**ELECTRONIC SUPPLEMENTARY MATERIAL for Stuart, Inger & Voris**

### *Sampling*

Specimens were collected in the field in Cambodia, Thailand, and Borneo by the authors and shortly preserved in 10% buffered formalin after fixing pieces of liver in 95% ethanol or 20% DMSO-salt saturated storage buffer, or freezing pieces of heart, liver, and muscle in liquid nitrogen. Specimens and tissue samples were later deposited at The Field Museum (FMNH), Chicago, and specimens were transferred to 70% ethanol upon arrival there. Voucher specimens and tissue samples from additional localities in Vietnam, Thailand, Peninsular Malaysia, and Sumatra were borrowed from the holdings of the FMNH and other institutions (Table 1).

### *Extraction, Amplification, and Sequencing of DNA from Fresh Tissues*

Total genomic DNA was extracted from fresh tissues (tissues that were preserved at the time of collection for the purpose of genetic analysis) using PureGene Animal Tissue DNA Isolation Protocol (Gentra Systems, Inc.). Primers for amplifying and sequencing mitochondrial DNA were designed from amphibian sequences in GenBank (Table 2). A fragment of mitochondrial DNA that encodes part of the cytochrome oxidase c subunit III (COXIII) gene, the complete tRNA glycine, the complete NADH dehydrogenase subunit 3 (ND3) gene, and part of the tRNA arginine was amplified by PCR (the polymerase chain reaction; 94$^{o}$C 45s, 49$^{o}$C 30s, 72$^{o}$C 1 min) for 35 cycles using the primer pair L-COXIII/Arg-HND3III. A fragment of mitochondrial DNA that encodes part of the 16S ribosomal RNA (16S) gene was amplified by PCR (94$^{o}$C 45s, 60$^{o}$C 30s, 72$^{o}$C 1 min) for 35 cycles using the primer pair L-16SRanaIII/H-16SRanaIII. An additional fragment of mitochondrial DNA that encodes part of the tRNA methionine, the complete NADH deydrogenase subunit 2 (ND2) gene, and part of the tRNA tryptophan was amplified from samples of *O. livida* by PCR (94$^{o}$C 45s, 49$^{o}$C 30s, 72$^{o}$C 1 min) for 35 cycles using the primer pair Met-LND2/Trp-HND2.

PCR products were electrophoresed in a 1% low melt agarose TALE gel stained with ethidium bromide and visualized under ultraviolet light. The bands containing DNA were excised and agarose was digested from bands using GELase (Epicentre Technologies). PCR products were sequenced in both directions by direct double strand cycle sequencing using Big Dye version 3 chemistry (Perkin Elmer). The amplifying primers, and in the case of ND2 a forward and reverse internal primer, were used in the sequencing reactions. Cycle sequencing products were precipitated with ethanol, 3 M sodium acetate, and 125 mM EDTA, and sequenced with a Prism 3100 Genetic Analyzer (ABI) or 3730 DNA Analyzer (ABI). Sequences were edited and aligned using Sequencher v. 4.1 (Genecodes).

The aligned *O. livida* dataset used in the phylogenetic analyses contained 2,150 mitochondrial DNA characters, consisting of 1,431 protein-coding, 623 rRNA, and 96 tRNA characters. The aligned *R. chalconota* dataset contained 1,082 mitochondrial DNA characters, consisting of 393 protein-coding, 615 rRNA, and 74 tRNA characters. Sequences were deposited in GenBank (accession numbers DQ650352-DQ650632).

### *Extraction, Amplification, and Sequencing of Historical DNA from Museum Type Specimens*

A small piece of abdominal muscle or liver was removed from a syntype female of *O. chloronota* (BMNH 1947.2.28.6; collected prior to 1875) and the neotype female of *O. livida* (BMNH 1889.3.25.48; collected in 1887). DNA was extracted from this tissue using a protocol modified from Kearney & Stuart (2004). Extractions were performed using UV-sterilized supplies inside a Purifier PCR Enclosure (Labconco) in a separate room from where fresh tissues of the *O. livida* group had been previously extracted and amplified. Tissues were washed three times (2 h, 2 h, 12 h) with 1.5 mL of GTE Buffer to bind excess formalin (Shedlock et al., 1997) and twice in 1 mL $dH_20$, and then incubated at 56$^{o}$C for 5 days in 300 µL of TNES Buffer (10 mM Trizma Base, 100

mM NaCl, 10mM EDTA, 2% SDS, 39mM DTT) with daily additions of 300 µg of proteinase-K. The remaining extraction procedure followed the DNeasy Tissue Kit (Qiagen) protocol for animal tissues, with these modifications: 300 µL AL Buffer and 400 µL of 100% ethanol were used rather than 200 µL of each, two spins of 500 µL of the extraction product through the DNeasy mini column was necessary to accommodate the larger extraction volume, a second spin was added for 1 minute at full speed after discarding the Buffer AW2 flow-through fluid, and 75 µL of Buffer AE was added to the DNeasy membrane rather than 100-400 µL, after which the membrane was incubated at 65$^{o}$C for 5 min before centrifuging.

Five fragments of 181-339 nucleotide basepairs (bp; after primer sequences were trimmed) of 16S were amplified by PCR (94$^{o}$C 45s, 54$^{o}$C 30s, 72$^{o}$C 1 min) for 40 cycles using the primer pairs L-16SRanaIII/H-R20016S, L-R14016S/H-R37516S, L-R14016S/H-R48016S, L-R21516S/H-R48016S, and L-R43016S/H-16SRanaIII (Table 2). Primers were designed so that the resulting fragments overlapped by 42-265 bp (after primer sequences were trimmed). This measure ensured that fragments of contaminant DNA were not concatenated into chimeric sequences that might be erroneously judged to be authentic (Olson & Hassanin, 2003). The 25 µl PCR reactions utilized 4 µl of bovine serum albumin (BSA; New England BioLabs) to prevent PCR inhibitors, a relatively large amount (4 µl) of DNA template to overcome low extraction yield, the high-quality Taq polymerase AmpliTaq Gold (Roche), and extra cycles (40 total) of the PCR reaction. PCR products were sequenced, edited, and aligned as described above.

A total of 361 bp was obtained from the *O. chloronota* syntype. A total of 600 bp was obtained from the *O. livida* neotype, and this represented the complete fragment of 16S that was obtained from fresh tissues (above).

***Phylogenetic Analyses***

Phylogenies were reconstructed using the maximum parsimony optimality criterion and mixed-model Bayesian inference. The *O. livida* dataset was rooted with *Amolops* cf. *chapaensis* and *O. bacboensis*, and the *R. chalconota* dataset was rooted with *R. cubitalis* and *R. erythraea*.

Maximum parsimony analyses were performed using PAUP* 4.0b10 (Swofford, 2002). A heuristic search of the *O. livida* dataset was performed with equal weighting of nucleotide substitutions, stepwise addition with 100 random addition replicates, and TBR branch swapping limited to 1,000 trees per replicate. The search recovered >70,000 equally most parsimonious trees (L=1966) and strict consensus showed that these trees differed only by the arrangement of individuals within clades. A heuristic search of the *R. chalconota* dataset was performed with equal weighting of nucleotide substitutions, stepwise addition with 1000 random addition replicates, and TBR branch swapping. The search recovered 541 equally most parsimonious trees (L=846) and strict consensus showed that these trees differed only by the arrangement of individuals within clades. Nodal support was evaluated with 500 nonparametric bootstrap pseudoreplications (Felsenstein, 1985) using the heuristic search option with TBR branch swapping limited to 10,000,000 rearrangements per replicate.

Mixed-model Bayesian analyses were performed using MrBayes 3.1 (Ronquist & Huelsenbeck, 2003). The datasets were separated into first codon position, second codon position, third codon position, rRNA, and tRNA data partitions. The model of sequence evolution that best described each of the five data partitions was inferred using the Akaike Information Criterion as implemented in Modeltest 3.7 (Posada & Crandall, 1998). The models selected by Modeltest for the *O. livida* dataset were GTR+G for the first codon position partition, GTR+I+G for the second codon position and rRNA partitions, TIM+I+G for the third codon position partition, and TVM+G for the tRNA partition. The models selected by Modeltest for the *R. chalconota* dataset were SYM+G for the first codon position partition, TVM+I for the second codon position partition, TrN+G for the third codon position partition, GRT+G for the rRNA partition, and HKY+G for the tRNA partition. Some of these models are not implemented in MrBayes 3.1, and so the next more complex model available in the program was used for those partitions. Four independent

Bayesian analyses were performed on each dataset. In each analysis, six chains were run for 10,000,000 generations using the default priors, trees were sampled every 5000 generations, and the first 25% of trees were discarded as 'burn-in.' A 50% majority rule consensus of the sampled trees was constructed to calculate the posterior probabilities of the tree nodes. The *O. lividа* and *R. chalconota* analyses resulted in standard deviations of split frequencies among the four runs of 0.008995 and 0.007749, respectively. Both analyses also had relatively stationary trace plots of clade probabilities, as viewed using AWTY (Wilgenbusch *et al*., 2004). These two measures suggest that the four runs of each analysis had sufficiently converged and that topologies were sampled in proportion to their true posterior probability distribution.

Table 1. Tissue samples sequenced in this study. Locality abbreviations used are BCA = Biodiversity Conservation Area; Dist. = District; NP = National Park; NR = Nature Reserve; Prov. = Province; WS = Wildlife Sanctuary. Institutional abbreviations used are AMNH = American Museum of Natural History, New York; BMNH = The Natural History Museum, London; FMNH = Field Museum of Natural History, Chicago; FRIM = Forest Research Institute Malaysia, Kuala Lumpur; ROM = Royal Ontario Museum, Toronto; UTA = University of Texas at Arlington. Brackets indicate coordinates were determined by the author rather than by the original collector.

| Voucher | Field/Tissue No. | Locality |
|---|---|---|
| *Odorrana bacboensis* | | |
| FMNH 255611 paratype | HKV 62713 | Vietnam, Nghe An Prov., Con Cuong Dist., Pu Mat NR, 18°56'N 104°45'E |
| *Odorrana* cf. *chapaensis* | | |
| AMNH 163775 | AMCC 106479 | Vietnam, Ha Giang Prov., Yen Minh Dist., Du Gia Commune, 22°52’21”N 105°13’50"E |
| *Odorrana banaorum* | | |
| FMNH 262874 | HKV 65476 | Cambodia, Ratanakiri Prov., Ta Veng Dist., Virachey NP, 14°11'16.3"N 107°17'36.1"E |
| FMNH 262875 | HKV 65477 | Cambodia, Ratanakiri Prov., Ta Veng Dist., Virachey NP, 14°11'16.3"N 107°17'36.1"E |
| FMNH 262878 | HKV 65480 | Cambodia, Ratanakiri Prov., Ta Veng Dist., Virachey NP, 14°11'16.3"N 107°17'36.1"E |
| FMNH 262889 | HKV 65865 | Cambodia, Mondolkiri Prov., O’Rang Dist., Seima BCA, 12°18'08.4"N 107°03'08.1"E |
| FMNH 262796 | HKV 65570 | Cambodia, Mondolkiri Prov., O’Rang Dist., Seima BCA, 12°16'24.6"N 107°03'53.1"E |
| FMNH 262800 | HKV 65839 | Cambodia, Mondolkiri Prov., O’Rang Dist., Seima BCA, 12°18'58"N 107°05'59"E |
| FMNH 262888 | HKV 65841 | Cambodia, Mondolkiri Prov., O’Rang Dist., Seima BCA, 12°18'58"N 107°05'59"E |
| FMNH 262801 | HKV 65840 | Cambodia, Mondolkiri Prov., O’Rang Dist., Seima BCA, 12°18'58"N 107°05'59"E |
| FMNH 262890 | HKV 65867 | Cambodia, Mondolkiri Prov., O’Rang Dist., Seima BCA, 12°18'08.4"N 107°03'08.1"E |
| FMNH 262802 | HKV 65866 | Cambodia, Mondolkiri Prov., O’Rang Dist., Seima BCA, 12°18'08.4"N 107°03'08.1"E |
| FMNH 262891 | HKV 65868 | Cambodia, Mondolkiri Prov., O’Rang Dist., Seima BCA, 12°18'08.4"N 107°03'08.1"E |
| FMNH 262740 | HKV 65905 | Cambodia, Mondolkiri Prov., O’Rang Dist., Seima BCA, 12°18'58"N 107°05'59"E |
| FMNH 262804 | HKV 65918 | Cambodia, Mondolkiri Prov., O’Rang Dist., Seima BCA, 12°18'08"N 107°03'08"E |
| FMNH 262900 | HKV 65919 | Cambodia, Mondolkiri Prov., O’Rang Dist., Seima BCA, 12°18'08"N 107°03'08"E |
| FMNH 262901 | HKV 65920 | Cambodia, Mondolkiri Prov., O’Rang Dist., Seima BCA, 12°18'08"N 107°03'08"E |
| ROM 39862 | - | Vietnam, Gia Lai Prov., An Khe Dist., Krong Pa, 14°20’38”N 108°28’45"E |
| ROM 39901 paratype | - | Vietnam, Gia Lai Prov., An Khe Dist., Tram Lap, 14°26’39”N 108°32’97"E |
| ROM 39913 paratype | - | Vietnam, Gia Lai Prov., An Khe Dist., Tram Lap, 14°26’39”N 108°32’97"E |
| *Odorrana chloronota* | | |
| BMNH 1947.2.28.6 syntype | - | India, Darjeeling, [26°45’00”N 88°15’00”E] |
| FMNH 268916 | 50887 | Thailand, Krabi Prov., Khao Phanom Bencha NP, 08°14’26”N 98°54’51"E |
| THNHM uncataloged | 50942 | Thailand, Krabi Prov., Khao Phanom Bencha NP, 08°14’26”N 98°54’51"E |
| FMNH 263418 | THNHM 4451 | Thailand, Prachuap Kirikhan Prov., Hua Hin Dist., Kaeng Krachan NP, 12°32’16”N 99°27’41"E |
| FMNH 263417 | THNHM 4452 | Thailand, Prachuap Kirikhan Prov., Hua Hin Dist., Kaeng Krachan NP, 12°32’16”N 99°27’41"E |

| Voucher | Field/Tissue No. | Locality |
|---|---|---|
| FMNH 263416 | THNHM 4493 | Thailand, Prachuap Kirikhan Prov., Hua Hin Dist., Kaeng Krachan NP, 12°32’16”N 99°27’41"E |
| THNHM 09970 | THNHM 4495 | Thailand, Prachuap Kirikhan Prov., Hua Hin Dist., Kaeng Krachan NP, 12°32’16”N 99°27’41"E |
| *Odorrana* cf. *chloronota* | | |
| FMNH 265929 | HKV 65996 | Thailand, Loei Prov., Phu Rua Dist., Phu Luang WS, 17°20’02.8"N 101°30’32.4"E |
| FMNH 265931 | HKV 66219 | Thailand, Loei Prov., Phu Rua Dist., Phu Luang WS, 17°15’32.4"N 101°30’22.8"E |
| FMNH 265932 | HKV 66222 | Thailand, Loei Prov., Phu Rua Dist., Phu Luang WS, 17°15’32.4"N 101°30’22.8"E |
| FMNH 265934 | HKV 66258 | Thailand, Loei Prov., Phu Rua Dist., Phu Luang WS, 17°20’42.8"N 101°30’27.9"E |
| FMNH 265939 | HKV 66273 | Thailand, Loei Prov., Phu Rua Dist., Phu Luang WS, 17°21'05.5"N 101°30'13.4"E |
| FMNH 265942 | HKV 66276 | Thailand, Loei Prov., Phu Rua Dist., Phu Luang WS, 17°21'05.5"N 101°30'13.4"E |
| FMNH 265944 | HKV 66278 | Thailand, Loei Prov., Phu Rua Dist., Phu Luang WS, 17°21'05.5"N 101°30'13.4"E |
| *Odorrana hosii* | | |
| THNHM uncataloged | 50903 | Thailand, Krabi Prov., Khao Phanom Bencha NP, 08°14’26”N 98°54’51"E |
| FMNH 268778 | 50904 | Thailand, Krabi Prov., Khao Phanom Bencha NP, 08°14’26”N 98°54’51"E |
| FMNH 268244 | 66734 | Thailand, Ranong Prov., Namtok Ngao NP, [09°56’N 98°43’E] |
| FMNH 268247 | 66735 | Thailand, Ranong Prov., Namtok Ngao NP, [09°56’N 98°43’E] |
| FMNH 268253 | 66739 | Thailand, Ranong Prov., Namtok Ngao NP, [09°56’N 98°43’E] |
| FMNH 268246 | 66761 | Thailand, Ranong Prov., Namtok Ngao NP, [09°56’N 98°43’E] |
| FMNH 268252 | 66763 | Thailand, Ranong Prov., Namtok Ngao NP, [09°56’N 98°43’E] |
| FMNH 268250 | 66764 | Thailand, Ranong Prov., Namtok Ngao NP, [09°56’N 98°43’E] |
| FMNH 268249 | 66765 | Thailand, Ranong Prov., Namtok Ngao NP, [09°56’N 98°43’E] |
| FMNH 268245 | 66767 | Thailand, Ranong Prov., Namtok Ngao NP, [09°56’N 98°43’E] |
| *Odorrana livida* | | |
| FMNH 268251 | 66779 | Thailand, Ranong Prov., Namtok Ngao NP, [09°56’N 98°43’E] |
| FMNH 263415 | THNHM 4453 | Thailand, Prachuap Kirikhan Prov., Hua Hin Dist., Kaeng Krachan NP, 12°32’16”N 99°27’41"E |
| THNHM 09971 | THNHM 4494 | Thailand, Prachuap Kirikhan Prov., Hua Hin Dist., Kaeng Krachan NP, 12°32’16”N 99°27’41"E |
| BMNH 1889.3.25.48 neotype | - | Myanmar, Thagata Juwa, [16°11’00”N 98°31’39”E] |
| *Odorrana* cf. *livida* | | |
| FMNH 265919 | HKV 66206 | Thailand, Loei Prov., Phu Rua Dist., Phu Luang WS, 17°16’48.7"N 101°31’07.5"E |
| FMNH 265920 | HKV 66207 | Thailand, Loei Prov., Phu Rua Dist., Phu Luang WS, 17°16’48.7"N 101°31’07.5"E |
| FMNH 265922 | HKV 66209 | Thailand, Loei Prov., Phu Rua Dist., Phu Luang WS, 17°16’48.7"N 101°31’07.5"E |
| FMNH 265923 | HKV 66217 | Thailand, Loei Prov., Phu Rua Dist., Phu Luang WS, 17°15’32.4"N 101°30’22.8"E |
| FMNH 265925 | HKV 66220 | Thailand, Loei Prov., Phu Rua Dist., Phu Luang WS, 17°15’32.4"N 101°30’22.8"E |
| *Odorrana morafkai* | | |
| FMNH 253837 topotype | HKV 60014 | Vietnam, Gia Lai Prov., An Khe Dist., Buon Loi, 14°20'N 108°36'E |
| FMNH 253838 topotype | HKV 60015 | Vietnam, Gia Lai Prov., An Khe Dist., Buon Loi, 14°20'N 108°36'E |
| FMNH 262871 | HKV 65441 | Cambodia, Ratanakiri Prov., Ta Veng Dist., Virachey NP, 14°11'16.3"N 107°17'36.1"E |

| Voucher | Field/Tissue No. | Locality |
|---|---|---|
| FMNH 262872 | HKV 65442 | Cambodia, Ratanakiri Prov., Ta Veng Dist., Virachey NP, 14°11'16.3"N 107°17'36.1"E |
| FMNH 262731 | HKV 65456 | Cambodia, Ratanakiri Prov., Ta Veng Dist., Virachey NP, 14°12'00.5"N 107°18'29.8"E |
| FMNH 262876 | HKV 65478 | Cambodia, Ratanakiri Prov., Ta Veng Dist., Virachey NP, 14°11'16.3"N 107°17'36.1"E |
| FMNH 262877 | HKV 65479 | Cambodia, Ratanakiri Prov., Ta Veng Dist., Virachey NP, 14°11'16.3"N 107°17'36.1"E |
| FMNH 262879 | HKV 65481 | Cambodia, Ratanakiri Prov., Ta Veng Dist., Virachey NP, 14°11'16.3"N 107°17'36.1"E |
| FMNH 262886 | HKV 65569 | Cambodia, Mondolkiri Prov., O'Rang Dist., Seima BCA, 12°16'24.6"N 107°03'53.1"E |
| FMNH 262734 | HKV 65835 | Cambodia, Mondolkiri Prov., O'Rang Dist., Seima BCA, 12°18'58"N 107°05'59"E |
| FMNH 262735 | HKV 65836 | Cambodia, Mondolkiri Prov., O'Rang Dist., Seima BCA, 12°18'58"N 107°05'59"E |
| FMNH 262736 | HKV 65837 | Cambodia, Mondolkiri Prov., O'Rang Dist., Seima BCA, 12°18'58"N 107°05'59"E |
| FMNH 262737 | HKV 65838 | Cambodia, Mondolkiri Prov., O'Rang Dist., Seima BCA, 12°18'58"N 107°05'59"E |
| FMNH 262738 | HKV 65864 | Cambodia, Mondolkiri Prov., O'Rang Dist., Seima BCA, 12°18'08.4"N 107°03'08.1"E |
| FMNH 262803 | HKV 65904 | Cambodia, Mondolkiri Prov., O'Rang Dist., Seima BCA, 12°18'58"N 107°05'59"E |
| ROM 39907 paratype | - | Vietnam, Gia Lai Prov., An Khe Dist., Tram Lap, 14°26'39"N 108°32'97"E |
| ROM 39947 paratype | - | Vietnam, Gia Lai Prov., An Khe Dist., Tram Lap, 14°26'39"N 108°32'97"E |
| *Rana cubitalis* | | |
| FMNH 265818 | HKV 65999 | Thailand, Loei Prov., Phu Rua Dist., Phu Luang WS, 17°20'02.8"N 101°30'32.4"E |
| *Rana erythraea* | | |
| FMNH 257282 | HKV 63681 | Cambodia, Siem Reap Prov., Siem Reap Dist., Siem Reap Town, 13°22'29"N 103°50'44"E |
| *Rana chalconota* | | |
| UTA 53665 topotype | MBH 5308 | Indonesia, Java, Barat, Desa Sukamahi, near Bogor |
| UTA 53685 | ENS 7634 | Indonesia, Sumatra, Selatan, Lahat, outside of Pagaralam on road to Lahat |
| *Rana* cf. *chalconota* B1 | | |
| FMNH 268572 | 15527 | Indonesia, Sumatra Barat, Padang, Limau Manis, 00°55'S 100°28'E |
| FMNH 268591 | 15534 | Indonesia, Sumatra Barat, Padang, Limau Manis, 00°55'S 100°28'E |
| FMNH 268579 | 15657 | Indonesia, Sumatra Barat, Padang, Limau Manis, 00°55'S 100°28'E |
| *Rana* cf. *chalconota* B3 | | |
| FMNH 268985 | 51685 | Malaysia, Sarawak, Bukit Sarang, 02°39'12.2"N 113°03'09"E |
| FMNH 267814 | 51068 | Malaysia, Sarawak, Bukit Sarang, 02°39'12.2"N 113°03'09"E |
| FMNH 267819 | 51160 | Malaysia, Sarawak, Bukit Sarang, 02°39'12.2"N 113°03'09"E |
| FMNH 267823 | 51219 | Malaysia, Sarawak, Bukit Sarang, 02°39'12.2"N 113°03'09"E |
| FMNH 267817 | 51080 | Malaysia, Sarawak, Bukit Sarang, 02°39'12.2"N 113°03'09"E |
| FMNH 267818 | 51157 | Malaysia, Sarawak, Bukit Sarang, 02°39'12.2"N 113°03'09"E |
| FMNH 268820 | 51173 | Malaysia, Sarawak, Bukit Sarang, 02°39'12.2"N 113°03'09"E |
| FMNH 267815 | 51076 | Malaysia, Sarawak, Bukit Sarang, 02°39'12.2"N 113°03'09"E |
| FMNH 267821 | 51182 | Malaysia, Sarawak, Bukit Sarang, 02°39'12.2"N 113°03'09"E |
| FMNH 267816 | 51078 | Malaysia, Sarawak, Bukit Sarang, 02°39'12.2"N 113°03'09"E |

| Voucher | Field/Tissue No. | Locality |
|---|---|---|
| FMNH 268983 | 51640 | Malaysia, Sarawak, Bukit Sarang, 02°39'12.2"N 113°03'09"E |
| FMNH 267822 | 51216 | Malaysia, Sarawak, Bukit Sarang, 02°39'12.2"N 113°03'09"E |
| FMNH 267824 | 51234 | Malaysia, Sarawak, Bukit Sarang, 02°39'12.2"N 113°03'09"E |
| FMNH 267825 | 51242 | Malaysia, Sarawak, Bukit Sarang, 02°39'12.2"N 113°03'09"E |
| *Rana* cf. *chalconota* B5 | | |
| FMNH 268573 | 15560 | Indonesia, Sumatra Barat, Padang, Limau Manis, 00°55'S 100°28'E |
| FMNH 268574 | 15568 | Indonesia, Sumatra Barat, Padang, Limau Manis, 00°55'S 100°28'E |
| FMNH 268575 | 15575 | Indonesia, Sumatra Barat, Padang, Limau Manis, 00°55'S 100°28'E |
| FMNH 268580 | 15664 | Indonesia, Sumatra Barat, Padang, Limau Manis, 00°55'S 100°28'E |
| FMNH 268585 | 15987 | Indonesia, Sumatra Barat, Padang, Sikayan Ubi, 00°53'S 100°28'E |
| FMNH 268586 | 15994 | Indonesia, Sumatra Barat, Padang, Sikayan Ubi, 00°53'S 100°28'E |
| *Rana labialis* | | |
| FRIM 1539 | JS 00327 | Malaysia, Kedah, Gunung Jerai, Lower Tupah River, 05°47'N 100°26'E |
| FRIM 1735 | JS 00330 | Malaysia, Kedah, Gunung Jerai, Lower Tuupah River, 05°47'N 100°26'E |
| FRIM 829 | JS 00497 | Malaysia, Kedah, Gunung Jerai, Perigi Cascade, 05°47'N 100°26'E |
| *Rana* cf. *labialis* | | |
| FRIM 1736 | JS 00381 | Malaysia, Kedah, Gunung Jerai, Batu Hampar River, 05°47'N 100°26'E |
| FRIM 1418 | JS 00390 | Malaysia, Kedah, Gunung Jerai, Batu Hampar River, 05°47'N 100°26'E |
| FRIM 826 | JS 00408 | Malaysia, Kedah, Gunung Jerai, Batu Hampar River, 05°47'N 100°26'E |
| FRIM 1401 | JS 00393 | Malaysia, Kedah, Gunung Jerai, Batu Hampar River, 05°47'N 100°26'E |
| *Rana raniceps* | | |
| FMNH 267958 | 51158 | Malaysia, Sarawak, Bukit Sarang, 02°39'12.2"N 113°03'09"E |
| FMNH 267960 | 51198 | Malaysia, Sarawak, Bukit Sarang, 02°39'12.2"N 113°03'09"E |
| FMNH 267961 | 51244 | Malaysia, Sarawak, Bukit Sarang, 02°39'12.2"N 113°03'09"E |
| FMNH 267962 | 51259 | Malaysia, Sarawak, Bukit Sarang, 02°39'12.2"N 113°03'09"E |
| FMNH 267963 | 51261 | Malaysia, Sarawak, Bukit Sarang, 02°39'12.2"N 113°03'09"E |
| FMNH 267964 | 51310 | Malaysia, Sarawak, Bukit Sarang, 02°39'12.2"N 113°03'09"E |

Table 2 . Oligonucleotide primers used to amplify and sequence frog mitochondrial DNA in this study. 'L' and 'H' refer to light and heavy strands, respectively. 'A' and 'S' refer to amplifying and sequencing, respectively.

| Primer | Product | Use | Sequence |
|---|---|---|---|
| L-COXIII | ND3 | A, S | 5'-CCGCATGATACTGACACTT-3' |
| Arg-HND3III | ND3 | A, S | 5'-AACTGTCTTTTTTGGACTAGC-3' |
| Met-LND2 | ND2 | A, S | 5'-CAATGTTGGTTAAAATCCTTCC-3' |
| Trp-HND2 | ND2 | A, S | 5'-AGGCTTTGAAGGCCTTTGGTC-3' |
| L-ND2am | ND2 | S | 5'-TTATAGCCTTCTCCTCCATCG-3' |
| H-ND2bana | ND2 | S | 5'-CTATGATTTTTCGAAGTTGAG-3' |
| H-ND2dhsxs | ND2 | S | 5'-ATTCATCCTAGGTGGCCGAT-3' |
| L-ND2hos | ND2 | S | 5'-ACTTCGGAAAATTATAGCCTTCTC-3' |
| H-ND2hos | ND2 | S | 5'-GAGAAATATGGCGGTTGTCAT-3' |
| L-ND2pdd | ND2 | S | 5'-CGGAATTGGCCAAACTCAAC-3' |
| H-ND2pdd | ND2 | S | 5'-TTTGGGTCATGAGGTTGATA-3' |
| L-ND2thai | ND2 | S | 5'-CAACTTCGAAAGATCATAGC-3' |
| L-ND2xs | ND2 | S | 5'-GACTGATCTTATCGACCTGAC-3' |
| L-16SRanaIII | 16S | A, S | 5'-GAGTTATTCAAATTAGGCACAGC-3' |
| H-16SRanaIII | 16S | A, S | 5'-CATGGGGTCTTCTCGTCTTAT-3' |
| H-R20016S | 16S | A, S | 5'-TTCTTGTTACTAGTTCTAGCA-3' |
| L-R14016S | 16S | A, S | 5'-AATTACTAAAACATCCACTAACCC-3' |
| H-R37516S | 16S | A, S | 5'-TAAAATTTGCCGAGTTCCTTC-3' |
| H-R48016S | 16S | A, S | 5'-CAAGTGATTATGCTACCTTCG-3' |
| L-R21516S | 16S | A, S | 5'-AGTAACAAGAACTTGCCATTC-3' |
| L-R43016S | 16S | A, S | 5'-CTGTTTACCAAAAACATCGCCT-3' |

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