A NEW SPECIES OF RANID FROG (AMPHIBIA: ANURA: RANIDAE) OF THE *HYLARANA SIGNATA* COMPLEX FROM PENINSULAR MALAYSIA

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Abstract:We describe a new species of ranid frog from the *Hylarana signata* Complex in Peninsular Malaysia based on morphological and genetic differentiation. The new species can be distinguished from its congeners by the following combination of characters: (1) adult males reaching 37.4–37.6 mm SVL; (2) nuptial pads absent in males; (3) humeral glands in males large (4.2 mm); (4) webbing on toes reduced, one phalanx free of web on post-axial side of Toe II and pre-axial side of Toe V; (5) dorsolateral stripe straight, continuous, red or orange in color; (6) middorsal region black, unmarked; (7) flanks black, coloration unstratified; (8) flanks, dorsal surfaces of limbs, and upper lip with large, round, yellow spots; (9) venter grayish-brown, with light spots on throat and light reticulations on ventrum. The new species is phenotypically most similar to the distantly allopatric *H. siberu* (endemic to Siberut Island, south of Sumatra, Indonesia) but differs by having larger, more dense and more rounded spots on the flanks and dorsal side of limbs, larger spots along the entire upper lip as opposed to smaller spots restricted to the proximal half of the upper lip, and having light, distinct spots on the throat and light reticulations on the ventrum (vs. solid ventrum without distinct markings). We use mitochondrial data (12S–16S ribosomal RNA gene fragments) to estimate genealogical relationships and genetic divergences between the new species, *H. siberu*, a related, undescribed Sumatran population, and other members of the *H. signata* Complex. These data unequivocally support the specific recognition of the new taxon and provide insights into its evolutionary relationships.

*Key words:*  *Hylarana debussyi*; *H.* *siberu*; Morphology; Sumatra; Systematics; Taxonomy

The *hylarana* *signata* Complex comprises at least nine species that occur throughout Sundaland: *H. banjarana* from the Malay Peninsula; *H. siberu* from Siberut Island, Indonesia; *H. picturata* from the Malay Peninsula and Borneo; *H. signata* from the Malay Peninsula, Sumatra, and Borneo; and *H. mangyanum*, *H. moellendorffi*, *H. grandocula*, and *H. similis* from the Philippines (Brown and Guttman, 2002; Brown and Siler, 2013). Delimiting species in this complex has been historically problematic due to phenotypic similarities between species and highly variable intraspecific coloration (Boulenger, 1920; Inger, 1954, 1966; Zainudin and Sazali, 2012). This is most apparent in Peninsular Malaysia where the species names *H. signata* and *H. picturata* have been applied inconsistently and interchangeably over the years (Taylor, 1962; Berry, 1975; Brown and Guttman, 2002). Species from this complex are generally characterized as riparian forest frogs with a dark-brown to black dorsum covered with orange spots, and having a distinct, orange dorsolateral stripe (Inger, 1954, 1966). Paradoxically, although interspecific variation may be somewhat conserved (Brown and Guttman, 2002), polymorphism within populations/species is pronounced enough to render the identification of diagnostic morphological characters for species delimitation problematic (Zainudin and Sazali, 2012).

The most recent study of this complex described high elevation populations of the *H. signata* Complex from the Malay Peninsula as a distinct species (*H. banjarana*) based on adult and larval morphological differences (Leong and Lim, 2003). Subsequently, another distinct population was discovered from a lowland primary forest in central Peninsular Malaysia (Leong and Lim, 2004). Known from only one specimen at that time, it was designated as *H. siberu* (=*Rana siberu*), which was only known from Siberut Island, off the southern coast of Sumatra (Dring et al., 1989). The hypothesized conspecificity of these two populations was based on the following shared morphological characters: (1) entirely black dorsum without spots/blotches; (2) uninterrupted dorsolateral stripes from snout tip to vent, stripes red/deep orange in life; (3) lips, limbs and lower flanks with spots (vs. transverse bars), yellow in life; (4) males with enlarged humeral glands, paired subgular vocal sacs, without nuptial pads (Dring et al., 1989; Leong and Lim, 2004). An additional specimen was subsequently collected from the immediately adjacent area, approximately 9.2 km apart from the original site (Chan and Norhayati, 2009), which allowed a more thorough evaluation of the taxonomic and phylogenetic placement of that population. Recognizing the pitfalls of describing new species based on just two specimens, we evaluate these specimens within the framework of a lineage-based, Unified Species Concept (De Queiroz, 2005) and use morphological diagnosibility, phylogenetic relationships, genetic divergence, and geographic isolation as criteria for assessing lineage independence. Results from our analyses provide sufficient evidence to justify the recognition of this lineage as a new species.

Materials and Methods

*Sampling and morphology.—Hylarana baramica* and *H. glandulosa* were used as outgroups based on prior studies of the *H. signata* Complex (Brown and Guttman, 2002; Wiens et al., 2009; Brown and Siler, 2013). The ingroup includes four endemic Philippine species: *H. mangyanum, H. moellendorffi, H. grandocula,* and *H. similis*; sampling populations of *H. picturata* and *H. signata* from Sumatra and Borneo; *H. siberu* and an undescribed population from Sumatra, Indonesia; *H.* *banjarana* and the new species from Peninsular Malaysia (Table 1). For morphological comparisons, the new species was compared to all members of the *H*. *signata* Complex including the holotype and paratypes of *H. siberu* and *H. banjarana*, syntypes of *H. picturata*, and the holotype of *H. signata*. Only male specimens were used for comparisons to avoid possible measurement bias from sexual dimorphism. Voucher specimens of comparative material are listed in Appendix I of Brown and Guttman (2002). Data for *H. banjarana* were obtained from Leong and Lim (2003). Toe webbing formula follows Savage and Heyer (1997). The following 14 characters were examined to the nearest 0.1 mm: Snout-vent-length (SVL), tip of snout to vent; head length (HL), posterior margin of lower jaw to tip of snout; head width (HW), taken immediately posterior to eyes; snout length (SL), anterior corner of the orbit to tip of snout; internarial distance (IND), distance between nostrils; eye diameter (ED), distance between anterior and posterior corners of upper and lower eyelids; interorbital distance (IOD), distance across top of head between medial margins of orbits at their closest points; tympanum diameter (TD), horizontal width of tympanum at its widest point; brachium length (BL), axilla to flexed elbow; forearm length (FAL), flexed elbow to base of inner metacarpal tubercle; femur length (FL), vent to outer margin of flexed knee; tibia length (TBL), outer margin of flexed knee to outer margin of flexed tarsus; tarsal length (TL), outer margin of flexed tarsus to base of inner metatarsal tubercle; humeral gland length (HG), horizontal length of humeral gland. Measurements of the type and comparative material are summarized in Table 2.

The holotype has been deposited at the Raffles Museum of Biodiversity Research, Singapore; the paratype at University Kebangsaan Malaysia Herpetological Collection. Voucher abbreviations are as follow: BJE, Ben J Evans field number; DWNP, Department of Wildlife and National Parks, Malaysia; FMNH, Field Museum of Natural History; KU, University of Kansas; LSUHC, La Sierra University Herpetological Collection; MK, Mistar Kamsi field number; PNM, Philippines National Museum; THNC, Texas Natural History Collections, University of Texas, Austin; ZRC, Zoological Reference Collection, Raffles Museum of Biodiversity Research, Singapore.

*Molecular data.—*Genomic DNA was extracted from liver using a modified Guanidine Thiocyanate extraction protocol developed by M. Fujita (Esselstyn et al., 2008). A 2434 nucleotide base-pair fragment of mitochondrial DNA that encodes part of the 12S–16S rRNA and part of one flanking tRNA gene (tRNAval) was amplified in four fragments using the polymerase chain reaction (PCR) and thermal profiles and primers in Evans et al. (2003). We cleaned PCR products with ExoSAP-IT (USB) and sequenced cycle sequencing products in both directions on a 3130*xl* DNA Analyzer (Applied Biosystems) using the same primers and Big Dye v3 chemistry (Perkin Elmer). We assembled consensus sequences in Sequencher v. 4.1 (Genecodes), manually edited resulting contigs in McClade 4.07 (Maddison and Maddison, 2005) and excluded hypervariable regions for which unequivocal homology assessments could not be confidently ascertained.

*Phylogenetic analyses.—*An unpartitioned maximum likelihood (ML) analysis was conducted in RAxML version 7.2.8 (Stamatakis, 2006) using the GTR + Γ + I model of nucleotide substitution as selected under the Akaike Information Criterion (AIC; implemented in jModeltest v0.1.1; Posada and Crandall, 2008) with 100 replicate best-tree inferences, employing a random starting tree for each inference. We assessed clade support with 1000 bootstrap replicates. GAMMA + P-Invar model parameters were estimated up to an accuracy of 0.001 Log Likelihood units. A Bayesian analysis was performed in MrBayes v3.2.1 (Ronquist and Huelsenbeck, 2003) under the same nucleotide substitution model. We employed two separate MCMC analyses, each with four Metropolis-coupled chains (temperature setting = 0.02; exponential distribution with a rate parameter of 25 as a branch length prior). We ran analyses for 10 million generations, with parameters and topology sampling every 2000 generations, discarding the first 25% as burn-in. The program Tracer v1.4 (Rambaut and Drummond, 2007) was used to evaluate stationarity and convergence. Uncorrected pairwise *p*-distances were calculated in MEGA v5.2.1 (Table 3).

Results

*Phylogenetic Analyses*

Sequences included 554 (out of 1,015) variable characters for 12S + tRNAval and 753 (out of 1,435) for 16S. All tree topologies recovered high bootstrap support (ML) and posterior probabilities, which were congruent across all nodes. The resulting phylogeny clearly shows the new species nested within the *Hylarana signata* Complex with *H. banjarana* reconstructed as the first-diverging species in this clade. The next diverging lineages consisted of the Siberut Island endemic *H. siberu*,the new species from Peninsular Malaysia, and a related and undescribed high-elevation Sumatran species. The remaining *H. signata* Complex taxa fall into a clade from islands of Sundaland and the Philippines, with *H. picturata*, and *H. signata* estimated to be distantly related to the Peninsular Malaysian population (Fig. 1). Within its clade, the Peninsular Malaysian population is substantially genetically divergent from its closest relatives *H. siberu* (8% uncorrected *p*-distance) and *H.* sp. Sumatra (10%), which is consistent with interspecific divergences between other members of the *H. signata* Complex (Table 3). The phylogenetic placement of the entire *H. signata* Complex with regard to other closely related species of *Hylarana* is presented in Brown and Siler (2013).

*Systematics*

Results from the phylogenetic analyses indicate that specimens from central Peninsular Malaysia are: (1) members of the *H. signata* Complex; (2) closely related but not conspecific with *H. siberu*; and (3) distantly related to other co-occuring *H. signata* Complex taxa in Peninsular Malaysia (*H. banjarana* and *H. picturata*). Although we do not use molecular divergence to diagnose the new taxon, we note that these levels of divergences are equivalent or greater than most species level divergences in closely related *H. signata* Complex members (Brown and Siler, 2013). The exceptions are members of the *H. picturata* Complex which, although currently masquerading under a single species name, are suspected by numerous workers to represent a complex of distinct evolutionary lineages which now require taxonomic partitioning (Brown and Guttman, 2002; Brown and Siler, 2013; personal communication with L. L. Grismer and R. F. Inger). Here, we provide morphological evidence to show that this genetically divergent lineage can be phenotypically distinguished from all other species in its group. Having distinct, diagnosable, fixed character differences, bolstered by the only known occurrence of the new species as a distantly allopatric, biogeographically circumscribed lineage, strongly support the recognition of the Peninsular Malaysian specimens as a new species, which we describe as

Hylarana**centropeninsularis** *sp. nov.*

*(Figs. 2, 3A)*

*Rana siberu* Leong and Lim, 2004:261

*Hylarana siberu* Chan and Norhayati, 2009:295; Chan et al*.*, 2010:203

*Holotype*.—Adult male (ZRC1.10536; Fig. 2), collected by C.H. Lim on 17 March 2003 (ca. 2200 h) at Sungai Temir, within the Lakum forest reserve, Raub, Pahang, Malaysia (3°40’N, 101°55’E; 105 m above sea level; datum = WGS84).

*Paratype*.— Adult male (DWNP 1189; Fig. 3A), collected by Juliana Senawi on 27 April 2006 in pit-fall trap at Kuala Gandah, Pahang, Malaysia (3°35'N, 102°8'E; 90 m above sea level; datum = WGS84).

*Diagnosis*.—The new species can be differentiated from its congeners by the following combination of characters: adult males 37.4–37.6 mm SVL; nuptial pads absent in males; humeral glands in males large (4.2 mm); webbing on toes reduced, one phalanx free of web on post-axial side of Toe II and pre-axial side of Toe V; dorsolateral stripe straight, continuous, red to orange in color; middorsal region black, unmarked; flanks black, coloration unstratified; distinct spots on flanks, dorsal surfaces of limbs, and upper lip large, round, yellow; venter grayish-brown, with light spots on throat, and light reticulations on ventrum.

*Comparison with other species*.—*Hylarana centropeninsularis* can be readily distinguished from *H. banjarana, H. grandocula, H. mangyanum*, *H. moellendorffi, H. signata* and *H. picturata* by having a black, unmarked middorsal region (vs. blotched/spotted). It can be further differentiated from *H. grandocula, H. mangyanum, H. moellendorffi, H. signata* and *H. similis* by the absence (vs. presence) of nuptial pads in males, one phalanx free of web on post-axial side of Toe II and pre-axial side of Toe V (vs. webbed to discs on both toes), and larger humeral glands (mean = 4.2 vs. < 3.5); from *H. banjarana*, *H. moellendorffi* and *H. picturata* by having a continuous (vs. broken) dorsolateral stripe; from *H. banjarana* by the presence (vs. absence) of humeral glands in males; and from *H. grandocula* by having smaller SVL in males (mean = 37.5 vs. 43.6). *Hylarana centropeninsularis* differs from the phenotypically similar *H. siberu* by having larger, more dense and more rounded spots on the flanks and dorsal side of limbs; larger spots along the entire upper lip as opposed to smaller spots restricted to the proximal half of the upper lip; and having light, distinct spots on the throat and reticulations on the belly (vs. solid ventral coloration without distinct marking). Diagnostic characters are summarized across all members of the *H. signata* Complex in Table 4.

*Description of holotype.***—**SVL 37.4, HL 14.0, HW 12.0, SL 5.9, IND 3.7, ED 6.0, IOD 3.2, TD 4.8, BL 7.3, FAL 8.1, FL 8.1, TBL 19.9, TL 12.9, HG 4.2; adult male, testes enlarged, oval, finely granular, with orange granules on yellowish surface, anterior to kidneys. Head longer than wide (HL/HW = 1.2), snout rounded, sloping anteroventrally, projecting beyond lower jaw, snout length equal to eye diameter; canthus rostralis distinct, loreal region concave, vertical; nostrils oval, located laterally, closer to canthus than supralabial region, closer to rostrum than eye (NSD/END = 0.7); internarial distance half of distance between front of eyes (IND/EED = 0.6); eyes relatively large (ED/SL = 1.0; ED/HL = 0.4), eye diameter larger than interorbital distance (ED/IOD = 1.9); tympanum and tympanic annulus distinct, oval, diameter smaller than eye (TD/ED = 0.8), larger than distance to eye (TD/TED = 3.4); supratympanic fold prominent, extending obliquely from posterior margin of tympanum to dorsal portion of front limb insertion area; choanae tear-drop shaped, diameter 0.8 mm, tapering medially, separated by distance larger than their diameter; vomerine teeth small and indistinct, numbering four, arranged in short oblique row atop the dentigerous process of vomer; vocal sacs paired, internal subgular; tongue elongate, widening posteriorly with a deep central terminal notch, free for one third its length.

Arms relatively long and slender (BL/SVL = 0.2), brachial and forearm length subequal (BL/FAL = 0.9); enlarged humeral glands present on lateroventral surface of brachium; order of fingers from shortest to longest: II–IV–I–III (fingers I and IV subequal); fingers without web; finger tips dilated into small, pointed discs bearing circummarginal grooves; dorsal surface of articulation of ultimate and penultimate phalanges with transverse, rounded, inverted cup-like supra-articular cutaneous flap; subarticular tubercles prominently raised, oval, opaque; number of subarticular tubercles on each finger is given in parentheses following finger number denoted by Roman Numerals: I(1), II(1), III(2), IV(2); supernumerary tubercles indistinct, translucent, at the base of first phalanx on each finger; inner metacarpal tubercle large, oval, translucent; palmar tubercle oval, translucent, slightly smaller and not in contact with inner metacarpal tubercle; outer metacarpal tubercle elongate, translucent, in contact, same length, but half the width of palmar tubercle; nuptial pads absent (Fig. 2A).

Hindlimbs long, slender (FL/SVL = 0.5; TBL/SVL = 0.5; TL/SVL = 0.3), tibia slightly longer than femur (TBL/FL = 1.1); order or toes from shortest to longest: I–II–III–V-IV (toes III and V subequal); toe tips slightly dilated into small, pointed discs bearing circummarginal grooves; dorsal surface of articulation of ultimate and penultimate phalanges with transverse, rounded, inverted cup-like supra-articular cutaneous flap; web formula: I ½ − 2 II 1 −2½ III 1– 3- IV 3- − 1 V; subarticular tubercles prominently raised, translucent; number of subarticular tubercles on each toe is given in parentheses following toe number denoted by Roman Numerals: I(1), II(1), III(2), IV(3), V(2); inner metatarsal tubercle elongate, raised, translucent; outer metatarsal tubercle round, raised, translucent, smaller than inner (Fig. 2B).

*Color in life.***—**Dorsum completely black without markings; complete, orange dorsolateral stripe from rostrum, along the canthus, lateral margin of palpebrae, dorsolateral part of dorsum, and terminating at the sacrum where it forms a near complete loop; a single row of white spots along the upper and lower labials; flanks and dorsal side of limbs with round, creamy yellow spots; some spots connect to form short, elongated bars; venter grayish-brown; throat with whitish spots; belly with whitish reticulations.

*Color in preservative.***—**Dorsum dark brown; flanks and dorsal side of limbs a lighter shade of brown; dorsolateral stripe and spots/bars white; venter brown with light spots on throat and faint reticulations on belly (Fig. 2C–D).

*Variation.***—**The paratype closely matches the holotype in overall external morphology but has less spotting on the throat and more distinct reticulations on the ventrum. Measurements of the paratype (mm): SVL 37.6, HL 15.2, HW 12.5, SL 6.4, IND 3.6, ED 5.1, IOD 3.5, TD 2.2, BL 8.0, FAL 8.2, FL 17.7, TBL 19.2, TL 10.6, HG 4.2.

*Distribution.***—**The new species is currently known from two adjacent localities in central Peninsular Malaysia: Sungai Temir (=Temir River), Lakum Forest Reserve, Raub Pahang and Kuala Gandah, Lanchang, Pahang (Fig. 1).

*Natural History.***—**The holotype was caught in a pit-fall trap at least 100 m from the nearest stream in a lowland secondary forest (Chan and Norhayati, 2009), whereas the paratype was collected at night in an adjacent lowland primary forest from the edge of a temporary forest pool (ca. 1.5 x 1.0 m). This pool was among a swampy, waterlogged area away from streams. The new species was syntopic with the following anurans: *Hylarana labialis, H. erythraea, Polypedates macrotis, Rhacophorus appendiculatus, Philautus* sp. (Leong and Lim, 2004). These observations suggest that *H. centropeninsularis* is a swamp habitat specialist, which stands in contrast to other Peninsular Malaysian taxa *H. banjarana* and *H. picturata*, which are restricted to forest streams.

*Etymology.***—**The specific epithet is derived from the latin prefix “centro” (root=centrum) and the root “peninsularis,” in reference to the type and only known localities of the new species in central Peninsular Malaysia.

Discussion

We hypothesize that *H. centropeninsularis*, which is the sister species of *H. siberu* and *H.* sp. Sumatra, may now exhibit a relictual distribution. This assertion is based on phylogenetic affinity, morphological similarity and geographic proximity (Fig. 1; Table 2). One plausible scenario would be the existence of a widespread ancestral species that occurred in Sumatra and Peninsular Malaysia in the past. This is substantiated by the fact that the Strait of Malacca that separates Peninsular Malaysia and Sumatra is narrowest (ca. 65 km) and shallowest (ca. 40 m) at the central portion of Peninsular Malaysia and was land positive at or below 40 m below present-day levels for approximately 55% of the time in the last 17,000 years (Geyh et al*.*, 1979; Voris, 2000). The inundation of the Strait of Malacca could have served as the vicariant event that isolated the ancestral population(s), which subsequently diverged in isolation.

The new species has more in common with *H. siberu* in that both species occupy a generally similar ecological niche (lowland swamps) as opposed to *H.* sp. Sumatra, a montane species, which in that regard, is more similar to *H. banjarana* from Peninsular Malaysia (Leong and Lim, 2003). Given the small, patchy, microhabitat-specific, and apparently relictual nature of *H. centropeninsularis*, we would recommend prioritizing survey and conservation efforts in any identifiable lowland swamp habitats in the immediate near future. Not only are swamps and peat bog habitats insular in nature (surrounded by a generalized terrestrial habitat matrix), but these habitats are heavily imperiled and rapidly disappearing throughout Southeast Asia (Ng et al., 1994; Myers et al., 2000). The possibility that additional new species could await discovery in these unique habitats around the world should not be ignored (Biton et al., 2013).

*Hylarana* sp. Sumatra was collected from the type locality of poorly known *H. debussyi* (van Kampen) at 1000 m elevation in the Batak Mountains, Bandar Baru, Sumatra (M. Kamsi and D. Iskandar, *personal communication*; Fig. 1), initially leading us to consider the possibility of the application of this name to the distinct *H. signata* Complex species from high elevations of northern Sumatra. However, further inspection into the descriptions of *H. debussyi* (=*Rana debussyi*) in Boulenger (1920), van Kampen (1923) and the plate from the original description of the species (van Kampen, 1910, p. 23, pl. I, fig. 3) revealed that *H. debussyi* did not share the characters that would warrant its inclusion in the *H. signata* Complex (*sensu* Brown and Guttman, 2002). The following characters were provided by van Kampen (1923): brown above; sides, from tip of snout to vent, black, with a white streak from the tip of the snout along the upper lip, below the tympanum to the thighs; limbs pale brown, with dark cross-bars; yellowish white beneath. Moreover, Boulenger (1920) described it as allied to *H. luctuosa*, but having much in common with *H. nicobariensis*. These discrepancies, along with results from our molecular analyses, indicate that *H*. sp. Sumatra represents a distinct and undescribed lineage. The status of this and other, possibly undocumented, montane populations on Sunda Shelf islands should be prioritized as targets of future research. The taxonomic status of the multiple divergent lineages within the *H. picturata* Complex (Brown and Guttman, 2002) should likewise be the subject of scrutiny by taxonomists in the immediate future (Brown and Siler, 2013).

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Table 1*.***—**Samples used in this study and accompanying GenBank accession numbers. See Materials and Methods for museum abbreviations.

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| --- | --- | --- | --- |
| Species | Voucher | Locality | Genbank # |
| *Hylarana glandulosa* | FMNH 248254 | Brunei, Belait District | KF477638 |
| *Hylarana baramica* | FMNH 248218 | Brunei, Belait District | KF477628 |
| *Hylarana banjarana* | LSUHC 5128 | Malaysia, Pahang, Cameron Highlands | KF477644 |
| *Hylarana banjarana* | ZRC 8326 | Malaysia, Pahang, Cameron Highlands | KF477645 |
| *Hylarana* spSumatra | MK 334 | Northern Sumatra Island, Langkat, Bandar Baru, Batak Mountains | KF477646 |
| *Hylarana* spSumatra | MK 335 | Northern Sumatra Island, Langkat, Bandar Baru, Batak Mountains | KF477648 |
| *Hylarana centropeninsularis* | DWNP 1189 | Malaysia, Pahang, Kuala Gandah | KF477745 |
| *Hylarana siberu* | BJE 203 | Siberut Island, West Sumatra Province | KF477741 |
| *Hylarana siberu* | BJE 236 | Siberut Island, West Sumatra Province | KF477743 |
| *Hylarana picturata* | FMNH 235707 | Malaysia, Sabah, Kota Marudu | KF477729 |
| *Hylarana picturata* | ZRC 1.10886 | Borneo Island, Sabah, Mt. Kinabalu (Neotype Locality) | KF477731 |
| *Hylarana picturata* | FMNH 266930 | Sumatra Island, West Sumatra Province, Limau Manis | KF477717 |
| *Hylarana picturata* | FMNH 266944 | Sumatra Island, West Sumatra Province,Payakumbuh | KF477701 |
| *Hylarana signata* | FMNH 238842 | Mendolong, Sipitang Dustrict, Sabah, Malaysia | KF477746 |
| *Hylarana signata* | ZRC 1.12388 | Borneo Island, Sarawak, Matang | KF477748 |
| *Hylarana mangyanum* | KU 303566 | Philippines, Mindoro Island, Municipality of Paypayama, Barangay Carmundo, | KF477687 |
| *Hylarana mangyanum* | KU 303578 | Philippines, Mindoro Island, Municipality of Bongabong, Barangay Formon, | KF477686 |
| *Hylarana moellendorffi* | KU 309009 | Philippines, Palawan Island, Palawan Province, Municipality of Puerto Princesa City, Barangay Irawan | KF477696 |
| *Hylarana moellendorffi* | KU 327050 | Philippines, Palawan Island, Palwan Province, Municipality of Nara, Barangay Estrella Falls | KF477695 |
| *Hylarana grandocula* | KU 306492 | Philippines, Samar Island, Samar Proviunce Province, Municipality of San Jose de Baun, Barangay Poblacion | KF477660 |
| *Hylarana grandocula* | PNM 8848 | Philippines, Mindanao Island, Davao City Province, Municipality of Calinan, Barangay Malagos | KF477676 |
| *Hylarana similis* | TNHC 63007 | Philippines, Luzon Island, Camarines Norte Province, Municipality of Naga City, Barangay Panicuason, | KF477764 |
| *Hylarana similis* | PNM 5536 | Philippines, Luzon Island, Laguna Province, Municipality of Los Baños, University, of the Philippines campus, Mt. Makiling | KF477776 |

Table 2*.***—**Summary statistics of specimens examined. Ranges follow mean ± SD; NA = data not available. Voucher specimens are listed in Appendix I of Brown and Guttman (2002).

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | *centropeninsularis* sp. nov. | *banjarana* | *grandocula* | *mangyanum* |
|  | N=2 | N=5 | N=148 | N=62 |
| SVL | 37.5 ± 0.1  37.4 – 37.6 | 35.7 ± 1.0  34.6 – 37.3 | 43.6 ± 3.5 33.7 – 52.8 | 40.1 ± 3.2  34.0 – 46.4 |
| HL | 14.6 ± 0.8  14.0 – 15.2 | 13.4 ± 0.9  12.2 – 14.5 | 16.8 ± 1.4  13.8 – 20.2 | 15.9 ± 1.2  13.9 – 18.4 |
| HW | 12.3 ± 0.4  12.0 – 12.5 | 12.4 ± 0.4 11.9 – 12.8 | 13.8 ± 1.2  11.0 – 16.3 | 13.3 ± 1.1  10.7 – 16.1 |
| SL | 6.2 ± 0.4  5.9 – 6.4 | 5.1 ± 0.1 5.0 – 5.3 | 7.1 ± 0.7  5.5 – 8.8 | 6.7 ± 0.7  5.2 – 8.1 |
| IOD | 3.4 ± 0.2  3.2 – 3.5 | 3.4 ± 0.2  3.2 – 3.7 | 4.8 ± 0.5 3.7 – 6.0 | 4.2 ± 0.3  3.5 – 5.1 |
| IND | 3.7 ± 0.1  3.6 – 3.7 | 3.9 ± 0.2  3.7 – 4.1 | 4.5 ± 0.5  1.2 – 5.8 | 4.2 ± 0.3  3.4 – 5.0 |
| ED | 5.6 ± 0.6  5.1 – 6.0 | 5.2 ± 0.2  5.0 – 5.4 | 6.1 ± 0.6  4.5 – 7.5 | 5.7 ± 0.5  4.7 – 7.0 |
| TD | 3.5 ± 1.8  2.2 – 4.8 | 3.1 ± 0.2  2.9 – 3.5 | 3.8 ± 0.5  2.6 – 5.0 | 3.6 ± 0.4  3.0 – 4.5 |
| BL | 7.7± 0.5  7.3 – 8.0 | NA | 8.2 ± 0.9  6.1 – 11.0 | 7.6 ± 0.8  6.1 – 9.2 |
| FAL | 8.2 ± 0.1  8.1 – 8.2 | NA | 9.9 ± 1.0  7.9 – 12.3 | 9.0 ± 1.0  7.1 – 11.0 |
| FL | 17.7 ± 0.1  17.6 – 17.7 | NA | 21.2 ± 2.3  16.4 – 27.5 | 19.2 ± 1.7  15.1 – 23.5 |
| TBL | 19.6 ± 0.5  19.2 – 19.9 | 21.8 ± 0.8  20.9 – 22.9 | 23.3 ± 2.2  15.3 – 28.0 | 20.7 ± 1.3  17.6 – 23.6 |
| TL | 11.8 ± 1.6 10.6 – 12.9 | NA | 13.1 ± 1.1  10.9 – 15.6 | 11.8 ± 0.9  9.0 – 13.7 |
| HG | 4.2 ± 0.0 4.2 – 4.2 | NA | 1.9 ± 0.5  1.0 – 3.6 | 3.4 ± 0.3  2.5 – 4.3 |

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| --- | --- | --- | --- | --- |
| *moellendorffi* | *picturata* | *siberu* | *signata* | *similis* |
| N=102 | N=122 | N=3 | N=112 | N=125 |
| 38.5 ± 2.5  32.8 – 45.0 | 39.7 ± 3.6  32.8 – 47.8 | 37.0 ± 2.2  35.4 – 39.5 | 36.4 ± 1.4  33.7 – 41.1 | 38.8 ± 2.2  32.0 – 43.3 |
| 15.2 ± 0.9  12.8 – 17.0 | 15.3 ± 1.2  12.6 – 18.4 | 15.7 ± 0.1  15.6 – 15.9 | 14.3 ± 0.7 12.9 – 17.1 | 15.0 ± 1.0  11.3 – 18.3 |
| 12.9 ± 0.8  10.7 – 14.4 | 13.1 ± 1.1  11.3 – 15.6 | 13.0 ± 0.3 12.6 – 13.2 | 12.0 ± 0.6 10.6 – 13.4 | 12.5 ± 0.8  10.0 – 14.3 |
| 6.4 ± 0.5  5.2 – 7.6 | 6.4 ± 0.6  5.1 – 7.8 | 7.0 ± 0.5 6.5 – 7.4 | 5.9 ± 0.4 5.0 – 7.0 | 6.3 ± 0.5  4.7 – 7.6 |
| 4.4 ± 0.4  3.4 – 5.3 | 3.9 ± 0.4  3.2 – 5.1 | 4.2 ± 0.3  3.8 – 4.5 | 3.9 ± 0.4  3.1 – 4.9 | 4.1 ± 0.4  3.1 – 5.1 |
| 4.3 ± 0.3  3.4 – 5.0 | 3.7 ± 0.4  2.9 – 4.9 | 4.1 ± 0.2  4.0 – 4.3 | 3.7 ± 0.3  2.8 – 4.6 | 4.0 ± 0.4  3.1 – 5.7 |
| 5.7 ± 0.4  4.6 – 6.8 | 6.0 ± 0.6  4.4 – 7.7 | 5.3 ± 0.3  5.1 – 5.3 | 5.5 ± 0.4  4.6 – 6.9 | 5.6 ± 0.5  3.2 – 6.8 |
| 3.5 ± 0.3  2.8 – 4.5 | 3.5 ± 0.3  2.1 – 4.3 | 3.6 ± 0.3  3.3 – 3.9 | 2.9 ± 0.3  2.2 – 3.9 | 3.2 ± 0.4  2.4 – 4.3 |
| 7.4 ± 0.7  4.7 – 9.5 | 8.0 ± 0.7  6.3 – 10.1 | 8.0 ± 0.6  7.3 – 8.4 | 7.6 ± 0.6  6.0 – 9.0 | 7.4 ± 0.6  5.9 – 9.6 |
| 8.9 ± 0.8  7.4 – 10.8 | 9.4 ± 1.1  7.2 – 12.2 | 9.7 ± 0.5  9.2 – 10.1 | 8.9 ± 0.7  7.2 – 10.8 | 9.0 ± 0.7  7.1 – 10.6 |
| 19.6 ± 1.3  16.3 – 22.3 | 20.3 ± 1.7  17.0 – 24.3 | 18.7 ± 1.6  17.0 – 20.2 | 19.1 ± 1.1  16.2 – 22.1 | 19.0 ± 1.3  14.4 – 22.0 |
| 20.3 ± 1.4  17.1 – 23.9 | 21.8 ± 1.9  18.7 – 26.7 | 20.9 ± 0.8  20.0 – 21.6 | 20.7 ± 1.0  18.8 – 24.5 | 20.1 ± 1.1  17.6 – 22.4 |
| 11.6 ± 0.7  9.1 – 13.0 | 12.4 ± 1.0  11.0 – 14.9 | 12.1 ± 0.4  11.7 – 12.5 | 11.8 ± 0.6  10.5 – 13.4 | 11.5 ± 0.7  9.1 – 13.3 |
| 2.9 ± 0.6  1.4 – 4.3 | 3.3 ± 0.5  1.6 – 4.9 | 4.5 ± 0.3  4.3 – 4.8 | 1.5 ± 0.3  0.8 – 2.6 | 1.8 ± 0.4  0.6 – 3.0 |

Table 3*.***—**Uncorrected *p*-distances of sequences used in the phylogenetic analyses calculated using MEGA 5 (Tamura et al., 2011).

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|  |  | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 |
| 1 | *baramica* |  |  |  |  |  |  |  |  |
| 2 | *baramica* | 0.004 |  |  |  |  |  |  |  |
| 3 | *glandulosa* | 0.069 | 0.07 |  |  |  |  |  |  |
| 4 | *banjarana* | 0.158 | 0.155 | 0.155 |  |  |  |  |  |
| 5 | *banjarana* | 0.159 | 0.156 | 0.154 | 0.015 |  |  |  |  |
| 6 | *siberu* | 0.138 | 0.136 | 0.147 | 0.154 | 0.154 |  |  |  |
| 7 | *siberu* | 0.136 | 0.135 | 0.148 | 0.152 | 0.155 | 0.001 |  |  |
| 8 | *centropeninsularis* | 0.139 | 0.14 | 0.156 | 0.152 | 0.155 | 0.087 | 0.087 |  |
| 9 | sp. Sumatra | 0.152 | 0.151 | 0.158 | 0.154 | 0.158 | 0.105 | 0.105 | 0.106 |
| 10 | sp. Sumatra | 0.151 | 0.15 | 0.156 | 0.155 | 0.156 | 0.103 | 0.103 | 0.105 |
| 11 | *picturata* | 0.144 | 0.146 | 0.16 | 0.163 | 0.162 | 0.131 | 0.131 | 0.128 |
| 12 | *picturata* | 0.144 | 0.146 | 0.16 | 0.163 | 0.162 | 0.131 | 0.131 | 0.128 |
| 13 | *picturata* | 0.136 | 0.138 | 0.147 | 0.156 | 0.155 | 0.131 | 0.132 | 0.123 |
| 14 | *picturata* | 0.139 | 0.14 | 0.142 | 0.16 | 0.159 | 0.138 | 0.139 | 0.127 |
| 15 | *moellendorffi* | 0.146 | 0.143 | 0.167 | 0.174 | 0.177 | 0.147 | 0.147 | 0.151 |
| 16 | *moellendorffi* | 0.146 | 0.143 | 0.167 | 0.174 | 0.177 | 0.147 | 0.147 | 0.151 |
| 17 | *mangyanum* | 0.142 | 0.139 | 0.158 | 0.159 | 0.159 | 0.136 | 0.136 | 0.132 |
| 18 | *mangyanum* | 0.142 | 0.139 | 0.158 | 0.16 | 0.16 | 0.136 | 0.136 | 0.134 |
| 19 | *signata* | 0.144 | 0.146 | 0.15 | 0.171 | 0.175 | 0.136 | 0.136 | 0.123 |
| 20 | *signata* | 0.144 | 0.146 | 0.152 | 0.17 | 0.174 | 0.144 | 0.144 | 0.131 |
| 21 | *similis* | 0.16 | 0.162 | 0.168 | 0.181 | 0.184 | 0.139 | 0.139 | 0.147 |
| 22 | *similis* | 0.159 | 0.16 | 0.168 | 0.179 | 0.181 | 0.132 | 0.132 | 0.143 |
| 23 | *grandocula* | 0.162 | 0.163 | 0.171 | 0.181 | 0.184 | 0.131 | 0.131 | 0.146 |
| 24 | *grandocula* | 0.154 | 0.155 | 0.164 | 0.175 | 0.177 | 0.127 | 0.127 | 0.136 |

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| 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 |
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| 0.003 |  |  |  |  |  |  |  |
| 0.127 | 0.126 |  |  |  |  |  |  |
| 0.127 | 0.126 | 0 |  |  |  |  |  |
| 0.14 | 0.14 | 0.083 | 0.083 |  |  |  |  |
| 0.144 | 0.144 | 0.085 | 0.085 | 0.021 |  |  |  |
| 0.144 | 0.143 | 0.114 | 0.114 | 0.106 | 0.109 |  |  |
| 0.144 | 0.143 | 0.114 | 0.114 | 0.106 | 0.109 | 0 |  |
| 0.134 | 0.132 | 0.103 | 0.103 | 0.097 | 0.098 | 0.061 | 0.061 |
| 0.134 | 0.132 | 0.103 | 0.103 | 0.097 | 0.098 | 0.061 | 0.061 |
| 0.143 | 0.142 | 0.103 | 0.103 | 0.097 | 0.095 | 0.103 | 0.103 |
| 0.14 | 0.139 | 0.107 | 0.107 | 0.097 | 0.098 | 0.105 | 0.105 |
| 0.135 | 0.134 | 0.105 | 0.105 | 0.102 | 0.097 | 0.093 | 0.093 |
| 0.134 | 0.132 | 0.105 | 0.105 | 0.103 | 0.099 | 0.093 | 0.093 |
| 0.138 | 0.136 | 0.103 | 0.103 | 0.106 | 0.105 | 0.102 | 0.102 |
| 0.134 | 0.132 | 0.107 | 0.107 | 0.101 | 0.097 | 0.094 | 0.094 |

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| --- | --- | --- | --- | --- | --- | --- |
| 17 | 18 | 19 | 20 | 21 | 22 | 23 |
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| 0.001 |  |  |  |  |  |  |
| 0.09 | 0.091 |  |  |  |  |  |
| 0.093 | 0.091 | 0.021 |  |  |  |  |
| 0.098 | 0.098 | 0.091 | 0.091 |  |  |  |
| 0.091 | 0.091 | 0.09 | 0.093 | 0.011 |  |  |
| 0.098 | 0.098 | 0.101 | 0.103 | 0.023 | 0.019 |  |
| 0.09 | 0.09 | 0.089 | 0.091 | 0.024 | 0.019 | 0.026 |

Table 4*.***—**Diagnostic morphological characters of members in the *H. signata* Complex. NA = Data not available.

|  |  |  |
| --- | --- | --- |
|  | *banjarana* | *grandocula* |
| Mean SVL (mm) | 35.7 | 43.6 |
| Mean humeral gland length (mm) | absent | 1.9 |
| Nuptial pad | present | present |
| Middorsal texture | coarsely granular | smooth to  finely granular |
| Middorsal color-pattern | brown with  black reticulations | gray to brown; 63.5% dark flecks  and blotches,  36.5% unmarked |
| Dorsolateral stripe shape | straight; broken | straight; 95.2% complete, 4.8% broken |
| Dorsolateral stripe color | brown | white to yellow |
| Dorsal side of limbs | 100% dark bars | 84.7% dark bars,  15.3% absent |
| Throat color | gray to brown  with light spots | gray to black |
| Venter color | gray to brown  with light spots | light gray |
| Webbing on post-axial side of Toe II; pre-axial side of Toe V | slightly less than  two phalanges free  on Toe II and V | webbed to disc on  Toe II and Toe V |

|  |  |  |  |
| --- | --- | --- | --- |
| *mangyanum* | *moellendorffi* | *picturata* | *siberu* |
| 40.1 | 38.5 | 39.7 | 37 |
| 3.4 | 2.9 | 3.3 | 4.5 |
| present | present | present | absent |
| smooth to  moderately granular | moderately to  coarsely granular | moderately to  coarsely granular | smooth to  finely granular |
| dark brown to black; 61.1% with yellow, medial  projections,  21.9% blotched,  17% unmarked | dark brown to black; 97.1% distinct  round, yellow spots,  2.9% reticulate | black; 100% distinct  round, orange spots and bars | black, unmarked |
| wavy; 98.1% complete,  1.9% broken | irregular; 5.4% broken,  57.1% spot rows,  37.5% no pattern | irregular; 11.4% broken,  77.7% spot rows,  10.9% no pattern | straight, continuous |
| white to yellow | yellow to orange | yellow to orange | orange |
| 93.4% dark bars,  6.6% absent | 76.0% dark bars,  24.0% absent | 100% dark bars | yellow to  orange spots |
| gray to brown | 40.1% gray,  30.2% pale yellow,  9.0% brown,  20.7% black | 46.6% brown with  distinct white spots,  38.2% light gray,  13.1% brown, 2.1% black | light gray |
| gray to brown | 39.5% light gray,  37.2% pale yellow, 17.4% brown with  distinct white spots,  5.9% black | 46.6% brown with  distinct white spots,  39.2% light gray,  14.2% solid brown | light gray |
| webbed to disc on  Toe II and Toe V | webbed to disc on  Toe II and Toe V | webbed to disc on  Toe II and Toe V | NA |

|  |  |  |
| --- | --- | --- |
| *signata* | *similis* | *centropeninsularis*  sp. nov. |
| 36.4 | 38.8 | 37.5 |
| 1.5 | 1.8 | 4.2 |
| present | present | absent |
| smooth to  finely granular | smooth to  finely granular | smooth to finely  granular |
| black to dark brown; 100% distinct  round, yellow spots and  bars | 20.1% gray with  dark flecks and blotches, 79.9% dark gray to black, unmarked | black, unmarked |
| straight; 64.8% complete,  35.2% broken | straight; 95.2% complete,  4.8% broken | straight; continuous |
| yellow | white to yellow | orange |
| 98.6% dark bars,  1.4% absent | 76.5% dark bars,  23.5% absent | yellow spots |
| 44.1% brown  with distinct white spots, 26.6% solid brown, 24.3% light gray, 5.0% black | 63.9% light gray,  36.1% dark gray, brown, or black | gray to brown with light spots |
| 42.5% brown with  distinct white spots, 29.2% solid brown, 28.3% light gray | 74.6% light gray,  8.6% black, 6.8% pale or white, 5.8% creamy yellow, 4.2% blotched brown | gray to brown with  light reticulations |
| webbed to disc on  Toe II and Toe V | webbed to disc on  Toe II and Toe V | one phalanx free  on Toe II and V |

Fig. 1.—Maximum likelihood (ML) tree of the *Hylarana signata* Complex based on a RAxML analysis of 12S–16S rRNA (and part of one flanking transfer RNA genes (tRNAval) gene. Numbers above branches represent bootstrap support for ML/Bayesian posterior probabilities. Distribution ranges of species groups are color coded to correspond to the distribution map.

Fig. 2.—The holotype, showing A: Palmar view of manus; B: Plantar view of pes; C: Dorsum; D: Ventrum. Note greatly enlarged humeral gland (A, C) and reduced webbing of pes (B).

Fig. 3.—A:Paratype of *Hylarana centropeninsularis*; B: *Hylarana siberu*from Siberut Island, Sumatra (photo: J. A. McGuire); C: *Hylarana* sp Sumatra from northern Sumatra (photo: D. Iskandar); D: *Hylarana* (=*Rana*) *debussyi* adaptedfrom van Kampen (1910, p. 23, pl. I, Fig. 3).

1. Correspondence: e-mail, chanko@ku.edu [↑](#footnote-ref-1)