digits whitish; short brown strips transversely on head ventrum from post-orbit region to the neck, and from trunk to the knees; roof of the mouth black, yellow upper and lower jaws, red-pink tongue (Figures 2, 3, 4, and 5).

Natural history, habitat, and distribution

An adult male individual (UNP 111) of *Gekko* cf. *brooksii* was obtained near Sarasah Uwak waterfall (0°54'28"S, 100°28'54"E) in the Nagari (Village) Limau Manis, Pauh Sub-district, Padang City, West Sumatra, Indonesia at an altitude of 345 meters above sea level (m asl) on the evening of May 31, 2022. The ecosystem of the Sarasah Uwak waterfall (Figure 6) is characterized as a secondary forest on the slopes of the Bukit Barisan mountain range in West Sumatra.

Figure 2. Photos of living individual of *Gekko* cf. *brooksii* (UNP 111) from West Sumatra, Indonesia; A. Ventrolateral view, B. Dorsal view, and C. Ventral view. Images not to scale

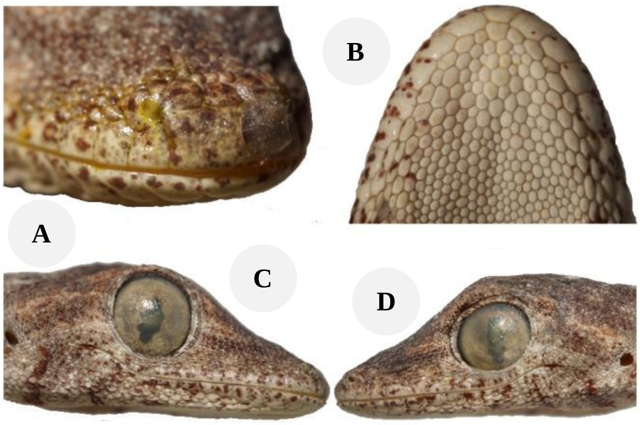

Figure 3. Head views of *Gekko* cf. *brooksii* (UNP 111) from West Sumatra, Indonesia. A. Nostril and the scales that contacted to it, B. ventral view of the head, C. right lateral view of the head, and D. left lateral view of the head. Images not to scale

Figure 4. Pre-cloacal region and femoral pores of *Gekko* cf. *brooksii* (UNP 111) from West Sumatra, Indonesia

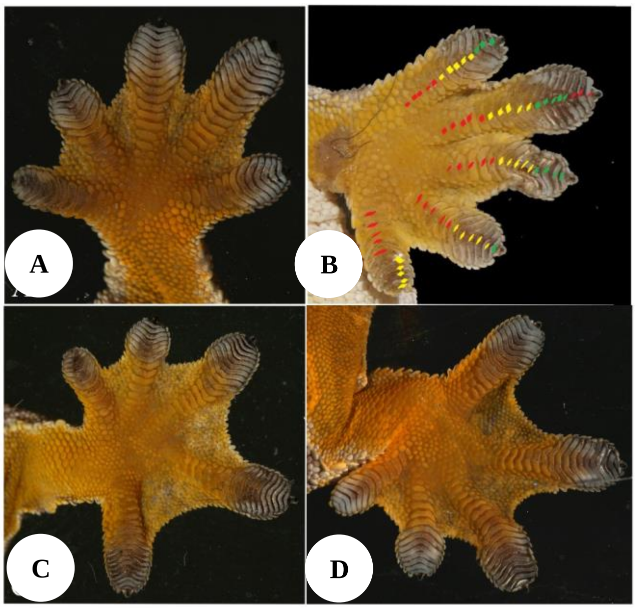

Figure 5. Lamellae under each toe and finger of *Gekko* cf. *brooksii* (UNP 111) from West Sumatra, Indonesia. A-B. left and right fingers, respectively, C-D. left and right toes, respectively. The red, green, and yellow marks in B indicate how number of subdigital lamellae were counted

The primary water feature in the vicinity is a rocky stream measuring approximately 1.0-2.5 m in width, positioned some 6-8 m from the gecko's encountered site. This stream converges into a broader rocky stream, spanning 8-15 m in width, where a water dam has been established by the local authorities. The distance from the gecko's encountered site to the waterfall is approximately 700 m. The specimen was discovered on a leaf of a young Breadfruit plant (*Artocarpus communis* J.R.Forst. & G.Forst.), located about 1 m from the hiking trail. This gecko doesn't seem to show any movement. A team member successfully captured it by hand but experienced an unexpected bite on the finger. The nearby vegetation consists of several tall trees but dominated by herbaceous plants not exceeding 1 m in height. Local residents have planted Durian fruit trees (*Durio zibethinus* Murray), which grow significantly taller than the surrounding bushes. At the beginning, the weather during the night surveys was covered by dark cloud. Around 9 PM, the field survey was halted as a precautionary measure against potential flooding due to heavy rainfall.

The references on the distribution of genus *Gekko* subgenera *Lomatodactylus* are rare, therefore, we only visualised the known localities of our specimen from West Sumatra (*G.* cf. *brooksii*, UNP 111), *G. browni* from Selangor (LSUHC 15106) and Sarawak, Malaysia (Ota et al. 1996), *G. brooksii* (Boulenger 1920), and *G. iskandari* (Brown et al. 2000). The geographic distribution of these taxa is shown in Figure 7.

Discussions

Based on our recently collected specimens from West Sumatra, we provide a brief overview of the identity, phylogenetic placement, description, habitat, and current distribution of *Gekko browni* in this study. Additionally, our study confirmed the new national record of *G. browni* in Indonesia, indicating that the discovery of reptile taxa in Sumatra has not come to a halt. Our finding also brings the number of species in the genus *Gekko* to seven in Sumatra, i.e., *G. gecko, G. albomaculatus, G. browni, G. brooksii, G. horsfieldii, G. kuhlii,* and *G. monarchus* (Uetz et al. 2023). Based on this, Sumatra currently has four subgenera within the genus *Gekko*, i.e., *Lomatodactylus, Ptychozoon, Gekko,* and *Archipelagekko.*

Due to rarity of occurences with members of the genus *Gekko* in Sumatra, its distributional ranges may still not be fully understood. Furthermore, just one individual is used to describe the majority of the identified species mentioned in this study, e.g., *G. browni* (Russell 1979), *G. brooksii* (Boulenger 1920), and *G. iskandari* (Brown et al. 2000), where only the ND2 gene sequence for *G. iskandari* is currently available. This group's species rarity may be attributed to their specialisation in living in the forest's upper canopy. For instance, *Luperosaurus sorok* Das, Lakim and Kandaung 2008 was observed by Fukuyama et al. (2022) at a height of roughly 24.7 m to 60 m above the ground. Our specimen (UNP 111) was collected from West Sumatra, only about 1.5 metres above the ground. One plausible reason for this could be that that individual fell from a height following strong winds (Brown et al. 2000; Das et al. 2008). There is a critical need to inventory gecko diversity in unexplored canopy strata of tropical rainforests that occupy specific habitat niches, which may not be covered by traditional reptile surveys. Several authors have suggested some alternative methods, e.g., Bromeliad patch sampling (McCracken and Forstner 2008; Aguilar-Cruz et al. 2022), and utilisation of epiphytic fern (Kurita et al. 2019). To the best of our knowledge, such methods are rarely practiced in Indonesia, which may be reason why reptile biodiversity in the high canopy layer is potentially under-explored.

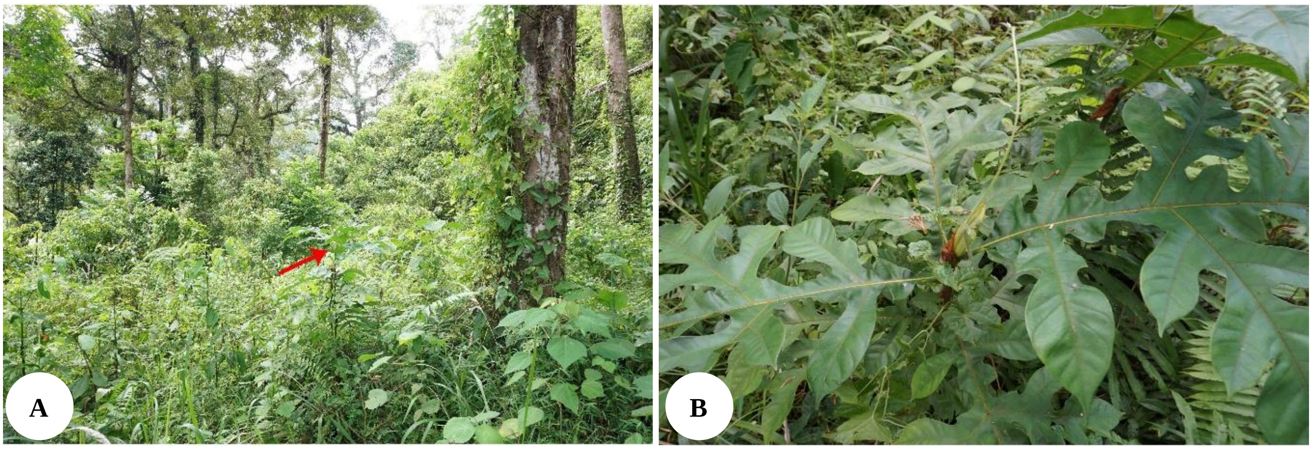

Figure 6. Habitat at the encountered site of *Gekko* cf. *brooksii* (UNP 111) from West Sumatra, Indonesia. A. General view of the habitat of the captured *G. browni* showing dense-vegetation secondary forest, red arrow indicates the resting site where the species captured, and B. young Breadfruit plant where the species was resting

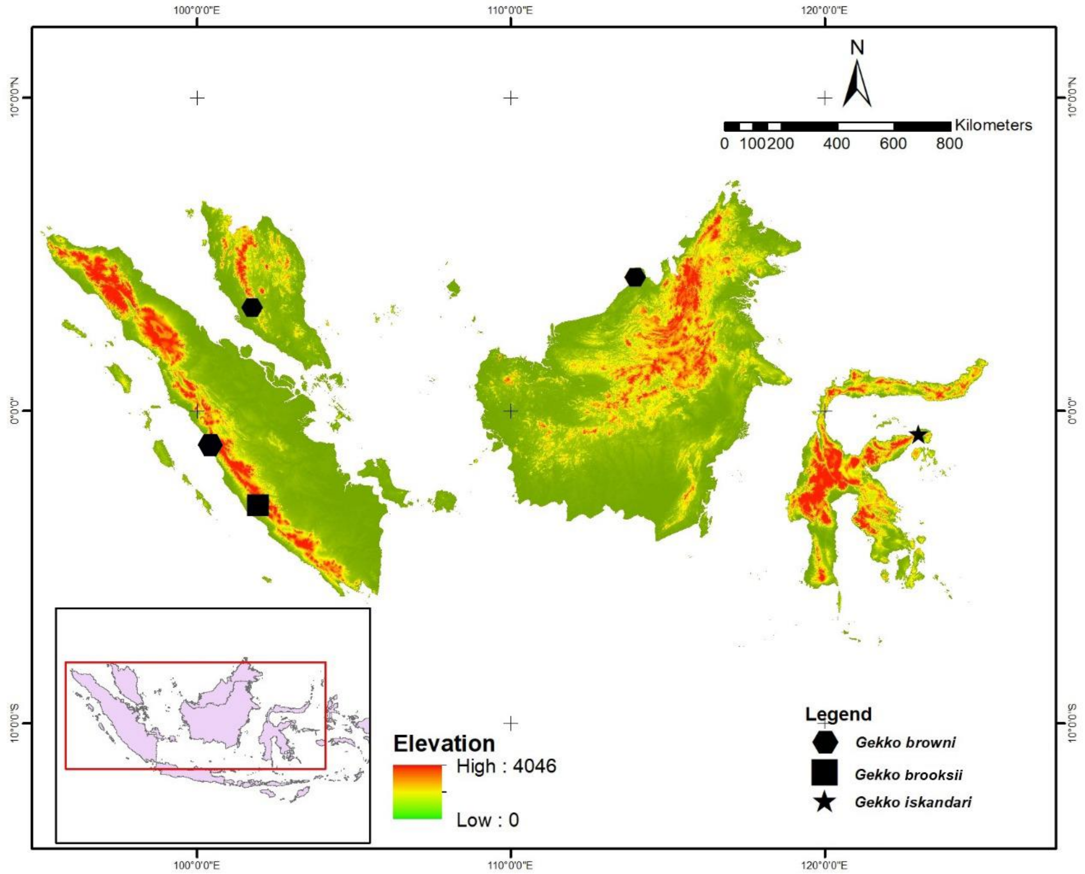

Figure 7. Geographic distribution of genus *Gekko* subgenera *Lomatodactylus* in Indonesia, including our collected specimen of *Gekko* cf. *brooksii* (UNP 111) from West Sumatra, Indonesia and two type specimens of *G. browni* from Malaysia Peninsula and Borneo

We report new information on morphological characteristics based on our newly collected specimen of *G.* cf. *brooksii* from West Sumatra (UNP 111). Most notable is the striking bright yellow coloration on the ventral parts of the limbs, trunk, pre- and post-cloacal regions. Unfortunately, there is no direct coloration description for *G. browni* collected from Selangor, Malaysia, as the initial description was based on a specimen that had been preserved for approximately nine years (Russel 1979). Another specimen of *G. browni* from Sarawak, Malaysia (Ota et al. 1996) had a similar colour on ventral surface of limbs, pre-anal and post-cloacal region, however, the trunk showed white coloration. Nonetheless, there is no detailed colour description of *G. brooksii* but the ventral of the body is white (Boulenger 1920). However, there is still a possibility that the white color is due to the preservation effect. The yellow venter of *G.* cf. *brooksii* from West Sumatra is similar to *G. iskandari*, except the presence of blue spots in the later species. In addition, the dorsal surface of fore-and hind-limbs cutaneous expansion was yellow in *G. iskandari* (Brown et al. 2000) but pale-grey to brown in *G.* cf. *brooksii* from West Sumatra. Another striking character is the coloration inside the mouth, which was not previously reported in both *G. browni*, *G. brooksii* and *G. iskandari*. This character was observed in *L. sorok* (Fukuyama et al. 2022), which suggests that this character is a defense behavior. Still, there are no reports on the functionality of the yellow body ventrum although this character is shared by other species in other gekkonid, e.g., *Hemiphyllodactylus flaviventris* Sukprasert, Sutthiwises, Lauhachinda & Taksintum, 2018 (Sukprasert et al. 2018).

It can be assumed that gekkonids inhabiting the high canopy strata of tropical rainforests in Sumatra remain largely unknown, limiting our understanding of their biology, biogeographical history, evolution, ecology, and determining appropriate conservation measures. Despite intensive exploration history in this island, survey efforts targeting unexplored areas in Sumatra will inevitably reveal more distribution records or new species that may not have been discovered yet. This has been demonstrated by recent studies (Harvey et al. 2015, 2017) which suggest that Sumatra may have a greater diversity of herpetofauna than than is currently documented. Therefore, intensive and comprehensive synergistic exploration is urgently needed to uncover the hidden diversity of Sumatra.

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